

GenCore version 5.1.3  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 17, 2003, 09:57:04 : Search time 101.5 Seconds  
(without alignments)  
6567.449 Million cell updates/sec

Title: US-09-743-492-1  
Perfect score: 6444  
Sequence: 1 gatccgcagcgaagactcc.....attgataatacagatttct 3467

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+\_n2p\_model -DEV=xlp  
-O=/cgn2.1/USPRO\_SPOOL/US09743492/runat\_17012003\_093836.11545/app\_query.fasta\_1.3655  
-DB=PIR.73 -QFMT=fastan -SUPER=irpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=biom62 -TRANS=humand0.cdi -LIST=45  
-DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09743492 @CGN\_1\_1\_178 @runat\_17012003\_093836.11545 -NCPU=6 -ICPU=3  
-NO\_XLPPY -NO\_MMAP -LARGESQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMOUT=120  
-WARN\_TIMOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
1: PIR.73:\*  
2: pir1:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3236	50.2	1897	1	TDHUKL
2	3176.5	49.3	1290	2	A56493
3	3172	49.2	1898	2	S46216
4	3057	47.4	1882	2	A57068
5	2926	45.4	1912	2	A56178
6	2874.5	44.6	1691	1	D54689
7	2874.5	44.6	1894	1	C54689
8	2867.5	44.5	1499	2	F50146
9	2850	44.2	1501	2	F50146
10	2847	44.2	1907	2	S50893
11	2844	44.1	1863	2	S46217
12	2753.5	42.7	1496	1	A48758
13	2509	38.9	1231	2	S53089
14	2503	38.8	2029	1	TDFFLK

15	2450.5	38.0	1437	2	T31093	probable protein-t
16	2377	36.9	2051	2	T30938	receptor tyrosine
17	1869	29.0	398	2	F56540	protein-tyrosine-p
18	1836.5	28.5	1585	2	T19121	probable protein-t
19	1551	24.1	802	1	A36065	protein-tyrosine-p
20	1538	23.9	1262	1	B48758	protein-tyrosine-p
21	1525	23.7	796	1	JC1285	protein-tyrosine-p
22	1518	23.6	829	1	A47373	protein-tyrosine-p
23	1429	22.2	700	1	S12053	protein-tyrosine-p
24	1423	22.1	699	2	JC6132	protein-tyrosine-p
25	1307	20.3	1452	1	S17670	protein-tyrosine-p
26	1306	20.3	1452	1	S17669	protein-tyrosine-p
27	1243	19.3	1457	1	A48066	protein-tyrosine-p
28	1236	19.2	1440	2	JC6312	protein-tyrosine-p
29	1168	18.1	1445	1	A48148	protein-tyrosine-p
30	1166.5	18.1	1436	2	JC5290	protein-tyrosine-p
31	1162	18.0	1442	1	B48148	protein-tyrosine-p
32	1142	17.7	1422	2	T42636	protein-tyrosine-p
33	1135.5	17.6	1442	2	S72441	protein-tyrosine-p
34	1117.5	17.3	2314	1	A46151	protein-tyrosine-p
35	1089.5	16.9	1301	1	A41622	protein-tyrosine-p
36	1048.5	16.3	1237	2	A54080	protein-tyrosine-p
37	1038	16.1	1273	1	TDRTLT	leukocyte common a
38	1035.5	16.1	1304	1	A46546	leukocyte common a
39	1017	15.8	1291	1	A28334	leukocyte common a
40	1013	15.7	1200	2	T43148	protein-tyrosine-p
41	1011.5	15.7	1462	1	B36182	probable protein-t
42	894	13.9	1409	2	T42522	protein-tyrosine-p
43	876.5	13.6	1422	2	T30111	protein-tyrosine-p
44	702	10.9	1711	1	A51148	hypothetical prote
45	697	10.8	256	2	A40169	protein-tyrosine-p

## ALIGNMENTS

## RESULT 1

TDHUKL

leukocyte antigen-related protein precursor - human

N:Alternate names: leukocyte common antigen homolog

N:Contants: protein-tyrosine-phosphatase (EC 3.1.3.48)

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 22-Jun-1999

C:Accession: S03841; J10051

R:Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.

J. Exp. Med. 168, 1523-1530, 1988

A:Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region

A:Reference number: J10051; MUID:89035978; PMID:2972792

A:Accession: S03841

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1897 <STR>

A:Cross-references: EMBL:Y00815; NID:g34266; PIDN:CNA68754.1; PID:g34267

C:Genetics:

A:Gene: GDB:PTPRF; LAR

A:Map position: 1p34-1p34

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homolog

C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembra

F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-1897/Product: leukocyte antigen-related protein #status predicted <MAT>

F:17-1250/Domain: extracellular #status predicted <EXT>

F:37-99/Domain: immunoglobulin homology <IMM1>

F:139-199/Domain: immunoglobulin homology <IMM2>

F:236-290/Domain: immunoglobulin homology <IMM3>

F:308-390/Domain: fibronectin type III repeat homology <FN3A>

F:403-489/Domain: fibronectin type III repeat homology <FN3B>

F:501-583/Domain: fibronectin type III repeat homology <FN3C>

F:596-685/Domain: fibronectin type III repeat homology <FN3D>

F:698-798/Domain: fibronectin type III repeat homology <FN3E>

F:810-893/Domain: fibronectin type III repeat homology <FN3F>

F:905-989/Domain: fibronectin type III repeat homology <FN3G>

F:1001-1078/Domain: fibronectin type III repeat homology <FN3H>

F:1251-1274/Domain: transmembrane #status predicted <TM>  
F:1275-1897/Domain: intracellular #status predicted <INT>  
F:1285-1897/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:1365-1586/Domain: protein-tyrosine-phosphatase homology <PPP>  
F:1554-1877/Domain: protein-tyrosine-phosphatase homology <PPP>  
F:44-97/146-197/243-288/Disulfide bonds: #status predicted  
F:107/240/285/711/956/Binding site: carbohydrate (asn) (covalent) #status predicted  
F:1538/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:144/Binding site: substrate phosphate (Arg) #status predicted  
F:1829/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1835/Binding site: substrate phosphate (Arg) #status predicted

## Alignment Scores:

Pred. No.:	3,92e-206	Length:	1897
Score:	3236.00	Matches:	607
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	50.22%	Indels:	0
DB:	1	Gaps:	0

US-09-743-492-1 (1-3467) x TDHULK (1-1897)

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QY 6 GCAGTAGAAGACTCTTGTGCTGGCCACCTCTGTGACCTGTGAGATGCGAGGCTCAAC 65
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Db 1291 GLEuLysAspSerLeuLeuAlaHisSerSerProValGluMetArgArgLeuAsn 1310

QY 66 TACGAGACCCGAGGTATGCGAGACACCCACCCATCCCATCCAGCCGACCTGGGACAC 125
    |||
Db 1311 TyrGlnThrProGluMetArgAspHisProProlleProIleThrAspLeuAlaAspAsn 1330

QY 126 ATCGAGCGCTCAAAAGCCACGATGGCTCAAGTTCTCCAGAGATGATGATCCATCGAC 185
    |||
Db 1331 IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGluTyrGlnSerIleAsp 1350

QY 186 CCGTAGACGAGCTGACGTGGGAGATCAAACTGGAGGTGAGAACACCCCAAGACCGC 245
    |||
Db 1351 ProGluGlnGlnPheThrProGluAsnSerAsnLeuGluValAsnLysProLysAsnArg 1370

QY 246 TATGCGATGTCATCGCTTACGACACCTGTGAGTCACTTACCTCATGATGCGCTC 305
    |||
Db 1371 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 1390

QY 306 CCGGAGAGTCACTACATCAATGCACTACATCGATGCTACCGACGACGATGCTTAC 365
    |||
Db 1391 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 1410

QY 366 ATGCGACGCGAGGGGCGCCCTCCGAGACCATGGGCGATTCTGAGAAATGTTGGGAA 425
    |||
Db 1411 IleAlaThrGlnGlyProLeuProlleuThrMetGlyAspPheTyrPargMetValTyrGlu 1430

QY 426 CAGCGACGCGCTGTGATGATGACACGCTGAGAGAGAGTCCCGGTTAAATGT 485
    |||
Db 1431 GlnArgThrAlaThrValValMetMetThrArgLeuGlnGluLysSerArgValLysys 1450

QY 486 GATAGTAGTGGCCAGCCGCTGGGACGAGACCTGTGGCTTATTCAGGTACCTGTG 545
    |||
Db 1451 AspGlnTyrTrpProAlaArgGlyThrGlnThrCysGlyLeuIleGlnValThrLeuLeu 1470

QY 546 GACGACGAGGTGGGCGACATACATGTCGACCTTGGACCTCCACCAAGAGTGGCTCC 605
    |||
Db 1471 AspThrValGluLeuAlaThrTyrThrValAlaThrPheAlaLeuHisLysSerGlySer 1490

QY 606 AGTGAGAGCGTGAGTGGCTGCTGATGTCATGCTGAGCTGGCCGACGACCATGAGTTCCT 665
    |||
Db 1491 SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTyrProAspHisGlyValPro 1510

QY 666 GAGTACCACTCCCATCTGGCTTCTCTACGACGGGTCAAGGCTGCAACCCCTACAC 725
    |||
Db 1511 GlnTyrProThrProIleLeuAlaPheLeuArgArgValLysAlaLysAsnProLeuAsp 1530

QY 726 GCAGGCGCCAGTGTGTGACATGACGCGGGGCTGGGCGCCACCGGCTGTTATCATGTG 785
    |||
Db 1531 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 1550
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QY 786 ATGATGCCATGTTGAGCGGATGACAGCAGAGAGAGCGGTGACATCTATGCCACGTG 845
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QY 846 ACTGCATGCATCAGACAGAGAACTACATGCTGTCAGACGAGAGACCACTACGTTGTC 905
    |||
Db 1571 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 1590

QY 906 CATGAGCGGCTGTGGAGGCTCCACCTGGCGGCCACACAGAGGTGCTGCCCCGACCTG 965
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Db 1591 HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu 1610

QY 966 TATGCCCATCCAGAGCTGGGCAAGTGCCTCAGAGGAGAGTGTGACCCCATGAGAG 1025
    |||
Db 1611 TyrAlaHisIleGlnLysLeuGlyGlnValProProGluGlnSerValThrAlaMetGlu 1630

QY 1026 CTGAGATTCAAGTTGCTGGCCAGCTCCAGGCCACACAGCTCCGCTTCATCAGCGCCAC 1085
    |||
Db 1631 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 1650

QY 1086 CTGCGCTCCAGACAGTTCAGAACCGGCTGGTGAACATCATGACCCCTACGATTCAC 1145
    |||
Db 1651 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 1670

QY 1146 GTGTGCTGCAGCCCATCCGCTGTGTGGAGGGCTCTGACTCATCATCAATGCCAGCTTC 1205
    |||
Db 1671 ValCysLeuGlnProIleArgGlyValGluLysSerAspTyrIleAsnAlaSerPheLeu 1690

QY 1206 GATGCTTATAGACAGACAGAGCCCTACATACCTACACAGGGGCTGTGGACAGAGCAC 1265
    |||
Db 1691 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlnProLeuAlaGlnSerThr 1710

QY 1266 GAGGACTCTGCGCGATGCTTGGGAGACAAATCCACATCATGCTGATGCTGACCAAG 1325
    |||
Db 1711 GluAspPheThrPargMetLeuThrProlleHisSerThrIleIleValMetLeuThrLys 1730

QY 1326 CTTCGGGAGATGGGACGAGGAGAAATGCCACGACTGAGCGACGAGAGCGCTGCTGCG 1385
    |||
Db 1731 LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg 1750

QY 1386 TACAGACTCTTTGTTGTGACCCGATGCTGATGACATGACCCGACTATATCTGCGT 1445
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Db 1751 TyrGlnTyrPheValIleAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 1770

QY 1446 GAGTTCAAGTCCAGGATGCCCGGAGTGGCGAGTCAAGAGCAATCCGCGACTTCAGTTC 1505
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Db 1771 GluPheLysValIleThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1790

QY 1506 ACAGACTGGCCAGACAGGCGCTGCCCAAGACAGAGGAGATTGATGACTTCATCGGG 1565
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Db 1791 ThrAspTrpProGluGlnGlyValProLysThrGlyGlnGlyPheIleAspPheIleGly 1810

QY 1566 CAGTGCATTAAGACACAGAGACAGTGTGGACAGATGGGCTATACAGGTGCTACTGCACT 1625
    |||
Db 1811 GlnValHisLysThrLysGlnGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1830

QY 1626 GCTGCGGTGGGCGCACCGGGGTGTCATCTGACATGACATGCTGTCGAGCGCATGGC 1685
    |||
Db 1831 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValIleGluArgMetArg 1850

QY 1686 TATGAGGCGGTGTCGACATGTTTCAGACGCTGAAGACCTGCTACACAGCTGCTGCC 1745
    |||
Db 1851 TyrGlnGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 1870

QY 1746 ATGCTGACAGACAGAGACAGTATACAGTGTGCTACCGTGGCGCTGTGAGTACCTGGC 1805
    |||
Db 1871 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGly 1890

QY 1806 AGCTTGACCACTATGCAAGC 1826
    |||
Db 1891 SerPheAspHisTyrAlaThr 1897
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RESUT.F.2
A56493
Leucocyte common antigen-related protein (LAR) - rat (fragment)
N:Alternate names: LAR receptor-linked tyrosine phosphatase
N:Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence
C:Accession: A56493; I55393
R:Zhang, J.S.; Longo, F.M.
J. Cell Biol. 128, 415-431, 1995
A:Title: LAR tyrosine phosphatase receptor: alternative splicing is preferential to the
A:Reference number: A56493; MUID:95146548; PMID:7844155
A:Accession: A56493
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1290 <RES>
A:Cross-references: EMBL:X83505; NID:9732918; PIDN:CA58495.1; PID:9732919
R:Longo, F.M.; Mattignetti, J.A.; Le Beau, J.M.; Zhang, J.S.; Barnes, J.P.; Brosius, J.
J. Biol. Chem. 268, 26503-26511, 1993
A:Title: Leukocyte common antigen-related receptor-linked tyrosine phosphatase. Regulation
A:Reference number: I55393; MUID:94075340; PMID:8253779
A:Accession: I55393
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 831-1290 <RES>
A:Cross-references: EMBL:U00477; NID:9392565; PIDN:AAC04306.1; PID:9392566
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology
Oy
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F:80-166/Domain: fibronectin type III repeat homology <3FR>
F:667-1290/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1047-1270/Domain: protein-tyrosine-phosphatase homology <PPP2>
F:931/Active site: Cys (phosphocysteine intermediate) #status predicted
F:937/Binding site: substrate phosphate (Arg) #status predicted
F:1222/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1228/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:
Pred. No.:          3,18e-202          Length:          1290
Score:              3176.50            Matches:           599
Percent Similarity: 97.57%            Conservative:      4
Best Local Similarity: 96.93%          Mismatches:       4
Query Match:        49.29%            Indels:           11
DB:                  2                  Gaps:             1

US-09-743-492-1 (1-3467) x A56493 (1-1290)

Oy 6  GGACTGAAGAGACTCTTCTGCTGGCCACCTCTGACCTGTGGAGATCGGAGGCTCAAC 65
Db 673 GlyLeuLysASPserLeuLeuAlaHisSerSerASPProValGluMetArgLeuAsn 692
Oy 66  TACGAGACCCCAAGG-----ATGCGAGACAC 92
Db 693 TyrlGlnInrProGlySerSerAlaProSerCysProAsnIleSerSerMetArgAspHis 712
Oy 93  CCACCATCCCATCCACCGACTGTGGCGGACAACATCGAGCGCTCAAGGCCAACAGATGGC 152
Db 713 ProProlleProIleThrAspLeuAlaAspAsnIleGluArgLeuLysAlaAsnAspGly 732
Oy 153 CTGAAGTTCTCCCAAGGAGATAGTTCATGCACCCGTGGACAGCAGTTCCAGTGGAGAT 212
Db 733 LeuLysPheSerGlnGluTyrGluSerIleAspProGlyGlnGlnPheThrProGluAsn 752
Oy 213 TCAAACTGGAGGAGGAAACAAGCCCAAGAACGGATATGCATGTCATGCCTACGACCAC 272
Db 753 SerAsnSerGluValAsnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAspHis 772
Oy 273 TCTCGAGTCATCCTTACTCTATGCATGCGCTCCCGGAGATGACTCATCAATGCCAAC 332
Db 773 SerArgValLeuLeuThrSerIleAspGlyValProGlySerAspTyrIleAsnAlaAsn 792
Oy 333 TACATCGATGGCTACCGCAGCAGAGATGCTTACATGCGCACGACAGGCCCCCTGCCGAG 392

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Db 1492 serGluLysArgSLeuLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 1511  
 QY 666 GAGTACCACACTCCATCTGCGCTTCTTACAGACGGGTCAAGGCCCTGCAACCCCTAGAC 725  
 Db 1512 GtUTyrProThrProIleLeuAlaPheLeuArgValLysAlaCysAsnProLeuAsp 1531  
 QY 726 GCAGGGCCATGGTGTGACTTCAGCGGGGGTGGCGGACCGGCTTCATCGTG 785  
 Db 1532 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 1551  
 QY 786 ATTGATCCATGTTGGAGCGATGAACAGACAGAGCGGTGACATCTATGGCCAGTG 845  
 Db 1552 IleAspAlaMetLeuGlnArgMetLysHisGlnLysThrValAspIleTyrGlnHisVal 1571  
 QY 846 ACCTGATCGATCAGACAGAGAACTCATGTGTCACAGCGAGACCAAGTACGTTCATC 905  
 Db 1572 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGlnAspGlnTyrValPheIle 1591  
 QY 906 CATGAGCGCGTGTGAGGCTGCGACGTGGCGGCACACAGAGGTGCTGCCGCAACCTG 965  
 Db 1592 HisGlnAlaLeuLeuGlnAlaAlaMetCysGlyHisThrGlnValLeuAlaArgAsnLeu 1611  
 QY 966 TATGCCACATCCAGAAAGCTGGCGCAAGTGCCTCCAGGGAGAGTGAACCCCATGAG 1025  
 Db 1612 TyrAlaHisIleGlnLysLeuGlnValProProGlyGlnSerValThrAlaMetGln 1631  
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 QY 1146 GTGTGTCTCAGCCCATCCGCTGGTGTGAGGGCTCTGACTACATCATGCGCAACTCTGTG 1205  
 Db 1672 ValCysLeuGlnProIleArgGlyValGlnGlySerAspTyrIleAsnIleSerPheLeu 1691  
 QY 1206 GATGCTTATAGACAGACAGAAAGCCTTACATGCTACACAGGGGCTGTGGCAGAGACACC 1265  
 Db 1692 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGlnSerThr 1711  
 QY 1266 GAGGACTTTCGGGCGCATGTATGGGAGCAATTCACCATCATGCTCATGCGACCAAG 1325  
 Db 1712 GluAspPheTrpArgMetLeuTrpGlnHisAsnSerThrIleLeuValMetLeuThrLys 1731  
 QY 1326 CTTCGGAGATGGGCGAGGAGAAATGCCACAGTACTGTGGCCAGACGCGCTTCTGCTCGC 1385  
 Db 1732 LeuArgGlnMetGlyArgGlnLysCysHisGlnTyrTrpProAlaGlnArgSerAlaArg 1751  
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 QY 1446 GAGTTCAAGGTACCGATGCCGCGGATGGGAGTCAAGGACATCCGGGACGATCCAGTTG 1505  
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 QY 1566 CAGGTGCATTAAGACCAAGAGCAGTTTGGACAGAGGATGGGCTATCACGGTGCACCTCAAGT 1625  
 Db 1812 GlnValHisLysThrLysGlnPheGlnPheGlnAspGlyProIleThrValHisCysSer 1831  
 QY 1626 GCTGGGCTGGGGCGACCGGGGTTCATCACTCAGAGATGCTCTGGAGGCGCATAGCGG 1685  
 Db 1832 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGlnArgMetLeuArg 1851  
 QY 1686 TATGAGGCGGTGTCACATGTTTTCAGACCGTGAAGACCTGCGTACAGAGCTCTGCTGCC 1745  
 Db 1852 TyrGlnGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 1871

QY 1746 ATGTGACAGACAGACAGACCATATCAGTGTGCTACCGTGGGCGCTGAGTACTCTCGC 1805  
 Db 1872 MetValGlnThrGlnAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGlnTyrLeuGly 1891  
 QY 1806 AGCTTGACCATATGCAACG 1826  
 Db 1892 SerPheAspHisTyrAlaThr 1898  
 RESULT 4  
 A:57068  
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type f - mouse (fragment)  
 M:alternate names: leukocyte antigen-related protein LAR  
 C:species: Mus musculus (house mouse)  
 C:date: 03-Oct-1995 #sequence\_revision 09-Mar-1996 #text\_change 23-Jul-1999  
 C:accession: A57068; S40280  
 R:schaeppeld, R.Q.D.; van den Maadenberg, A.M.J.M.; Schepens, J.T.G.; Olde Weghuis, Genomics 27, 124-130, 1995  
 A:title: The mouse gene Pprf encoding the leukocyte common antigen-related molecule  
 A:reference number: A57068; MUID:95394448; PMID:7665159  
 A:accession: A57068  
 A:status: not compared with conceptual translation  
 A:molecule type: mRNA  
 A:residues: 1-582 <SCH>  
 A:cross-references: GB:Z37988; NID:9993005; PIDN:CAA86070.1; PID:9993006  
 R:henricks, W.; Brugman, C.; Zeewen, P.; Schepens, J.; Mieringa, B.  
 submitted to the EMBL Data Library, June 1993  
 A:description: Assessment of the expression levels of murine protein-tyrosine phosphatase  
 A:reference number: S40280  
 A:accession: S40280  
 A:molecule type: mRNA  
 A:residues: 116-221 <HEN>  
 A:cross-references: EMBL:Z23049; NID:9438135; PIDN:CAA80584.1; PID:9438136  
 C:genetics: Pprf  
 A:gene: Pprf  
 C:superfamily: leukocyte antigen-related protein; fibronectin type III repeat homolog  
 C:keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembr  
 F:1-582/Domain: leukocyte common antigen cytosolic domain Homology (fragment) <IAC>  
 F:50-271/Domain: protein-tyrosine-phosphatase homology <PRP1>  
 F:339-562/Domain: protein-tyrosine-phosphatase homology <PRP2>  
 F:223/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:229/Binding site: substrate phosphate (Arg) #status predicted  
 F:514/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:520/Binding site: substrate phosphate (Arg) #status predicted  
 Alignment Scores:  
 Pred. No.: 2,24e-194 Length: 582  
 Score: 3057.00 Matches: 572  
 Percent Similarity: 99.14% Conservative: 5  
 Best Local Similarity: 98.28% Mismatches: 5  
 Query Match: 47.44% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-743-492-1 (1-3467) x A57068 (1-582)  
 QY 81 ATGCGAGACACCCACCCATCCCATACCGACCTGGCGGACAAATCGAGCGCTCAAA 140  
 Db 1 MetArgAspHisProIleProIleThrAspLeuAlaAspAsnIleGlnArgLeuLys 20  
 QY 141 GCCAACGATGGGCGCTCAAGTCTCCAGAGGTATGATGATCATGCAACCTGGACGCGAGTTC 200  
 Db 21 AlaAsnAspGlyLeuLysPheSerGlnGlyTyrGlnSerIleAspProGlyGlnGlnPhe 40  
 QY 201 ACCTGGAGCAATTCAAACCTGAGGTGAACCAAGCCCAAGAACCGTATGCGAATGTCATC 260  
 Db 41 ThrTrpGlnAsnSerAsnSerGlnValAsnLysProLysAsnArgTyrAlaAsnValIle 60  
 QY 261 GCCTACGACCACTCTCGAGTCACTCTTACCTTATGATGATGGCGTCCCGGAGTGAATAC 320  
 Db 61 AlaTyrAspHisSerArgValLeuLeuThrSerIleAspGlyValProGlySerAspTyr 80  
 QY 321 ATCAATGCCAATCAATCATGCTACCGCAACGACAAATGCTCAATCGCGACGAGGCG 380

Db	81	ILEASNAIAASNTGTTILEASRGITUTYATGlyGSLASNAIAATGTTILEAIATHGInGly	100
OY	381	CCSCSTGSSGAGACATGGGCGATTTCTGAGAAATGGTGTGGAGACAGGSCAGGCGACT	440
Db	101	PROLEUPROGIIUTHTMETGTYASPRHETPRATGMEVATLTPRLGInGInATHr	120
OY	441	GTGGCAGATGACAGCGGCTGGAGGAGAAATCCGGGGTAAATGTAATGATGACAGTGGCA	500
Db	121	VALVALMETMETTLATGLeGInGlyLysSerATGVALLYLysGlySPRLInTTPRO	140
OY	501	GCCCGTGAGCAGGACSTGTGGCTATATCAAGTATGACSTGTGTGGACAGTGGAGSTG	560
Db	141	VALATGInGlyTHrGInTHTGTLyLeuLIEGLVALTHrLeuVALASPRHrVALGInLeu	160
OY	561	GCCACATPACSTGTGGCACCTTGSCACSTCCASAAAGTGGCTCCAGTGAAGAGSTGAG	620
Db	161	ALATHrGTLyTHrMETATGTHrPHEAILeuInLysSerGTLySerGTLyLysATGIn	180
OY	621	CTGGGCTAGTTCTGTTCAAGGCTGGGCGGACAGCAATGAGAGTTCTGATGACCCAGCTCC	680
Db	181	LEUATGInPRHrGInPRHrMEALATTPRPOASPRHISGLYATPRGIIUTHTPOTHrPRO	200
OY	681	ATCCGTGGCTCTCTACACAGGGGTCAAGGGCTGACAAACCCCTTAGACAGCAGGCGGCTAG	740
Db	201	ILEUVALPRHrLeuATGATGVALYLYSALCYASPRPROLEUASPRALGTLyPRHrMETAL	220
OY	741	GTGCACTGACAGCGGGCGGTGGGCGGACGCGCTGCTCATGCTGATGATGATCCATGTTG	800
Db	221	VALHISCYSSrERALGlyVALGATGATGThrGILCYASPRHrLEVALILEASPRALMETLeu	240
OY	801	GAGGGGATGAAAGCAGAGAGAGGCTGGATATGAGCGACGTGACATGCGATGCGATCA	860
Db	241	GLIUTRMEGLYSHISGILYSPThrVALASPILETGTLyHISVALThrGlySMETATGSR	260
OY	861	CAGAGCAACTCATGCTGTGSCAGAGGAGAGACCATAGTGTCTCATCATGAGCGCTGCTG	920
Db	261	GInPRGInSPThrMETVALGInTHrGInASPRGInTLYVALPRHrLEHISGLYALeULeu	280
OY	921	GAGGCTGCCAGTGGCGGCGCACAGAGAGTGGCTGGCGGCAACCTGTATGCCCCACATCCAG	980
Db	281	GLIUTALIAMETCYSGILYHISThrGILYVALLeuVALAARGASInLeuTALHISThrGLIn	300
OY	981	AAGGTGGGCGCAAGTCCCTCCAGGGGAGAGTGTATCCCGCATGGAGCTCCAGTTCAAGTTG	1040
Db	301	LYSLeuSLyGInVALPRORPGIyGInUSerVALThrALAMETGLyLeuGInPRHrGlyLeu	320
OY	1041	CTGGCCAGCTCCAAAGGCGGCGACAGTCCCGCTTATGACGGGCAACCTGGCTGCGCAACAG	1100
Db	321	LEUVALASNSrLYSALIAHISThrSerATGPRHrVALSerLIALASInLeuPRCYASInLYS	340
OY	1101	TTTCAAGAACGGGTGTGAACATCATGCGCTTACGGAATGACCCGTGTGTCTGGACGCC	1160
Db	341	PHrLYSASPrARGLeuVALASInILEMETPROTGTLyUETHrARGALCYLsLeuGInPRO	360
OY	1161	ATCCGTGGTGTGAGAGGCTGTGACTATCATATATGCCAGCTTCTGGATGGTATATGACAG	1220
Db	361	ILEATGTLyVALGInGlySsrASPrTLYILEASNALASrPHELeuASPRGLyTyrATGIn	380
OY	1221	CAGAAAGCGTACATAGCTATACAGAGGGGCGCTGGCAGAGACAGCAGAGCATTTGGGGG	1280
Db	381	GInLYSALATyTTLLeAIATPrGInGlyPROLeuVALAGLUSerThrCInASPRHrPRATG	400
OY	1281	ATGCTATGGGAGACAAATTCCACCATCATGTCATGCTGACCAAGCTTGGGAGATGGGC	1340
Db	401	METLeuTPRGLInHISASNSrThrLIEILEVALMETLeuThrLYSLeuARGSLyMETGLY	420
OY	1341	AGGAGAAATGCCACAGTACTGGCCAGACAGAGCGCTGTCTGCTGCTACCATGATTTTGT	1400
Db	421	ARGSLyLYSCYSHISGInTLYTTPROALAGLUAARGSerALARGTycLInThrPRHrVAL	440
OY	1401	GTTTACCCGATGGCTAGTACAACAATGGCCCAGTATATCTCTGCGTGAAGTTCAAGGTCAAG	1460

Db 441 ValAlprProMetAlaGluTyrAsnMetProGlnTyrIleLeuArgGluIphelystValThr 460

QY 1461 GATGCCCGGGATGGGACGATCAAGACAAATCCGGCAGTTCCAGTTACAGACTGGCCAGAG 1520

Db 461 AspAlaIArgSpGlyGlnSerArgThrIleArgGlnPheGlnPheThrAspTrpProGlu 480

QY 1521 CAGGGCGTCCCAAGACAGGGGAGGATTCATGTAAGCTTCATCGGGCAGGTGATGAAGCC 1580

Db 481 GlnGlyValProLysThrGlnIleGlnIleGlnIlePheIleAspPheIleGlyGlnAlaHisLysThr 500

QY 1581 AAGGACAGATTGGACAGAGATGGGCTATACAGCGTGACACTGCAGTCCGTGGCCGCCGC 1640

Db 501 LysGlnGlnPheGlyGlnAspGlyProIleThrValHisCysSerAlaGlyValGlyArg 520

QY 1641 ACCGGGCTGTTCATCACTCTGAGCATCGTCTCGAGCGCATGCGCTATGAGGGCTGTC 1700

Db 521 ThrGlyValPheIleThrLeuSerIleValLeuGlnArgMetArgTyrGlnIleValAla 540

QY 1701 GACATGTTTCACACCGGTGAAGACCCGTGCTACACAGCGTCCGCATGGTGACAGACAG 1760

Db 541 AspMetPheGlnThrValLysThrLeuArgThrGlnAlaArgProAlaMetValGlnThrGlu 560

QY 1761 GACGATGATCAGCTGTGCTACCGTCCGGCCCTCGAGTACCTCGGCAAGCTTTGACCACATAT 1820

Db 561 AspGlnTyrGlnIleuGlnCysTyrArgAlaIleuGlnIuTyrLeuGlySerPheAspHisTyr 580

QY 1821 GCACAGC 1826

Db 581 AlaThr 582

RESULT 5

A56178

Protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - human

N.Alternate names: protein-tyrosine-phosphatase Bpp-2

C.Species: Homo sapiens (man)

C.Date: 03-Oct-1995 #sequence revision 03-Oct-1995 #text change 21-Jan-2000

R.Accession: A56178; S12052; B44929

R.Pulido, R.; Krueger, N.X.; Sierra-Pages, C.; Salto, H.; Streuli, M.

J. Biol. Chem. 270, 6722-6728, 1995

A.Title: Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta isoforms.

A.Reference number: A56178; MUID:95204468; PMID:7896816

A.Accession: A56178

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-1912 <PUL>

A.Cross-references: GB:L8929; NID:g755652; PIDN:AAC4149.1; PID:g755653

R.Krueger, N.X.; Streuli, M.; Salto, H.

EMBO J. 9, 3241-3252, 1990

A.Title: Structural diversity and evolution of human receptor-like protein tyrosine F

A.Reference number: S12049; MUID:91006018; PMID:2170109

A.Accession: S12052

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 390-1912 <KRU>

A.Cross-references: GB:X54133; NID:g35789; PIDN:CAM38068.1; PID:g35790

A.Note: The sequence from Fig. 5B is inconsistent with that from Fig. 5A in having 56

R.Adachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hinoda, Y.; Imai, K.;

Cancer Res. 52, 737-740, 1992

A.Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.

A.Reference number: A44929; MUID:92119637; PMID:1370651

A.Accession: B44929

A.Molecule type: mRNA

A.Residues: 1756-1804, 'C', 1806-1845 <ADA>

A.Cross-references: GB:S78086; NID:g243545; PIDN:AMB21147.1; PID:g243546

A.Experimental source: pre-B cell NALM-6

A.Note: sequence extracted from NCBI backbone (NCBIN:78086, NCBIPI:78087)

A.Note: the authors did not report the entire codon for residue 90

C.Genetics:

A.Gene: GDB:PTPRD

A.Cross-references: GDB:131384; OMIM:601598

A.Map position: 9p24-9p24

C.Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homolog

**Keywords:** glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane  
 F\_38-100/Domain: immunoglobulin homology <IIM1>  
 F\_140-209/Domain: immunoglobulin homology <IM2>  
 F\_250-304/Domain: immunoglobulin homology <IM3>  
 F\_711-811/Domain: fibronectin type III repeat homology <3FR>  
 F\_1193-1912/Domain: leukocyte common antigen cytosolic homology <LAC>  
 F\_1669-1892/Domain: protein-tyrosine-phosphatase homology <PTR2>  
 F\_1553/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F\_1559/Binding site: substrate phosphate (Arg) #status predicted  
 F\_1844/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F\_1850/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:

Pred. No.:	1,296-185	1912
Score:	2326.00	538
Percent Similarity:	95.99%	37
Best Local Similarity:	89.83%	24
Query Match:	45.41%	0
DB:	2	0
	Gaps:	0
	Indels:	0

US-09-743-492-1 (1-3467) X A56178 (1-1912)

QY	30	CAC	TCCCTCTACCCCTGTGGAGATGGCGAGGCTCAACTACACACCCACGATATGGCAGAC	89
Db	1314	H	isrprothrissrprovalgileuadargyleuasnphleglnthrpogllimelaaser	1333
QY	90	CAC	CCACCCATCCCTCCATCCACCCGAGCGGCGAGCAACATCGACGGCTCAAGCCACGAT	149
Db	1334	H	isrprotrilleprroleileuolguleuallaaaphisllieglunargleuylalaaasnsp	1353
QY	150	G	GCCTCAAGTTCTCCACGAGATGATGATCCATCGACCCCTGGACACAGTTCACGTGGAG	209
Db	1354	A	snlleuylspheaserenglnuyrgluserlileasprroglynglnphethrrpglu	1373
QY	210	A	ATTTCAACCTGGAGGTGAACAAAGCCACAGAACCCCTTATGGAAATGCATCGCTACGAC	269
Db	1374	H	isrstaasnleuolvalasnlysprolysasnarglytalaaasnvalillialaryasp	1393
QY	270	C	ACTCTCGACTACCTTACCTTACCTTATCGATGGCGCTCCCGGAGTGCATACATATGCC	329
Db	1394	H	isrserargylalleuuseralalieglnlglyleprroglyserasptylvalaaala	1413
QY	330	A	ACTACATCGATGGCTTACCGCAGACAGAAATGCTTACATCGCCACGACGGCCCTGGCC	389
Db	1414	A	asnpyrlleasplgylaryargylsglnaanaatyrllleaialthnglnlglyserleupro	1433
QY	390	G	GAGACCATGGCGCATTTTCGGAGAAATGGTGTGGAAACAGCGACGGCCACATGTGTCATG	449
Db	1434	G	lutthrpheliglyasphethrrpargmethietrrpelnlglnlathyseralthlthvalvalmet	1453
QY	450	A	TGACACAGCGCTGAGAGAGAGATCCCGGGTAAATGTGATCAGTACTGGCCACGCCGTGGC	509
Db	1454	M	ethrrlyslenglnlunlathyseralvalylscysasprglnluytrpproservargly	1473
QY	510	A	CCGAGAACCTGGGCTTATTCAGAGTGAACCGCTGGTGACACAGTGGACACTGGCCACATAC	569
Db	1474	T	hnelunthnislsgyleuvalglnvalthrrleuasnsprrthvalglnleuadlathrrtyr	1493
QY	570	A	CTGTGGGCACTCTTCACATCCACAGAAGATGGCTCCAGTGAAGACCGTACGACTCGTACG	629
Db	1494	C	ysvalalarghrphelaleuulaytrlysasnlglyserseglunlyarglvalalargln	1513
QY	630	T	TTTCAGTTACGTGCGCTGGCCACAGCAATGGAGTTCTCGATACCCCAACTCTCCATCTGGCC	689
Db	1514	P	heglmrphethrllatrrproasphrslsglyvalrproglunthsrprothrprophelaula	1533
QY	690	T	TTCTACAGACGGGTCAAGCGCTGCACACCCCTACAGACGAGGGCCATGTGTCTACATGC	749
Db	1534	P	heleuadargylalylsthrscysasnrrprotrproasphrllaeaglyprtomelvalvalhiscys	1553
QY	750	A	AGCGCGGCGCTGGGCGCACACCGGCTGCTTCATCGTATGTGATGCCATGTTGGACGAGTG	809

Db	1554	SerIaGIValGIaYArgThrGIcYsPheIleValIIleAspAlaMetLeuGIaArgIle	1573
QY	810	AAGCAGAGAAAGACGGTGGACATCTATGTGGCCACGGTACCTGCATGCGATTCACAGAGAAC	869
Db	1574	LysHISGIuLySThrValAspIleTyrGIcLysValIThrLeuMetArgAlaGIaArgAsn	1593
QY	870	TACATGTGTGCAGACGGAGGACAGTACGTGTTCATGCTCAAGAGCGCTCTGGAGCGTGGC	929
Db	1594	TyrMetValGIcThrGIaAspIleTyrIThrPheIleHISAspAlaLeuGIcValaVal	1613
QY	930	ACGTGGCGCCACACAGAGAGTGTGGCCGCAACCTGTATGCCATCCATCCAGACATGGGGC	989
Db	1614	ThrCysGIaAsnThrGIaValProIaArgAsnLeuTyrAlaTyrITleGIaLysLeuThr	1633
QY	990	CAAGTGGCTCCAGGGGAGAGTGTGACGGCCATGAGAGCTGCGAGTTCATGCTTGTGGCCAGC	1049
Db	1634	GIaITleGIuThrGIcLysAlaValIThrGIcLeuGIuLeuGIuPheLysArgLeuAlaSer	1653
QY	1050	TTCAGAGCCCAACAGCTCCCGCTTCATCAGCGCCAAACCTGGCCCTGCACACAGTTCAGAAC	1109
Db	1654	SerIySaIaITHisThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLysAsn	1673
QY	1110	CGGGTGTGACATCATATGCTCCATGACAAITTGACCCCTGTGTGTGTGACCCCATCCGTGTGT	1169
Db	1674	ArgLeuValaAsnITleMetProTyrGIuSerIThrArgValaCysLeuGIaProITleArgGIu	1693
QY	1170	GTGGAGCGCTGTGATCATCATCATGATCCAGCTTCCTGGATGGTATAGACACAGAGCGCC	1229
Db	1694	ValGIuGIuSerAspTyrITleAsnAlaSerPheIleAspGIuTyrArgGIaGIaLysAla	1713
QY	1230	TACATAGCTACACAGAGGCGCTGTGGCAGAGAGCCAGACCGAGACTTGTGGCGCATGCTATGG	1289
Db	1714	TyrITleAlaIThrGIaGIuProLeuValaGIuThrIThrGIaAspPheIThrArgMetLeuITyr	1733
QY	1290	GAGCAGCATTCACCATCATATGTGATGTGACCAAGCTTCCGGAGATGGCAGAGGAGAA	1349
Db	1734	GIuHISaAsnSerThITleValaValaMetLeuIThrLysLeuArgGluMetGIaYArgGIuLys	1753
QY	1350	TGCCACGAGTACGTGGCCAGCAGAGCGCTGTGCTGCTCCACAGTACTTGTGTTGATACCCG	1409
Db	1754	CysHISGIaITyrITrProAlaGIaArgSerAlaArgITyrGIaITyrPheValaValaAspPro	1773
QY	1410	ATGGCTAGTACACACATGCCCCAGTATATCTGCTGCGTAGTTCACAGTACAGGATGCCGG	1469
Db	1774	MetaIaGIuITyrAsnMetProGIaITyrITleLeuArgGIuPheLysValIThrAspAlaArg	1793
QY	1470	GATGGGCGAGTACAGACACAATCCGAGATGCCAGTTCCAGTTCACAGACTGCCACAGAGCGGTG	1529
Db	1794	AspGIcLysIaSerArgIThrValaArgIThrPheGIaIThrAspITrProGIuGIaVala	1813
QY	1530	CCCAAGACAGCGCAGAGGATTAATTGACTTCACTCGGGCAGGTGCATTAAGACCAAGAGAGAG	1589
Db	1814	ProIySSerGIuGIuIThrPheIleAspPheIleITleGIaITaLysIThrLysGIuGIa	1833
QY	1590	TTTGGACAGGATGGCGCTATACAGGTTGCACGTGCACAGTGTGGCGCTGGAGCGCGGGGTG	1649
Db	1834	PheGIcLysAlaAspGIuProITleSerValaHISySSerAlaGIaValaITyrArgIThrGIuAla	1853
QY	1650	TTTCATCACTGTGAGATGTGTCTGGAGCGCATGGCGCTATAGAGGCGGTGTGACATGTGTT	1709
Db	1854	PheITleIThrIleSerITleValaITleuITaArgMetaITyrGIuGIaValaValaAspIThrPhe	1873
QY	1710	CAGACCGTAGAAGACCTGCTGATACAGAGCGTCTGCTGCATAGTGCAGACAGAGACAGAT	1769
Db	1874	GIaIThrValaLysMetLeuArgIThrGIaIThrArgITrProAlaMetValaGIaIThrGIaAspITyr	1893
QY	1770	CAGCTGTCTACACGCTGGCGCGCTGGAGTACCTGGCGACCTTGGACCACTATGACAAG	1836
Db	1894	GIaIThrSerITyrArgAlaAlaLeuGIaITyrITleuGIuSerIThrPheAspHISITyrAlaIThr	1912



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Db 1593 ProlyserGlyGluGlyPheIleAspPheIleGlyGlnValHisLysThrLysGluGln 1612  
QY 1590 TTITGACAGAGATGGCCCTATACAGGTGACAGTGTGCGCGCCGACCGAGGTG 1649  
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Db 1613 PheGlyGlnAspGlyProIleSerValHisCysSerAlaGlyValAlaGlyThrGlyVal 1632  
QY 1650 TTCATACGCTGACGATCGCTCGGAGCGCATGCGCTATGAGGCGCGTGCAGATGTTT 1709  
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Db 1633 PheIleThrLeuSerIleValLeuGlnArgMetArgTyrGluGlyValAlaSplIlePhe 1652  
QY 1710 CAGACGCTGACAGACCTGCGTACACAGCGCTCGCATGGTGACAGACAGACAGTAT 1769  
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Db 1653 GlnThrValLysMetLeuArgThrGlnArgProAlaMetValGlnThrGluAspGlnTyr 1672  
QY 1770 CAGCTGTGCTACCGTGGCGCCCTGAGATACCTCGGACGCTTTGACCACTATGACAG 1826  
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Db 1673 GlnPheCysTyrArgAlaAlaLeuGlnTyrLeuGlySerPheAspHisTyrAlaThr 1691  
RESULT 7  
C54689  
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form B precursor  
N:Alternate names: Mppr delta type B/C  
N:Contains: protein tyrosine phosphatase, receptor type delta, splice form C  
C:Species: Mus musculus (house mouse)  
C:Date: 25-Apr-1995 #sequence\_revision 19-May-1995 #text\_change 12-Feb-1999  
C:Accession: C54689; B54689  
R:Minuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.  
Mol. Cell. Biol. 13, 5513-5533, 1993  
A:Title: Mppr delta, a putative murine homolog of Hppr delta, is expressed in specialized  
A:Reference number: A54689; MUID:93360986; PMID:8355697  
A:Accession: C54689  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1894 <M12>  
A:Experimental source: brain; splice form B  
A>Note: sequence inconsistent with nucleotide translation  
A>Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBI:137487)  
A:Accession: B54689  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-352, 'H', 354-535, 'S', 537-601, 1002-1894 <M12>  
A:Experimental source: brain; splice form C  
A>Note: sequence inconsistent with nucleotide translation  
A>Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBI:136530)  
C:Superfamily: Leukocyte antigen-related protein; fibronectin type III repeat homology;  
ogy  
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoprotein; phosphoric monoester hyd  
F:45-107/Domain: immunoglobulin homology <IMM1>  
F:245-299/Domain: immunoglobulin homology <IMM2>  
F:317-399/Domain: fibronectin type III repeat homology <FN3A>  
F:1278-1894/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:1652-1874/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:1536/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1542/Binding site: substrate phosphate (Arg) #status predicted  
F:1806/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1832/Binding site: substrate phosphate (Arg) #status predicted  
Alignment Scores:  
Pred. No.: 3.3e-182 Length: 1894  
Score: 2874.50 Matches: 534  
Percent Similarity: 95.168 Conservative: 36  
Best Local Similarity: 89.158 Mismatches: 26  
Query Match: 44.618 Indels: 3  
DB: 2 Gaps: 3  
US-09-743-492-1 (1-3467) x C54689 (1-1894)  
QY 30 CACTCTCTGACCTGTGAGATGCGAGGCTCACTACAGACCCGAGTATGCGAG 89  
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Db 1299 HisProThrAspProValGlnLeuArgArgLeuAsnPheGlnThrProGlyMetAlaSer 1318  
QY 90 CAGCCAGCATCCCATACCGAGCTGGCGGAGACACATGAGGCGCTCAAGCAACGAT 149

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Db 1319 HisProThrIleProIleLeuGlnLeuAlaAspHisIleGluThrGlyLeuAlaAsnAsp 1338  
QY 150 GGCCTCAAGTTCTCCAGAGATATGATCCATGACCCCTGGACAGCATTCACGTGGAG 209  
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QY 210 AATTCAACTGTGAGGTGAACAGCCAGAACCCGCTATGCCAATGTCATCGGCTACGAC 269  
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QY 270 CACTCTGACATACCTTACCTACATGATGGCGGCGCGAGTGCATCATATGCC 329  
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QY 330 AACTACATGATGCTACACCGACAGAAATGCTACATGCCACGAGGCGCCCTGCC 389  
|||||.....  
Db 1399 AsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGlySerLeuPro 1418  
QY 390 GAGACCATGGCGCATTTCTGAGATAGTGTGGGAACGGCGCACGGCCATGTGTCATG 449  
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Db 1419 GluThrPheGlyAspPheThrPargMetIleTrpGluGlnGlu--AlaThrValAlaMet 1437  
QY 450 ATGACACGGCTGGAGAGAAATGCCGGAATATGATGATGATGAGCCAGCCGCGG 509  
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Db 1438 MetThrLysLeuGlnGluArgSerArgValLysCysAspGlnTyrTrpProSerArgGly 1457  
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Db 1458 ThrGluThrHisGlyLeuValGlnValThrLeuLeuAspPheValGluLeu--ThrTyr 1476  
QY 570 ACTGTGCGACCTTTCGCACCTCCACAGAGTGGCTCCAGTGAAGAGCGTGAGCTGCGT 629  
|||||.....  
Db 1477 CysValArgThrPheAlaLeuTyrAsnAsnGlySerSerLysArgLysValArgGln 1496  
QY 630 TTTCAGTTCATGCGCTGGCGACGACCATGAGTTCGATGAGCAACATCCATCCTGGCC 689  
|||||.....  
Db 1497 PheGlnPheThrAlaTrpProAspHisGlyValProGlnHisProThrProPheLeuAla 1516  
QY 690 TTTCCTAGACGGGTCAAGGCTGCAACCCCTGACAGCGAGGCCCATGTGTGCTGCTGC 749  
|||||.....  
Db 1517 PheLeuArgArgValLysThrCysAsnProProAspAlaGlyProMetValAlaHisCys 1536  
QY 750 AGCGGGGGCTGGGGCGGACCGGCTGCTATGCTGATGATGATGATGATGATGATGATG 809  
|||||.....  
Db 1537 SerAlaGlyValGlyArgTyrThrGlyCysPheIleValIleAspAlaMetLeuGluArgIle 1556  
QY 810 AACGACGAGAAAGCGGAGCATCTATGGCCAGCTGACCTGACGATGACAGAGAGAAC 869  
|||||.....  
Db 1557 LysHisGlnLysThrValAspIleTyrGlyHisValThrLeuMetArgAlaGlnArgAsn 1576  
QY 870 TACATGGTGACAGGAGACACAGTACGTTGATCCATGAGGCGCTGTGAGGCTGCC 929  
|||||.....  
Db 1577 TyrMetValGlnThrGluAspGlnTyrIlePheIleHisAspAlaLeuGlnAlaVal 1596  
QY 930 ACTGTGGGCGACACAGAGTGCCTGCCCGGACACCTGATATCCACATCCAGAGCTGGGC 989  
|||||.....  
Db 1597 ThrCysGlyAsnThrGlnValProAlaArgAsnLeuTyrAlaTyrIleGlnLysLeuThr 1616  
QY 990 CAGTGCCTTCACAGGAGGATGACCGGACGATGACGATGATGATGATGATGATGATGATG 1049  
|||||.....  
Db 1617 GlnIleGluThrGlyLysAsnValThrGlyMetGluLeuGlnPheLysArgLeuAlaSer 1636  
QY 1050 TCCAGAGCCACACGTCGCCCTTCATCAGGCGCACCTGCGTGCACAAATTCAGAAC 1109  
|||||.....  
Db 1637 SerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLysAsn 1656  
QY 1110 CGCGTGTGACATCATGCCCTTACGAATGACCCGTGTGTGTGACAGCCATTCGTTGTT 1169  
|||||.....  
Db 1657 ArgLeuValAsnIleMetProTyrGlnSerGlyArgValCysLeuGlnProIleArgGly 1676  
QY 1170 GTGGAGGGCTGTGACTACATCATGACGATGCTGCTGATGATGATGATGATGATGATGATG 1229  
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Db 1677 ValGIuGIySerAsPtyrILLeasnAlaSerPheLeuAspGIyTyraRgInGIuLysAla 1696
QY 1230 TACATAGCTACACAGGGGCTCTGGCAGAGACACCGAGACTTCTGGCGATGCATAG 1289
    |||||
Db 1697 TyrILeAlaThrGInGlyProLeuAlaGIuThrThnGIuAsPheThrPrArgMetLeuTrp 1716
QY 1230 GAGCAACAATTCACCATCATCTCATGCTGACCAAGCTTGGAGATGGGACGGAGAAA 1349
    |||||
Db 1717 GIuHISAsnSerThrILeValAlaMetLeuThrILysLeuAlaRGIuMetGIyArGIuLys 1736
QY 1350 TGGCCACGACTATGGCAGCAGAGGCTCTGCTGCTACCACTACTTGTGTGACCCG 1409
    |||||
Db 1737 CysHISGIuTrpProAlaGIuArGIuSerAlaArGIyGIuTrpPheValAlaAspPro 1756
QY 1410 ATGCGTGAATACACATGCGCCACGATATCTGCGTGAATTCAGAGTCCAGGATGCCG 1469
    |||||
Db 1757 MetAlaGIuTyraSmeProGIuTrpILeLeuArGIuGIuPheLysValILhrspAlaArG 1776
QY 1470 GATGGGAGTCAAGAGCAATCCGGCAGTTCACAGTTCACAGACTGGCCAGAGAGGCGTG 1529
    |||||
Db 1777 Asp---GIuSerArGIyThrValArGIuInPheGIuInPheThrAspTrpProGIuInGIyVal 1795
QY 1530 CCCAGACAGGAGGAGGATTCATGACTCATCGGGCAGCTGATTAAGCCAAAGAGCAG 1589
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Db 1796 ProLysSerGIyGIuGIyPheILeAsPheILeGIyGIuValILhISyThrLysGIuGIu 1815
QY 1590 TTTGGACAGAGATGGGCTCATCAAGGTGCAGTGCAGTGTGCGTGGCGCCAGCGGAGTG 1649
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Db 1816 PheGIyGIuInAspGIyProILeSerValILhISySerAlaGIyValGIyArGIuThrGIyVal 1835
QY 1650 TTCATCACTCTGAGCATGCTCTCGAGGCGCATGCGCTATGAGGCGGTGTCACATGTTT 1709
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Db 1836 PheILeThrILeAsPheILeValILeGIuArGIyMetArGIyGIyValILaAspILePhe 1855
QY 1720 CAGACGCGAAGACCGCTGCGTACAGAGGCTCTGCCATGGTGCACAGAGAGACGATAT 1769
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Db 1856 GIuThrValILysMetLeuArGIuThrILhISyProAlaMetValILhISyGIuAspGIuTrp 1875
QY 1770 CAGCTGTCTACCGTGCAGGCGCTTGAGTACCTGCGCAGCTTTGACCACATATCAACG 1826
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Db 1876 GIuPheCysTyraRGIAlaILaLeuGIuTrpILeGIuLysSerPheAsPheILhISyArILhISy 1894

RESULT 8
150212
Protein: tyrosine-phosphatase (EC 3.1.3.48) - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C:Accession: 150212
R:Stocker, A.W.
Mech. Dev. 46, 201-217, 1994
A:Title: Isoforms of a novel cell adhesion molecule-like protein tyrosine phosphatase at
A:Reference number: 150212; MUID:95001563; PMID:7918104
A:Accession: 150212
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1499 <STO>
A:Cross-references: GB:L32780; NID:g485746; PIDN:AAA64460.1; PID:g485747
C:Genetics:
A:Gene: CRYPALPAL
C:Superfamily: Leukocyte antigen-related protein; fibronectin type III repeat homology;
Oy
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F:148-208/Domain: immunoglobulin homology <IMM1>
F:245-299/Domain: immunoglobulin homology <IMM2>
F:317-399/Domain: fibronectin type III repeat homology <3PR>
F:881-1499/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1257-1479/Domain: protein-tyrosine-phosphatase homology <PTP2>
F:141/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1147/Binding site: substrate phosphate (Arg) #status predicted
F:1432/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1438/Binding site: substrate phosphate (Arg) #status predicted

```

```

Pred. No.: 9,21e-182 Length: 1499
Score: 2867.50 Matches: 527
Percent Similarity: 94.32% Conservative: 38
Best Local Similarity: 87.98% Mismatches: 33
Query Match: 44.50% Gaps: 1
DB: 2
US-09-743-492-1 (1-3467) x 150212 (1-1499)
QY 30 CACTCTGAGTCACTTCACTCTATGATGAGCGTCCCGGAGTACTACATATGCC 89
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Db 902 HIsPProILeProValSerGIuLeuAlaGIuHISThrGInHISLeuLysAlaSnAsP 921
QY 90 CACCCACCCATCCCATCCATCCAGACCTGGCGGCAACATGCAGCGCTCAAAAGCAAGAT 149
    |||||
Db 922 HIsPProILeProValSerGIuLeuAlaGIuHISThrGInHISLeuLysAlaSnAsP 941
QY 150 GGCCTCAAGTCTCCAGAGATATGATGATCCATGCAGCTGGACAGCAGTTCACGTGGAG 209
    |||||
Db 942 AsnLeuLysLeuSerGIuInGIuTrpGIuSerILeAsPProGIyGIuInPheThrPrGIu 961
QY 210 AATTCAAACCTGAGGTGACAAAGCCCAAGAACCGCTATGCGAATGTCATGCCATACGAC 269
    |||||
Db 962 HIsSerAsnLeuGIuValAsnLysProLysAsnArGIyArILaSnValILeAlaTyraSP 981
QY 270 CACTCTGAGTCACTTCACTCTATGATGAGCGTCCCGGAGTACTACATATGCC 329
    |||||
Db 982 HIsSerArGIyValILeLeuLeuProILeGIuGIyILeValGIySerAsPtyrILLeAsnAla 1001
QY 330 AACTCATGATGAGTCTACCGCAAGCAAGATGCCCTATATGCCACGAGGCCCCCTGCC 389
    |||||
Db 1002 AsnTyrILeAspGIyTyraRGIyGIuInAsnAlaTyrILeAlaThrGInGIuProLeuPro 1021
QY 390 GAGACCATGGGAGATTTCTGGAGAAATGGTGGGAAACAGCGACGCGCCACTGGTGCATG 449
    |||||
Db 1022 GIuThrPheGIyAsPheThrPrArGIyValILhISyGIuInArGIySerAlaThrILeValILe 1041
QY 450 ATGACACGCGCTGGAGAGAGATCCGGGTAAATGTGATCACTAGTGGCCAGCCCTGGCG 509
    |||||
Db 1042 MetILhISyLeuGIuInGIuLysSerArGIyILeLysCysAsPGIuTyTrpProGIyArGIy 1061
QY 510 ACCGAGACTGTGGCCTTATTCAGTGACCCCTGTTGGACACAGTGGAGCTGGCCACATAC 569
    |||||
Db 1062 ThrAsPThrTyGIyMetILeGIuValILhISyLeuLysPThrILeGIuLeuAlaThrPhe 1081
QY 570 ACTGTGGCAGCTTGACACTCCCAAGAGTGGCTGCAGAGAGAGGTCAGTGGCTGCGTAC 629
    |||||
Db 1082 CysValArGIyThPheSerILeHISLysAsnGIySerSerGIuLysArGIuValILhISy 1101
QY 630 TTTCAATTCATGGCCTGGCCAGACCATGAGATGCTGAGTACCAACTCCATCCCTGGCC 689
    |||||
Db 1102 PheGIuInPheThrAlaILhISyProAsPheILhISyGIyValILhISyGIuTrpThrProPheLeuAla 1121
QY 690 TTCCTACGACGCGGTCAAGGCTGCAACCCCTAGACGACGAGGCGCCATGGTGGTGCATGTC 749
    |||||
Db 1122 PheLeuArGIyArGIyValILhISyThrCysAsnPropoAsPheILhISyValILhISy 1141
QY 750 ACCGCGGCGGTGGCGGCGACCGGCTGCATGCAGTGCATGATGATGATGATGATGATGATG 809
    |||||
Db 1142 SerAlaGIyValILeArGIyThrGIyCysPheILeValILeAsPAlaMetLeuILhISyLe 1161
QY 810 AAGCAGAGAAAGACGCTGACATCTATGCGCACAGTGCAGCTGCATGCATGCATGCATGC 869
    |||||
Db 1162 LysHISGIuLysThrValILaSPLeILeYrGIuHISValILhISyLeuMetArGIySerILhISy 1181
QY 870 TACATGTCGACAGAGAGACCAAGTATGCTGTTCATGCATGCATGCATGCATGCATGCATGC 929
    |||||
Db 1182 TyrMetValILhISyThrGIuAsPProILhISySerPheILhISyAsPAlaLeuLeuILhISy 1201
QY 930 ACGTGGCGGCAACAGAGAGTGGCTGGCGGCAACCTGTATGCCACATGCAGAGAGTGGCG 989
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Db 1202 AlaCysGIyAsnThrGIuValProAlaArGIyAsnLeuTyTrpThrTyTrILeGIuLysLeuAla 1221

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Alignment Scores:

[illegible]

R.Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J. *Biochem. J.* 302, 39-47, 1994

A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-A:Reference number: S46216; MUID:94347119; PMID:8068021

A:Accession: S46218

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-1501 <ZNA>

A:Cross-references: EMBL:U12329; NID:9294573; PIDN:ACG37657.1; PID:9294574

C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homolog ogy

C:KeyWords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrr F:47-109/Domain: immunoglobulin homology <IMM1>

F:149-209/Domain: immunoglobulin homology <IMM2>

F:246-300/Domain: immunoglobulin homology <IMM3>

F:413-506/Domain: fibronectin type III repeat homology <3R>

F:483-1501/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:965-1190/Domain: protein-tyrosine-phosphatase homology <PTP1>

F:1258-1481/Domain: protein-tyrosine-phosphatase homology <PTP2>

F:1142/Active site: Cys (phosphocysteine intermediate) #link PTP1 #status predicted

F:1148/Binding site: substrate phosphate (Arg) #link PTP1 #status predicted

F:1433/Active site: Cys (phosphocysteine intermediate) #link PTP2 #status predicted

F:1439/Binding site: substrate phosphate (Arg) #link PTP2 #status predicted

Alignment Scores:

Pred. No.:	1.33e-180	Length:	1501
Score:	2850.00	Matches:	523
Percent Similarity:	93.99%	Conservative:	40
Best Local Similarity:	87.31%	Mismatches:	36
Query Match:	44.23%	Indels:	0
DB:	2	Gaps:	0

US-09-743-492-1 (1-3467) x I58148 (1-1501)

QY 30 CACTCTCTGACCTCTGTGGAGATGCGGAGGCTCAACACAGCCAGGATGCGAGAC 89

Db 903 HSPolysAspProValGluMetArgArgIleAsnPhcGlnThrProGlyMetLeuSer 922

QY 90 CACCCACCATCCCATACGAGCTGCGGGGCAACATGAGAGCGCTCAAGCCACAGAT 149

Db 923 HSPProIleProlIerThrAspMetValGluHisMetGluGluValAsnAsp 942

QY 150 GGCTCAAGTTCTCCAGAGATGATGATGCATGACCCCTGGAGACAGATTCACGTGGAG 209

Db 943 SerLeuLysLeuSerGlnGluThrGluSerIleAspProGlyGlnGlnPheThrTrpGlu 962

QY 210 AATTCAAACTGTGGAGCTAACAAGCCCAAGAACCGCTATGCGAATGTCATGCCATACAC 269

Db 963 HisSerAsnLeuGluAlaAsnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAsp 982

QY 270 CACTCGAGATCATCTTACCTATGATGATGAGCGGCCCGGAGATGACTATCAATGCC 329

Db 983 HisSerArgValIleLeuGlnProLeuGluGluIleMetGlySerAspTyrIleAsnAla 1002

QY 330 AACTTCATCATGATGCTTACCGCAGACAGAACTGCTATACATGCGCAGACAGGCCCCCTGCC 389

Db 1003 AsnTyrValAspGlyTyrArgArgGlnAsnAlaTyrIleAlaThrGlnGlyProLeuPro 1022

QY 390 GAGACCATGGCGATTTCTTGAGAAATGTTGTGGAAACAGCCAGCCCATGTTGTCATG 449

Db 1023 GluThrPheGlyAspPheTrpArgMetValIleTrpGlnGlnArgSerAlaThrValIleMet 1042

QY 450 ATGACACGGCTGTGGAGAAATGCCCGGGTAAATGTATCATGACTGTGCCACGCCCTGGGC 509

Db 1043 MetThrArgLeuGluGluLysSerArgValLysCysAspGlnTyrTrpProAsnArgGly 1062

QY 510 ACCGAGACCTGTGCTTATCAGGTGACCTGTGGACACAGAGGAGCGGCCACATCAT 569

Db 1063 ThrGluThrTyrGlyPheIleGlnValThrLeuLeuAspThrMetGluLeuAlaThrPhe 1082

QY 570 ACTGTGCGACCTTCGCACTCACAGAGTGCTCCAGTGAAGAAGCGGTGACCTGCTGAC 629

Db 1083 CysValAcGluThrPheSerLeuHisLysAsnGluGlySerSerGluLysArgGlyValArgHis 1102



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QY 630 TTTCAGTTCAGGCGCTGGCCAGACCATGAGTTCCTGAGTACCAATCCATCTCGGCC 689
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Db 1103 PheGlnPheThrAlaTrpProAspHisGlyVal1ProGluTyrProThrProPheLeuAla 1122
QY 690 TTCCAGACGAGGCTGAAGCCCTGCAACCCCTAGACAGGAGGCGCATGGTGTGACATCC 749
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1123 PheLeuArgValGlyValLysThrCysAsnProProAspAlaGlyProValAlaHisCys 1142
QY 750 AGCGCGGCGTGGGCGCCAGACCGGCTTCATCATGATTCATGATTCATGATTCATGATTCAT 809
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1143 SerAlaGlyValGlyArgThrClYcysPheLeuVal1LeuAspAlaMetLeuLysArgTyr 1162
QY 810 AAGCAGAGAAGACGGTGGACATCTATGCGCCAGTGCATCGCATCGCATCAGAGAGAAC 869
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1163 ArgThrGluLysThrValAspValYrgLysHisVal1ThrLeuMetArgSerGlnArgAsn 1182
QY 870 TACATGGTGCAGAGGAGGACCATGATTCATCATGATTCATGATTCATGATTCATGATTCAT 929
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1183 TyrMetValGlnThrGluAspGlnTyrSerPheLeuHisGluAlaLeuLeuGluAlaVal 1202
QY 930 AGCTGCGGCGCACAGAGAGTGGCTGCGCCAGACCTGTATGCCATCCAGAGAGTGGCG 989
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Db 1203 GlyCysGlyAsnThrGluValProAlaArgSerLeuTyrThrTyr1LeuGlnLysLeuAla 1222
QY 990 CAATGCTCCAGGAGGAGAGTGTGACCGCCATGAGCTCGAGTTCAAGTTGCTGGCCAGC 1049
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Db 1223 GlnValGluProGlyGlnHisVal1ThrGlyMetGluLeuGluPheLysArgLeuAlaSer 1242
QY 1050 TCCAGGCGCCAGCTCCGCTGCTCATCAGCGGCGCAACGCTCCCTGCAACAGTTCAGAAC 1109
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Db 1243 SerLysAlaHisThrSerArgPheLeuThrAlaSerLeuProCysAsnLysPheLysAsn 1262
QY 1110 CGGCTGTGAACATCATCCCTACGAATTCACCCGCTGTGTCTGCTCAGCCCATCCGTGT 1169
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Db 1263 ArgLeuValAsn1LeuLeuProTyrGluSerSerArgValCysLeuGlnPro1LeuArgGly 1282
QY 1170 GTGAGGCGCTGATACATCATCCAGCTTCGTGATGTTATACAGACAGAGAGGCC 1229
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Db 1283 ValGluGlySerAspTyr1LeuAsnAlaSerPheLeuAspGlyTyrArgGlnLysAla 1302
QY 1290 TACATAGTATACAGGCGGCTGCTGCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1289
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1303 Tyr1LeuAlaThrGlnGlyProLeuAlaGluTyrThrGluAspPheTrpArg1AlaLeuTyr 1322
QY 1290 GAGCAATTCACCATCATGCTCATGCTGACCAAGCTTCGGAGAGTGGAGGAGAGAA 1349
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1323 GluAsnAsnSerThr1LeuValMetLeuThrLysLeuArgGluMetGlyArgGluLys 1342
QY 1350 TGGCAGCATGCTGGCGACGAGGCGCTGCTGCTGCTACACAGTACTTGTGTTGACCCG 1409
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Db 1343 CysHisGlnTyrTrpProAlaGluArgSerAlaArgTyrGlnTyr-PheValAlaAspPro 1362
QY 1410 ATGGCTGATCAACATGCCCCAGATATCCGCGGTGAGTTCAAGCTCAAGCATGCCGCGG 1469
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Db 1363 MetAlaGluTyrAsnMetProGlnTyr1LeuAspArgLysVal1ThrAsp1AlaArg 1382
QY 1470 GATGGCGAGTCAAGGACATCCGCGCATTCAGTTCACAGACTGGCCAGAGCGGCGCTG 1529
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Db 1383 AspGlyGlnSerArgThrValArgGlnPheGlnPheThrAspTrpProGluGlnLysAla 1402
QY 1530 CCCAAGACAGCGGAGGATTCATTGACTTCATCGGCGAGGTGCATTAAGACAGAGAGAG 1589
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Db 1403 ProLysSerGlyGluGlyPheLeuAspPheLeuGlyGlnVal1HisLysThrLysGluGln 1422
QY 1590 TTTGGACAGGATGGGCGCATGATCGGTCAGTGCATGCTGGGCTGGGCGGCGAGCGGCGT 1649
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Db 1423 PheGlyGlnAspGlyPro1LeuSerVal1HisCysSerAlaGlyVal1ArgThr1Val 1442
QY 1650 TTTCATCATCTGAGCATGCTCTGAGGAGCATGCTGCTGAGGCGGTGCTGACATGTTT 1709
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1443 Phe1LeuThrLeuSer1LeuValLeuGluLysArgMetArgTyrGluGlyVal1ValAsp1LeuPhe 1462

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QY 1710 CAGACCGTGAGAACCCCTCGCTACACAGCGTCTGCCCATGCTGCAGACAGAGACCATAT 1769
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Db 1463 GlnThrVal1ValLeuArgThrGlnArgProAlaMetValGlnThrGluAspGluTyr 1482
QY 1770 CAGCTGTGCTACCGTGGCGGCGCTGAGTACCTCGGACGCTTGACCATATGCAACG 1826
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1483 GlnPheCysPheGlnAla1AlaLeuGluTyrLeuGlySerPheAspHisTyrAlaThr 1501

RESULT 10
S50893
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type sigma precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S50893; S40281
R:Wagner, J.; Boerdboom, D.; Tremblay, M.L.
Eur. J. Biochem. 226, 773-782, 1994.
A:Title: Molecular cloning and tissue-specific RNA processing of a murine receptor-ty
A:Reference number: S50893; MUID:95112841; PMID:7529177
A:Accession: S50893
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1907 <MAG>
A:Cross-references: EMBL:X82288; NID:9587483; PIDN:CA57732.1; PID:9587484
R:Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
Submitted to the EMBL Data Library, June 1993
A:Description: Assessment of the expression levels of murine protein-tyrosine phospho
A:Reference number: S40280
A:Accession: S40281
A:Molecule type: mRNA
A:Residues: 1441-1501, 'E', 1503-1546 <HEN>
A:Cross-references: EMBL:Z23050; NID:9438137; PIDN:CA80585.1; PID:9438138
C:Superfamily: Leukocyte antigen-related protein; fibronectin type III repeat homolog
QY
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembr
F:149-209/Domain: immunoglobulin homology <IM1>
F:246-300/Domain: immunoglobulin homology <IM2>
F:413-506/Domain: fibronectin type III repeat homology <3FR>
F:1288-1907/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F:1375-1596/Domain: protein-tyrosine-phosphatase homology <PTR1>
F:1664-1887/Domain: protein-tyrosine-phosphatase homology <PTR2>
F:1548/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1554/Binding site: substrate phosphate (Arg) #status predicted
F:1839/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1845/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:
Pred. No.: 2,18e-180 Length: 1907
Score: 2847.00 Matches: 522
Percent Similarity: 93.9% Conservative: 41
Best Local Similarity: 87.15% Mismatches: 36
Query Match: 44.18% Indels: 0
DB: 2 Gaps: 0

US-09-743-492-1 (1-3467) x S50893 (1-1907)
QY 30 CACTCTCTGACCTGTGGAGATGCGAGAGCTCAACTACAGACCCAGATATGCGAGAC 89
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1309 HisProLysAspProValGluMetArgTyrGlnPheGlnThrProGluTyrLeuSer 1328
QY 90 CACCACCCATCCCATACACGACCTGGCGGACCAATCAGAGCGGCTCAAAACCAACAT 149
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Db 1339 HisProLysAspProValGluMetArgTyrGlnPheGlnThrProGluTyrLeuSer 1348
QY 150 GCCCTCAAGTTCCTCCAGAGATAGTTCATGACCTCGACAGCAGTTCACGTGGAG 209
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1349 SerLeuLysLeuSerGlnGluTyrGluSer1LeuAspProGluGlnPheThrTrpGlu 1368
QY 210 AATTCAAACTGAGAGTGAACAGACCCAGAAACCGCTATGCCAATGTCATCGCTACAGAC 269
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1369 HisSerAsnLeuGluAlaAsnLysProLysAsnArgTyrAlaAsnVal1LeuAlaTyrAsn 1388
QY 270 CACTTCGAGTCATCTTACCTTATCATGATGCGGCTCCCGGAGAGTACTACTCATATGCC 329
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

Db 1389 HisserArgValIleLeuGlnProLeuGlnGlyIleMetGlySerAspTyrIleAsnAla 1408  
 QY 330 AACTCATGATGGCTACCGCAGAGATGGCTTACATGGCCACGAGGGCCCTGCC 389  
 Db 1409 AsnTyrValAspGlyTyrTrgArgGlnAsnAlaTyrIleAlaThrGlnIleProLeuPro 1428  
 QY 330 GAGACCATGGGCGATTTCGGAGAAATGCTGGGAAACAGCGAGCGCCACTGTGCATG 449  
 Db 1429 GlnThrPheGlyAspPheThrArgMetValTrpGlnGlnArgSerAlaThrValAlaMet 1448  
 QY 450 ATGACACGGCTGGAGAGAAATCCGGTAAATGTGATCACTGAGCCACCGCTGGC 509  
 Db 1449 MetThrArgLeuGlnGlnIuysSerArgIleLysCysAspGlnTyrTrpProAsnArgIly 1468  
 QY 510 ACCGAGACCTGTGGCTTATTCAGGTGACCTGTGGACACAGTGGAGCTGGCCACATAC 569  
 Db 1469 ThrGlnThrTyrGlyPheIleGlnValThrLeuLeuAspThrMetGlnLeuAlaThrPhe 1488  
 QY 570 ACTGGCGCACCTTGCGATCCACAAGAGTGGCTCCAGTACGAGAGAGTGGAGCTGGC 629  
 Db 1489 CysValAlaGlnThrPheSerIleuHisLysAsnGlySerSerGlyLysArgGlnValAlaArgHis 1508  
 QY 630 TTTCAGTTCATGGCCTGGCGCAGACCATGGATGCTCTGATGATCCCAATCCATCCGTG 689  
 Db 1509 PheGlnPheThrAlaTrpProAspHisGlyValProGlnTyrProThrProPheLeuAla 1528  
 QY 690 TTCTCATGACGGGTCAAGGCTGCAACCCCTAGACGACGAGGCCCATGTGGTGCATGC 749  
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 QY 750 AGCGGGGGCGGGGGCGCGGCTGCTCATGGATGATGATGATGATGATGATGATGATGATG 809  
 Db 1549 SerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeuGlnAlaGlyIle 1568  
 QY 810 AAGCAGAGAAAGACGCTGACATCTATGGCCAGCTGACCTGATGGATGATGATGATGATG 869  
 Db 1569 LysThrGlnLysThrValAlaSerValTyrGlnHisValThrLeuMetArgSerGlnArgAsn 1588  
 QY 870 TACATGCTGACAGAGGAGGACCATGATGCTTCATCCATGAGCGCTGCTGAGAGCTGCC 929  
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 QY 930 ACGTGGCGGCGACAGAGTGGCTGCGCGGACCTGATGCCACATCCAGAGAGGGGCG 989  
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 QY 990 CAAGTGCCTCCAGGAGAGAGTGTGACCCGATGAGCTGATGATGATGATGATGATGATG 1049  
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 Db 1669 ArgLeuValAlaAsnIleLeuProTyrGlnLysSerArgValCysLeuGlnProIleArgGly 1688  
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 QY 1230 TACATGCTGACAGAGGCGCTGTGGCAGAGACCGAGAGACTTGTGGCGCATGCTATG 1289  
 Db 1709 TyrIleAlaThrGlnGlyProLeuAlaGlnThrThrGlnAspPheThrArgAlaLeuTyr 1728  
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QY 1410 ATGGCGAGTACAAATGCGCCAGTATATCTGCGGAGTTCAGGTCAAGGTACGAGTCCGG 1469  
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 Db 1809 ProLysSerGlyGlnGlyPheIleAspPheIleGlyGlnValHisLysThrLysGln 1828  
 QY 1590 TTGGGACAGAGGCGCTTCACGCGTCAACGCTGACGCTGAGCTGGGCGCGGCGGCTG 1649  
 Db 1829 PheGlyGlnAspGlyProIleSerValHisCysSerAlaGlyValGlyArgThrGlyAla 1848  
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 Db 1849 PheIleThrLeuSerIleValIleuGlnArgMetArgTyrGlnGlyValAlaAspIlePhe 1868  
 QY 1710 CAGACCGTGAAGACCTGCGTACACAGCGTCCCTGCGCATGCTGACAGACAGACAGTAT 1769  
 Db 1869 GlnThrValLysValLeuArgThrGlnArgProAlaMetValGlnThrGlnAspGlyTyr 1888  
 QY 1770 CAGCTGTGCTACCGTGGCGCCCTGGAGTACCTCGGACGCTTGCACCATGATGACAG 1826  
 Db 1889 GlnPheCysPheGlnAlaAlaLeuGlnTyrIleuGlySerPheAspHisTyrAlaThr 1907  
 RESULT 11  
 546217  
 protein-tyrosine-phosphatase (EC 3.1.3.48) type sigma precursor - rat  
 M:Alternate names: leukocyte common antigen-related phosphatase  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 07-May-1995 #sequence,revision 03-Nov-1995 #text\_change 23-Jul-1999  
 C:Accession: S46217; S51174; A49104  
 R:Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.  
 Biochem. J. 302, 39-47, 1994  
 A>Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-  
 A:Reference number: S46216; MUID:94347119; PMID:8068021  
 A:Accession: S46217  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-1863 <ZHA>  
 A:Cross-references: EMBL:L11587  
 R:Goldstein, B.J.  
 submitted to the EMBL Data Library, February 1993  
 A:Reference number: S51174  
 A:Accession: S51174  
 A:Molecule type: mRNA  
 A:Residues: 1-1788, 'G', 1790-1863 <GOL>  
 A:Cross-references: EMBL:L11587; NID:g205134; PIDN:AAC37656.1; PID:g205135  
 R:Yan, H.; Grossman, A.; Wang, H.; D'Eustachio, P.; Mossie, K.; Musacchio, J.M.; Sili  
 J. Biol. Chem. 268, 24880-24886, 1993  
 A>Title: A novel receptor tyrosine phosphatase-sigma that is highly expressed in the  
 A:Reference number: A49104; MUID:94043351; PMID:8227050  
 A:Accession: A49104  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-596, 'R', 598-603, 'I', 967-1788, 'G', 1790-1863 <VAN>  
 A:Experimental source: brain  
 A>Note: sequence extracted from NCBI backbone (NCBI:139669)  
 C:Superfamily: Leukocyte antigen-related protein; fibronectin type III repeat homolog  
 ogy  
 C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester  
 F:1-26/Domain: signal sequence #status predicted <SIG>  
 F:27-1863/Product: protein-tyrosine-phosphatase #status predicted <MNT>  
 F:149-209/Domain: immunoglobulin homology <IMM1>  
 F:246-300/Domain: immunoglobulin homology <IMM2>  
 F:318-400/Domain: fibronectin type III repeat homology <FN3A>  
 F:413-499/Domain: fibronectin type III repeat homology <FN3B>  
 F:511-592/Domain: fibronectin type III repeat homology <FN3C>  
 F:1244-1863/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:1331-1552/Domain: protein-tyrosine-phosphatase homology <PP1>  
 F:1504/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1510/Binding site: substrate phosphate (Arg) #status predicted  
 F:1795/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:1801/Binding site: substrate phosphate (Arg) #status predicted

## Alignment Scores:

Pred. No.:	3,44e-180	Length:	1863
Score:	2844.00	Matches:	522
Percent Similarity:	93.82%	Conservative:	40
Best Local Similarity:	87.15%	Mismatches:	37
Query Match:	44.13%	Indels:	0
DB:	2	Gaps:	0

US-09-743-492-1 (1-3467) x S46217 (1-1863)

```

QY 30 CACGCCCTGTGACCGTGGAGATGGAGCGCTCAATCAGACACCCGAGTATGGAGAC 89
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Db 1265 HisProlysaSprProvalGImetArgrgIleasnPhelnInthrProgluMetleuSer 1284

QY 90 CACCCACCATCCCATCCAGCAGCTGGCGGAGACACATCGAGCGCTCAAGCCAGCAT 149
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1285 HisProProIleProIleThrAspMetAlaGluHisMetGluArgleuAlaAsnAsp 1304

QY 150 GGCCTCAAGTCTCCAGAGATAGTCATCGACCTGGACAGCAGTTCAGCTGGAG 209
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1305 SerleuIleuSerGlnGluIleuSerIleAspProgluGlnPhenThrTrpGlu 1324

QY 210 AATCAACCTGGAGGTGAGAACAGCCCAAGACGCTATGGCATGTGATGCTGACAGC 269
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Db 1325 HisSerIleuGluAlaAsnIleuProIleAsnArgIleAlaAsnValIleAlaIleAsp 1344

QY 270 CACTCTGAGTACCTTATCTATCGATGCGCTCCCGGAGAGTACATCATATGCC 329
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1345 HisSerArgValIleleuGluProleuGluGlyIleMetGlySerAspTyrIleAsnAla 1364

QY 330 AACATACATCGATGGCTACCCGACAGAGATGCTTCATCGCAGCAGAGGCCCTGCC 389
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1365 AsnIleAlaIleValIleAlaIleValIleAlaIleValIleAlaIleValIleAlaIle 1384

QY 390 GAGACCATGGGCGATTTCTGAGATGGTGGGAGACGCGACGCGCCAGCTGGTCTAG 449
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1385 GluThrPheGlyAspPheThrPargMetValIleProgluGlnArgSerAlaThrValAlaMet 1404

QY 450 ATGACGCGGTGAGAGAAATCCCGGTAAATGTGATGACTGCTGCGCCAGCCCTGGC 509
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1405 MethIleArgleuGluGluIleuSerArgValIleLysCysAspGlnIleTyrProAsnArgIle 1424

QY 510 ACCGAGACCTGGCTTATTCAGAGTACCTGTGGACACAGTGGAGCTGGCCACATAC 569
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1425 ThrIleThrIleGlyPheIleGluValIleThrIleuAspIleMetGluIleuAlaThrPhe 1444

QY 570 ACTGTGGCAGCTTCGACCTCCACAGAGTGGCTCGAGTGAAGCGAGCTGCGTGCAG 629
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1445 CysValIleArgIlePheSerIleHisLysAsnGlySerGlnIleValArgIleValAlaArgHis 1464

QY 630 TTTTCAGTTCAGCTGGCGCCAGACCATGAGTTCCTGAGTACCCAACTCCCATCGCTGCC 689
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1465 PheIleIleThrIleAlaIleThrProAsnIleGlyValIleProgluIleTyrProIlePheIleuAla 1484

QY 690 TTTCTAGCAGCGGTCAAGGCTGCAACCCCTAGACGAGGCGCCCATGGTGGTGCATGC 749
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1485 PheIleuIleArgValIleValIleCysAsnProProAsnIleGlyProValIleAlaHisCys 1504

QY 750 AGCGGGCGGTGGGCGCGACCGGCTGCTCATGCTGATGTGATGATGATGATGATGATGATG 809
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Db 1505 SerIleAlaGlyValIleGlyThrGlyCysPheIleValIleAspAlaMetLeuGluArgIle 1524

QY 810 AAGCAGCAGAGAGCGTGCATATGACATGACGCTGACATGACGATGACGATGACGATGAC 869
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1525 ArgThrGluIleuThrIleValAlaValIleGlyHisValIleThrIleuMetArgSerGlnArgAsn 1544

QY 870 TACAATGCTGACAGCAGGAGCAGCACTACGCTTTCATCCATGAGCGCTGCTGGAGCTGCC 929

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Db 1545 TyrMetValGlnThrGluAspGluIleThrSerPheIleHisGluAlaLeuLeuGluAlaVal 1564
QY 930 ACGTGGCGCCACAGAGAGTCTGTCGCCGCAACCGTGTGGCCACATGCAGAGCTGGCC 989
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1565 GlyCysGlyAsnThrGluValIleProIleAsnSerIleuIleThrIleGlnIleuAla 1584

QY 990 CAAGTCCCTCCAGGGAGAGTGTGACCCGATGAGAGCTCGAGTTCAGTTCAGTTCGCGCCAGC 1049
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1585 GluValGluProgluGluHisValThrGluIleMetGluIleuGluPheIleArgLeuAlaSer 1604

QY 1050 TCCAAAGCCCGACAGCTCCCGCTTCATCAGCCGCAACCTGCGCTGCACAGTTCAGAGAC 1109
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1605 SerIleAlaIleThrSerArgPheIleThrIleAsnSerLeuProCysAsnIlePheLysAsn 1624

QY 1110 CGGCTGGTGAACATCATCCCTTACGAAATTCAGCCGCTGTGTGTCAGCCCATCCGATGCT 1169
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Db 1625 ArgLeuValAsnIleleuProTyrGluSerSerArgValCysLeuGlnProIleArgGly 1644

QY 1170 GTGAGGCGCTGTGACTACATCATATGCGCAGCTTCCTGTGATGCTTATAGACAGAGAGCC 1229
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Db 1645 ValGluGlySerAspTyrIleAsnAlaSerPheIleAspGlyTyrArgGlnGlnLysAla 1664

QY 1230 TACATAGCTACAGAGGCGCTCTGGCAGAGACACCGAGAGCTTCTGGCGCATGCTATGG 1289
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1665 TyrIleAlaIleThrGlnGlyProleuAlaGluIleThrThrGluAspPheThrPargAlaLeuTyr 1684

QY 1290 GAGCAATTCACCATCATCATGCTGATGCTGACCAAGCTTCGGAGATGCGAGGAGAGAA 1349
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Db 1685 GluAsnAsnSerThrIleValIleAlaMetLeuThrIleAsnArgIleGluMetGlyArgGluLys 1704

QY 1350 TGCCACGACTAGTGGCGCCAGCAGAGCGCTGCTGCTGCTACAGTACTTGTGTGGACCG 1409
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Db 1705 CysHisGlnIleTyrTrpProAlaGluArgSerAlaArgTyrGlnIlePheValIleAspPro 1724

QY 1410 ATGGCTGAGTACACATGCCCGCATATATCTCGTGTGATGCTTCAGGTACAGGATGCCCG 1469
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Db 1725 MetAlaGluTyrAsnMetProGlnIleThrIleuArgGluPheLysValIleAspAlaArg 1744

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Db 1745 AspGluIleAsnArgIleThrValIleArgIlePheIleThrIleAsnArgIleThrValIle 1764

QY 1530 CCCAAGACAGCGGAGGATTCATGACTTTCATCGGGGAGGTGATTAAGACCAAGAGACAG 1589
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Db 1785 PheGluGlnAspAlaProIleSerValHisCysSerAlaGluValIleGlyArgThrGlyVal 1804

QY 1650 TTTCACTACTGAGCATGCTGCTGAGGCGCATGGCGCTTGAAGGGGCGTGGATGATGTTT 1709
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1805 PheIleIleThrIleuSerIleValIleuGluIleuArgMetIleGlyGluGlyValIleAspIlePhe 1824

QY 1710 CAGACCGTGAAGACCTGCGCTACACAGCGCTCCGATGCTGACAGACAGAGACAGCATAT 1769
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1825 GlnThrValIleLysValIleuArgThrGlnArgProAlaMetValGlnThrGluAspGluTyr 1844

QY 1770 CAGCTGTGCTACCGTGGCGCGCTGGAGTACCTGGCAGCTTTGACACACTATGCAAGC 1826
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1845 GlnPheCysPheGlnAlaIleAlaLeuGluIleuGlySerPheAsnHisTyrAlaThr 1863

RESULT 12
A48758
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor-linked form p1 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 10-Sep-1999
R:Pan, M.G.; Rim, C.; Lu, R.P.; Florio, T.; Stork, P.J.S.
J. Biol. Chem. 268, 19284-19291, 1993
A:Title: Cloning and expression of two structurally distinct receptor-linked protein-
A:Reference number: A48758; MUID:93374907; PMID:8396131

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Db 1458 pNEGlnThrVallysalValleuArGTrnGlnArgProAlaMetValGlnThrLnuaspGlu 1477  
1767 TATCGACGCTGTACCGTCCGCGCCGAGTACCTCGCGACGCTTGACACATATCAACG 1826  
1478 TyrGlnPheCysPheGlnAlaAlaLeuGlu---LeuGlySerPheAspHisTyrAlaThr 1496

RESULT 13  
SS3089  
protein-tyrosine-phosphatase (EC 3.1.3.48) AnLAR - African malaria mosquito (fragment)  
N:Alternative names: Leukocyte antigen-related protein  
C:Species: Anopheles gambiae (African malaria mosquito)  
C:Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C:Accession: SS3089  
R:Spiers, S.  
submitted to the EMBL Data Library, March 1995  
A:Description: Anlar-a transmembrane, receptor-like protein tyrosine phosphatase from t  
A:Reference number: SS3089  
A:Accession: SS3089  
A:Molecule type: DNA  
A:Residues: 1-1231 <SPI>  
A:Cross-references: EMBL:X85217; NID:g732549; PIDN:CAA59483.1; PID:g732550  
C:Genetics:  
A:Introns: 1026/3, 1070/3, 1209/3  
C:Superfamily: Leukocyte antigen-related protein; fibronectin type III repeat homology;  
0y  
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane  
F:208-293/Domain: fibronectin type III repeat homology <3FP>  
F:619-1231/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:988-1211/Domain: protein-tyrosine-phosphatase homology <PTP>  
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F:1169/Binding site: substrate phosphate (Arg) #status predicted

Alignment Scores:  
Pred. No.: 4,74e-158 Length: 1231  
Score: 2509.00 Matches: 448  
Best Local Similarity: 87.94% Conservative: 77  
Best Percent Similarity: 75.04% Mismatches: 72  
Query Match: 38.94% Indels: 0  
DB: 2 Gaps: 0

US-09-743-492-1 (1-3467) x SS3089 (1-1231)

QY 36 TCTGACCTGTGGAGATGGGAGGCTCAACTACAGACCCAGTATGGAGACCA 95  
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QY 96 CCCATCCCCATCCAGACCTGGCGAGCAACATCGAGCGCTCAAGACCAAGATGCGCTC 155  
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QY 156 AAGTCTCCCGAGATATGATGATGCATCGACCTGGACAGCAATTCACGGGAGAAATCA 215  
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Db 675 LysPheSerGlnGluTyrLeuSerIleGluProGlyGlnGlnPheThrTTPAspHisSer 694  
QY 216 AACCTGGAGGTGACAAAGCCCAAGAACCGCTATGGCAATGTATCGCTACACACATCT 275  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 695 AsnMetGluValAsnLysPheProLysAsnArgrTyrAlaAsnValThrSerTyrAspHisSer 714  
QY 276 CGAGTCATCTTAACTCTATTCATGGCGCTCCCGGAGAGTACTACATCAATGCCAATAC 335  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 715 ArgValIleIleuProProIleGluLarGlyValProGlySerAspTyrIleAsnAlaAsnTyr 734  
QY 336 ATCGATGGCTACCCGAGACAGACAGAAATGCTTACATCGCCACGAGGCCCCCTGCCAGAC 395  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 735 CysAspGlyTyrArLysHisAsnAlaTyrValAlaThrGlnGlyProLeuGlnGluThr 754  
QY 396 ATGGCGAATTTCTGAGAGATGGTGTGGGAACAGCCACGCGACCATGTGATCATATGACA 455  
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 755 PheGlyAspPheThrPargIleMetCysTrpGluLeuLysSerSerThrIleValMetLeuThr 774  
QY 456 CGGCTGGAGGAGAACTCCCGGGTAAATGTGATCATGCTACGCGACCCGCTGGACCGAG 515

[illegible]

Db 1135 serglYnglInglypheIleasprheIleaglInvalInIstYthrIlysglInpneIly 1154  
 QY 1596 CAGGATGGGCTATGACGCTGACATGCTGGCGTGGCGGACCGGGGTTCATC 1655  
 Db 1155 GlnAspGlyProIleThrValHisCysSerAlaGlyValGlyArgThrIlyAlaPheIle 1174  
 QY 1656 ACTGAGCATGCTGGTGGAGGCAATGGCTGTAGAGGGGTGGACATGTTTCGACC 1715  
 Db 1175 ThrIleSerIleValIleuGlIuArgMetGlnTyrGlnIlyValIleuAspValPheGlnThr 1194  
 QY 1716 GTGAGACCCCTGACATGACGCGCTCTGCGATGGTGCAGACAGAGCAGCATACAGTGTG 1775  
 Db 1195 ValArgIleLeuArgSerIleArgProAlaMetValGlnThrGlnAspIleThrIlyGlnPhe 1214  
 QY 1776 TGCATACGCTGGCGCCCTGGAGTACTCGGCGAGCTTTGACCACTATGCAACG 1826  
 Db 1215 CysTyrArgAlaAlaIleuGlIuArgMetGlnTyrGlnIlyValIleuAspValPheGlnThr 1231

## RESULT 14

TDFLXK

protein-tyrosine-phosphatase (EC 3.1.3.48) DLAR precursor - fruit fly (Drosophila melanogaster)

N.Alternate names: leukocyte antigen-related protein

C.Species: Drosophila melanogaster

C.Date: 14-Dec-1990 #sequence\_revision 02-May-1994 #text\_change 22-Jun-1999

C.Accession: A36182

R.Steuli, M.; Krueger, N.X.; Tsai, A.Y.M.; Saito, H.

Proc. Natl. Acad. Sci. U.S.A. 86, 8698-8702, 1989

A.Title: A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila

A.Reference number: A36182; MUID:90046860; PMID:2554325

A.Accession: A36182

A.Molecule type: mRNA

A.Residues: 1-2029 &lt;STR&gt;

A.Cross-references: GB:M27700; MID:9157811; PIDN:AAA28668.1; PID:9157812

A.Gene: FlyBase:lar

C.Genetics:

A.Cross-references: FlyBase:FBgn0000464

C.Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

ogy

C.Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane

F.1-32/Domain: signal sequence #status predicted &lt;SIG&gt;

F.33-2029/Product: leukocyte antigen-related protein #status predicted &lt;MAT&gt;

F.33-1377/Domain: extracellular #status predicted &lt;EXT&gt;

F.50-113/Domain: immunoglobulin homology &lt;IMM&gt;

F.154-211/Domain: immunoglobulin homology &lt;IMM2&gt;

F.249-303/Domain: immunoglobulin homology &lt;IMM3&gt;

F.321-401/Domain: fibronectin type III repeat homology &lt;FN3A&gt;

F.416-502/Domain: fibronectin type III repeat homology &lt;FN3B&gt;

F.514-599/Domain: fibronectin type III repeat homology &lt;FN3C&gt;

F.610-699/Domain: fibronectin type III repeat homology &lt;FN3D&gt;

F.708-802/Domain: fibronectin type III repeat homology &lt;FN3E&gt;

F.811-896/Domain: fibronectin type III repeat homology &lt;FN3F&gt;

F.909-993/Domain: fibronectin type III repeat homology &lt;FN3G&gt;

F.1006-1091/Domain: fibronectin type III repeat homology &lt;FN3H&gt;

F.1101-1198/Domain: fibronectin type III repeat homology &lt;FN3I&gt;

F.1378-1402/Domain: transmembrane #status predicted &lt;TM&gt;

F.1403-2029/Domain: intracellular #status predicted &lt;INT&gt;

F.1417-2029/Domain: leukocyte common antigen cytosolic domain homology &lt;LAC&gt;

F.1497-1718/Domain: protein-tyrosine-phosphatase homology &lt;PTP&gt;

F.1786-2009/Domain: protein-tyrosine-phosphatase homology &lt;PTP2&gt;

F.57-111,161-209,256-301/Disulfide bonds: #status predicted

F.176/Binding site: carbohydrate (Asn) #status predicted

F.1670/Active site: Cys (phosphocysteine intermediate) #status predicted

F.1676/Binding site: substrate phosphate (Arg) #status predicted

F.1961/Active site: Cys (phosphocysteine intermediate) #status predicted

F.1967/Binding site: substrate phosphate (Arg) #status predicted

## Alignment Scores:

Align. No.: 1,29e-157 Length: 2029  
 Score: 2503.00 Matches: 447  
 Percent Similarity: 88.24% Conservative: 78  
 Best Local Similarity: 75.13% Mismatches: 70  
 Query Match: 38.84% Indels: 0  
 DB: 1 Gaps: 0

US-09-743-492-1 (1-3467) x TDFLXK (1-2029)

QY 36 TCTGACCTGTGTGAGATGCGGAGGCTCAACTACAGACCCAGATATGCGAGACACCA 95  
 Db 1433 SerAspProValAspMetArgArgIleuAspPheGlnThrProGlyIleuIleSerHisPro 1452  
 QY 96 CCCATCCCATATACCGACCTGGCGGACCAACATCGAGCGCTCAAAAGCCAAAGATGGCC 155  
 Db 1453 ProIleProIleSerGlnPheAlaAsnHisIleGlnIlyGlnIlySerAsnAspAsnGln 1472  
 QY 156 AAGTGTCCAGAGATGATGATGTCATGACCCCTGGACAGACAGTTCACGGGAGGATGCA 215  
 Db 1473 LysPheSerGlnIlyTyrIleuSerIleGlnProGlyGlnIlePheThrIlyPheAsnSer 1492  
 QY 216 AACCTGGAGTGAACAAGCCCAAGAACCCCTATGCGAATGTCAATGCTCCATGACACACT 275  
 Db 1493 AsnIleuGlnHisAsnIlySerIlyAsnAlaGlyAlaAsnValThrAlaThrAspHisSer 1512  
 QY 276 CGAGTCATCTTAACTCTATGCGATGGCTCCCGGAGTGAATCAATGCAATGCAATGCA 335  
 Db 1513 ArgValGlnIleuProAlaValGlnIlyValIlyGlySerAspTyrIleAsnAlaAsnTyr 1532  
 QY 336 ATCGATGGCTAACCGGCAAGCAAGATGCGCTACATCGCCAGCGAGGCCCTGGCCCGAGAC 395  
 Db 1533 CysAspGlyTyrArgIlyHisAsnAlaTyrValAlaThrIleuGlnIlyProIleuGlnIlyThr 1552  
 QY 396 ATGGCGGATTTGTGAGATGTGTGGGAACGCGACGCGACGCGCACTGGTGCATGATGACA 455  
 Db 1553 PheValAspPheThrArgMetCysTyrGlnIlyuIleuIlyThrAlaThrIleValMetMetThr 1572  
 QY 456 CGGCTGGAGAGAGATCCCGGGTAAATGATGATCACTGGCCAGCCGCTGGACACCGAG 515  
 Db 1573 ArgIleuGlnIlyArgThrArgThrArgIleuIlyCysAspGlnIlyTyrProThrArgGlyThrGln 1592  
 QY 516 ACGTGGGCTTATGAGTGAACCCCTGTGGAACAGTGCAGTGGCCATGACATGACTG 575  
 Db 1593 ThrTyrGlnGlnIlePheValThrIleThrGlnIlyGlnIleuAlaThrIlySerIle 1612  
 QY 576 CGCAGCTTGCACATCCCAAGAGTGGCTCAGTGAAGACCTGACGCTGCTGACTTTCAG 635  
 Db 1613 ArgThrPheGlnIleuIlyAspArgIleuIlyPheAsnAspArgArgIlyIleuGlnIleuGln 1632  
 QY 636 TTCATGCGCTGGCCAGACATGAGTGTCTGAGTACCCAACTCCATCTCGGCTTCTGA 695  
 Db 1633 PheThrAlaThrProAspHisGlyValProAspHisProAlaThrIleuGlnIlyPheIleu 1652  
 QY 696 CGACGGGTCAAGGCGCTGCAACCCCTGAAGCGAGCGCCATGGTGGCACTGCACGCG 755  
 Db 1653 ArgArgCysArgAlaIleuThrProProGlnIlySerGlyProValIleValHisCysSerAla 1672  
 QY 756 GCGGTGGCGGCGACCGGCTGTCATGATGATGATGATGATGATGATGATGATGATGATG 815  
 Db 1673 GlyValGlyArgThrIlyGlyIlyValIleValIleAspSerMetIleuIlyArgMetIly 1692  
 QY 816 GAGAGACGCTGACATCTATGCGGACGCTGACCTGATGCGATGACAGAGAACTATGAT 875  
 Db 1693 GlnTyrIleIleAspIleTyrGlnHisValThrCysIleArgAlaIleuIlyArgMetIly 1712  
 QY 876 GTGCACAGGAGAGACAGTACGATGATGATGATGATGATGATGATGATGATGATGATG 935  
 Db 1713 ValGlnThrGlnIlyProIlyThrIlePheIleHisAspAlaIleuIlyAlaIleIleCys 1732  
 QY 936 GGCACACAGAGATGCTCCCGCAACCTGATGCCACATGCCAGATGCCAGGCAAGTG 995  
 Db 1733 GlyValThrGlnValProAlaThrAsnIleuHisThrHisIleuGlnIlyIleuIleThr 1752  
 QY 996 CCTCCAGGGAGAGCTGACCGGCATGAGAGCTGAGATTAAGTTGCTGGCCAGCTCAAG 1055  
 Db 1753 GlnProGlyGlnThrIleSerIlyMetGlnValGlnPheIlyIlySerAsnValIly 1772  
 QY 1056 GCCACACGCTCCCGCTTATGACGCGCAACCTGCGCTGCAACAAGTTCAAGAACCGGCG 1115





QY	381	AAATGGGGCCCAAGTGGCTCCAGGGGAGAGTGTGACCGGCATGTGGACTGTGAGTCAAGTGC	1040
Db	1149	LysLeuMetSerLeuLeuSerGlySerAsnLeuThrLeuMetGluValGluPheLeuLys	1168
QY	1041	CTGGCCACGCTTCACAGGGCCACCGTCCCGCTTCATGAGCGCCAAACCTCGCTGCACAG	1100
Db	1169	LeuAlaAsnIleLeuThrSerSerSerGlnPheAlaSerLeuProSerAsnLys	1188
QY	1101	TTCAAGAACCGCGGTGTGAACATCATGCCCCCTACGAATTTGACCCGCTGTGTCTGCAGCCC	1160
Db	1189	PheLysAsnArgLeuValAsnIleLeuProTyrGluSerSerArgValThrLeuGlnLeu	1208
QY	1161	ATCCGTGTGTGGAGGGCTGTACTACATCAATGCCAGCTTCGTGGATGGTTATAGACAG	1220
Db	1209	IleArgGlyValAspGlySerAspTyrIleAsnAlaAsnPheIleAspGlyTyrArgTyr	1228
QY	1221	CAGAAGGCCTACATAGCTATACAGAGGGGCGCTGGCGCAGAGACCGAGACTGTCCGGCC	1280
Db	1229	LysLysAlaTyrIleAlaThrGlnGlyProLeuAlaSerThrThrGlnAspPheTrpArg	1248
QY	1281	ATGCTATGGGAGCACAATTCACCATCATCGTATGCTGACCAACCTTCGGAGATGGGC	1340
Db	1249	MetLeuTrpGlnAsnSerThrIleValValMetLeuValLysLeuArgGluMetCly	1268
QY	1341	AGGAGAAATGCCACCAGTACTGGCCAGCAGACCGCTGTCCGTACCACTATTGGT	1400
Db	1269	ArgGluLysCysLeuGlnTyrTrpProSerGluArgSerAlaArgTyrGlnTyrPheVal	1288
QY	1401	GTTGATCCCGATGGCTAGTACACATGCCCCAGTATATCTCTCGTGATTCAGAGTCAAG	1460
Db	1289	ValAspProMetValGlnTyrAsnMetProGlnTyrIleLeuArgGluPheLysValThr	1308
QY	1461	GATCCCGGGATGGGCGAGTAAAGAACAAATCCGCACTTCAGTTGACAGACTCGGCCAG	1520
Db	1309	AspAlaArgAspGlyGlnSerAlaGlyThrIleArgGlnPheGlnPheThrAspTrpProGlu	1328
QY	1521	CAGGGCTGCCCAAGACAGCGCGAGGATTCATTGACTTCATCGGCGAGTGCATAAAGC	1580
Db	1329	GlnGlyValProLysSerGlyGlnGlyPheValAspPheIleGlyGlnValHisLysThr	1348
QY	1581	AAGGACAGTTTGGACAGATGGGCTATACAGGTGCACATGCAGTGTGGCGTGGCCGC	1640
Db	1349	LysGlnGlnPheGlyGlnAspGlyProIleThrValHisCysGlyAlaGlyValSerArg	1368
QY	1641	ACGGGGGGTTCATCACTCTGAGCATCACTGCACTGCGATCGGTATGAGGGCTGTGC	1700
Db	1369	ThrIleValPheIleAlaLeuSerValValLeuGlnArgMetArgTyrGluGlyValVal	1388
QY	1701	GACATGTTTACAGACCGTGAAGACCGTCCGTACACAGCGTCTGCC-----	1745
Db	1389	AspLeuPheGlnThrValAlaLeuLeuAlaGlyThrGlnArgProCysCysValLysLeuArg	1408
QY	1746	---ATGCTGCAGACA---GAGGACCAAGTATCAAGTGTGCTACCGTGGCGCCCTGGAGTAC	1799
Db	1409	LeuGlnValGlnThrProGluAspHisTyrAlaPheCysTyrArgAlaAlaLeuGlnTyr	1428
QY	1800	CTGGCAGACTTTGACCACTATGCA	1823
Db	1429	LeuGlySerPheArgHisTyrAla	1436

Search completed: January 17, 2003, 10:15:51  
Job time : 182.5 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 17, 2003, 09:54:14 ; Search time 45.5 Seconds

(without alignments)  
6320.810 Million cell updates/sec

Title: US-09-743-492-1

Perfect score: 6444

Sequence: 1 gatccgcagctaaagactcc.....attgataatcagatttct 3467

Scoring table:  
BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame+np\_model -DEV=xlp  
-O=/cgn2.1/USPTO\_spool/US09743492/runat.17012003.093835.11506/app\_query.fasta.1.3655  
-DB=SwissProt 40 -OEMT=fastan -SUFFIX=rsp -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human0.cdi -LIST=45  
-DOCLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09743492 @CGN.1.1.72 @runat.17012003.093835.11506 -NCPU=6 -ICPU=3  
-NO\_XLPPX -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEROUT=120  
-WARN\_TIMEROUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3236	50.2	1897	1	PTPE_HUMAN
2	2826	45.4	1912	1	PTPD_HUMAN
3	2503	38.8	2029	1	LAR_DROME
4	1551	24.1	802	1	PTPA_HUMAN
5	1522	23.6	796	1	PTPA_RAT
6	1518	23.6	829	1	PTPA_MOUSE
7	1429	22.2	700	1	PTPE_HUMAN
8	1421	22.1	699	1	PTPE_MOUSE
9	1307	20.3	1452	1	PTPM_MOUSE
10	1306	20.3	1452	1	PTPM_HUMAN
11	1255	19.5	1439	1	PTPM_HUMAN
12	1243	19.3	1457	1	PTPM_MOUSE
13	1168	18.1	1445	1	PTPG_MOUSE
14	1162	18.0	1442	1	PTPG_HUMAN
15	1153.5	17.9	1430	1	PTPG_HUMAN
16	1142	17.7	1422	1	PTPG_CHICK
17	1125.5	17.5	2316	1	PTPZ_RAT
18	1117.5	17.3	2314	1	PTPZ_HUMAN

19	1089.5	16.9	1301	1	PTP9_DROME	P35832 drosophila
20	1038	16.1	1255	1	CD45_RAT	P04157 rattus norv
21	1035.5	16.1	1304	1	CD45_HUMAN	P08575 homo sapien
22	1011.5	15.7	1462	1	PTP6_DROME	P16620 drosophila
23	1004	15.6	1152	1	CD45_MOUSE	P06800 mus musculu
24	702	10.9	1711	1	PTPO_RAT	O64612 rattus norv
25	678.5	10.5	1705	1	PTPO_MOUSE	P70289 mus musculu
26	603.5	9.4	1631	1	PTP1_DROME	P35992 drosophila
27	596	9.2	1114	1	PT13_STYPL	P28205 styela plic
28	588	9.1	1238	1	PTP1_MOUSE	O64455 mus musculu
29	586	9.1	1997	1	PTP2_HUMAN	P23467 homo sapien
30	585	9.1	1337	1	PTP3_HUMAN	O12913 homo sapien
31	547.5	8.5	593	1	PTN9_HUMAN	P43378 homo sapien
32	526	8.2	593	1	PTN6_HUMAN	O06124 homo sapien
33	523	8.1	593	1	PTN6_RAT	P41499 rattus norv
34	522.5	8.1	595	1	PTN6_MOUSE	P29351 mus musculu
35	513	8.0	585	1	PTN6_MOUSE	P35235 mus musculu
36	502	7.8	595	1	PTN6_HUMAN	P29350 homo sapien
37	496.5	7.7	432	1	PTN1_RAT	P20417 rattus norv
38	496.5	7.7	845	1	CSN_DROME	P29349 drosophila
39	490.5	7.6	363	1	PTN2_RAT	P35233 rattus norv
40	490.5	7.6	415	1	PTN2_HUMAN	P17706 homo sapien
41	490	7.6	360	1	PTN7_HUMAN	P35236 homo sapien
42	489	7.6	432	1	PTN1_MOUSE	P35821 mus musculu
43	489	7.6	434	1	PTN1_CHICK	O13016 gallus gall
44	486.5	7.5	435	1	PTN1_HUMAN	P18031 homo sapien
45	485	7.5	2485	1	PTND_HUMAN	O12923 homo sapien

# ALIGNMENTS

RESULT 1  
ID PTPE\_HUMAN STANDARD; PRT; 1897 AA.  
AC P10586;  
DT 01-JUL-1989 (rel. 11, Created)  
DT 01-JUN-1989 (rel. 11, Last sequence update)  
DT 15-JUN-2002 (rel. 41, Last annotation update)  
DE LAR protein precursor (leukocyte antigen related) (EC 3.1.3.48).  
GN PTPEP OR LAR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Tonsil;  
RX MEDLINE=89035978; PubMed=2972792;  
RA Streuli M., Krueger N.X., Hall L.R., Schlossman S.F., Saito H.;  
RT "A new member of the immunoglobulin superfamily that has a  
RT cytoplasmic region homologous to the leukocyte common antigen.";  
RT J. Exp. Med. 168:1523-1530(1988).  
RN [2]  
RP MUTAGENESIS.  
RX MEDLINE=90046860; PubMed=254325;  
RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;  
RT "A family of receptor-linked protein tyrosine phosphatases in humans  
RT and Drosophila.";  
RN [3]  
RP MUTAGENESIS.  
RX MEDLINE=90316093; PubMed=1695146;  
RA Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;  
RT "Distinct functional roles of the two intracellular phosphatase like  
RT domains of the receptor-linked protein tyrosine phosphatases LCA and  
RT LAR.";  
RN [4]  
RP EMBO J. 9:2399-2407(1990).  
CC -!- FUNCTION: IT IS POSSIBLE THAT DIAR IS A CELL ADHESION RECEPTOR.  
CC IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY  
CC (PTPASE).  
CC -!- FUNCTION: THE FIRST PTPASE DOMAIN HAS ENZYMAIC ACTIVITY, WHILE  
CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE  
CC FIRST ONE.



QY 1206 GATGGTATAGACAGACAGAGAGGCTACATAGCTACACAGAGGCGCTTGACAGACAGC 1265  
 DB 1691 ASPGILYTYRARGINGLINSALATYRIEALATHGICGLYPROLEUALAGLUSERTHR 1710  
 QY 1266 GAGGACTTCTGGCGCATGCTATGGAGACAAATTCACCATCATGCTCATGCTGACCAAG 1325  
 DB 1711 GIUASPhetRPArgMetLeutRPGLIHLSAsnSerThrIleIValMetLeutRLys 1730  
 QY 1326 CTTCGGGAGATGGCGGAGAGAAATGCCACCACTACTGGCCAGACAGAGCGCTCTGCC 1385  
 DB 1731 IeuATgGluMeTcLYARgSLuLysCSYSHSgInTYTRPRoAlaGLuATgSerAlaAgy 1750  
 QY 1386 TACCACTACTTGTGTGTACCCAGAGGCTGATACAAATGATGCCAGATATCCGCGGT 1445  
 DB 1751 TYRGINTYRPhEVALValAspPROMeTALaGLUTYRAsnMeTProGInTYRIleLeuAgy 1770  
 QY 1446 GAGTTCAGAGTCACGAGATGCCGGAGTGGCGAGTCAGACAAATCCGGCAGTTCAGTTC 1505  
 DB 1771 GIuPhElySValTYRAspAlaRgAspGLYInSerArgThRIeArgInPhEgInPh 1790  
 QY 1506 ACAGACTGGCCAGACAGGCGCGTCCAGACAGAGGAGGATTCATTCATTCATCCAGG 1565  
 DB 1791 THRAsPTRPProGLInGLInLYAlProLYSThngLYGLInLYPhEILeAspPhEILeGLY 1810  
 QY 1566 CAGGTGATTAAGACCAAGAGCAGTTCGACAGATGGCGCTATCAGCGTGCATCGACT 1625  
 DB 1811 GInVALHISLYSThRLysGLInPhEgLYGLInAspGLYProIleThrVALHISCYSSer 1830  
 QY 1636 GCTGGCGTGGGCGGACCGCGGTTCATCATCTGAGCATCGTCCGTGAGCGCATCGCG 1685  
 DB 1831 ALAglYVALGLYARgThrgLYAlPhEILeThRLeUSeRIleValLeuGLuATgMeTARg 1850  
 QY 1666 TATGAGGGGCTGTGCACATGTTTCAGACCGCGTGAAGACCCCTGCTACACAGCTCTGCC 1745  
 DB 1851 TYRGInGLYVALValAspMeTPhEgInThRVALYSThLeARgThrgInARgProAla 1870  
 QY 1746 ATGGTGACAGACAGACAGTATCATGCTGTACCGCGCGCCCTGAGTACCTCGCGG 1805  
 DB 1871 MeTVALGInThrgLInAspGLInTYRGLInLeUCYSTYRArgAlaAlaLeuGLInTYRIleuGLY 1890  
 QY 1806 AGCTTTGACCACTATGCAACG 1826  
 DB 1891 SerPhEAspHISTYRAlaThR 1897  
 RESULT 2  
 PTPD\_HUMAN STANDARD: PRT; 1912 AA.  
 AC P23468;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Protein-tyrosine phosphatase delta precursor (EC 3.1.3.48) (R-PTP-delta).  
 GN PTPRD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 CC NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.  
 RX MEDLINE=95204468; PubMed=7896816;  
 RA Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;  
 RT "Molecular characterization of the human transmembrane protein-  
 RT tyrosine phosphatase delta. Evidence for tissue-specific expression of  
 RT alternative human transmembrane protein-tyrosine phosphatase delta  
 RT isoforms";  
 RT J. Biol. Chem. 270:6722-6728(1995).  
 RN [2]  
 RP SEQUENCE OF 390-1912 FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=91006018; PubMed=2170109;  
 RA Krueger N.X., Streuli M., Saito H.;  
 RT "Structural diversity and evolution of human receptor-like protein

RT tyrosine phosphatases";  
 RL EMBL J. 9:3241-33252(1990).  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: A number of isoforms are produced by  
 CC alternative splicing.  
 CC -1- PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN  
 CC FROM THE TRANSMEMBRANE SEGMENT.  
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 8 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL: L38929; AAC1749.1; -;  
 DR EMBL: X54133; CAA38068.1; -;  
 DR PIR: S12052; S12052.  
 DR HSSP: P18052; TYRO.  
 DR Genew: HGNC:9668; PTPRD.  
 DR MIM: 601598; -;  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR003962; FNIII\_repeat.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003598; Ig\_C2.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR InterPro: IPR000242; Tyr\_PP.  
 DR Pfam: PF00041; fn3; 8.  
 DR Pfam: PF00047; fn3; 3.  
 DR PRINTS: PR00102; Y\_phosphatase; 2.  
 DR PRINTS: PR00014; ENTYPFIII.  
 DR PRINTS: PR00700; PRTPHPTASE.  
 DR SMART: SM00060; FN3; 8.  
 DR SMART: SM00408; IGC2; 3.  
 DR SMART: SM00194; PTPC; 2.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE: PS50055; TYR\_PHOSPHATASE\_ptp; 2.  
 DR HydroLase: Receptor; Glycoprotein; Signal; Transmembrane; Repeat;  
 KW Immunoglobulin domain; Alternative splicing.  
 KW SIGNAL.  
 FT 1 20  
 FT CHAIN 21 1912  
 FT DOMAIN 21 1265  
 FT TRANSMEM 1266 1290  
 FT DOMAIN 1291 1912  
 FT DOMAIN 23 115  
 FT DOMAIN 118 225  
 FT DOMAIN 232 318  
 FT DOMAIN 320 414  
 FT DOMAIN 417 513  
 FT DOMAIN 516 606  
 FT DOMAIN 609 708  
 FT DOMAIN 711 822  
 FT DOMAIN 825 916  
 FT DOMAIN 918 1017  
 FT DOMAIN 1020 1137  
 FT DOMAIN 1375 1618  
 FT DOMAIN 1619 1912  
 FT ACT\_SITE 1553 1553  
 FT ACT\_SITE 1844 1844  
 FT SITE 1175 1178  
 FT CARBOHYD 254 254  
 FT CARBOHYD 289 289  
 FT CARBOHYD 724 724  
 FT CARBOHYD 832 832  
 FT VARSPPLIC 181 189  
 FT VARSPPLIC 226 229  
 FT -----  
 CC CLEAVAGE (POTENTIAL).  
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC MISSING (IN KIDNEY ISOFORM).  
 CC MISSING (IN KIDNEY ISOFORM).

FT VARSPLIC 775 783 MISSING (IN KIDNEY ISOFORM).  
FT VARSPLIC 609 1137 MISSING (IN FETAL BRAIN ISOFORM).  
FT MUTAGEN 1178 1178 R->A: 2.5-FOLD REDUCTION IN CLEAVAGE.  
SQ SEQUENCE 1912 AA; 214759 MW; 3AE8BCBD32182E26 CRC64;

## Alignment Scores:

Pred. No.: 5.63e-168 Length: 1912  
Score: 2926.00 Matches: 538  
Percent Similarity: 95.99% Conservative: 37  
Best Local Similarity: 89.82% Mismatches: 24  
Query Match: 45.41% Indels: 0  
DB: 1 Gaps: 0

US-09-743-492-1 (1-3467) x FRPD\_HUMAN (1-1912)

QY 30 CACTCTCTGACCCCTGTGAGATGCGAGGCTCACTACAGACCCCAAGTATGCGAGAC 89  
DB 1314 HisprothrraprrprovalGluLeuuarGargLeuasnphneGlnThrProGlyMetAlaSer 1333  
QY 90 CACCCACCCATCCCATACCCGACCTGGCGGACAAACATGAGCGGCTCAAAACCAACGAT 149  
DB 1334 HisprothrraprrprovalGluLeuuarGargLeuasnphneGlnThrProGlyMetAlaSer 1333  
QY 150 GGCCTCAAGTCTCCAGAGATGATGTCATCCAGCCTGGAGACAGATGTCACGTGGAG 209  
DB 1354 AsnLeuLysPheSerGlnGluThrGlnSerLeuAspProGlyGlnGlnPheThrTrpGlu 1373  
QY 210 AATTCAAACCTGAGAGTGAACAGACCCCAAGAACCCGATGCGAATGTCATGCGCTACGAC 269  
DB 1374 HisSerAsnLeuGluValAsnLysProLysAsnArgTyrrAlaAsnValIleAlaTyrrasp 1393  
QY 270 CACTCTGAGTATCTTAACTCTATGATGAGCGCTCCCGGAGTGACTATCAATGCC 329  
DB 1394 HisSerArgValLeuLeuSerAlaIleGluGlyLeuProGlySerAspTyrrValAsnAla 1413  
QY 330 AACTACATGATGGTGTACGAGAGCAAGATGCTACATGCGCAGGAGGCCCTGGCC 389  
DB 1414 AsnTyrrIleAspGlyTyrrArgLysGlnAsnAlaTyrrIleAlaThrGlnGlySerLeuPro 1433  
QY 390 GAGACGATGGCGATTTCTGAGATGCTGTGGAACAGCGCAGCGCAGCTGTGTCATG 449  
DB 1434 GluThrPheGlyAspPheThrArgMetIleThrGlnGlnArgSerAlaThrValIleMet 1453  
QY 450 ATGACAGCGGTGAGAGAGAGCTCCGGGTAAATGTATGATGACTGGCCAGCCGCTGAC 509  
DB 1454 MetThrLysLeuGlnGluThrArgSerArgValLysCysAspGlnTyrrProSerArgGly 1473  
QY 510 ACCGACACCTGTGGCTTATGATGAGCGCTGTGACAGACAGTGGAGCTGCCACATAC 569  
DB 1474 ThrGluThrHisGlyLeuValGlnValIleThrLeuAspThrValGluLeuAlaThrTyrr 1493  
QY 570 ACTGTGCGACCTTTCGACCTCCACAAAGATGCTCCAGTGAAGAGCGTGAAGCTGGCTAG 629  
DB 1494 CysValAlaGlnThrPheAlaLeuTyrrLysAsnGlySerSerGlnLysArgGluValArgGln 1513  
QY 630 TTTCAGATTCAGCGCTGGCGCAGACCATGAGTCTCTGAGTAAACCAATCCATCCTGGCC 689  
DB 1514 PheGlnPheThrAlaThrProAspHisGlyValProGlnHisProThrProPheLeuAla 1533  
QY 690 TTTCAGAGAGGAGTCAAGCGCTGCAACCCCTAGACGAGGCGCCATGAGTGGTGACAGC 749  
DB 1534 PheLeuAlaGlyValLysThrCysAsnProProAspAlaGlyProMetAlaValHisCys 1553  
QY 750 AGCGCGGCGTGGCGCGACCGGCTTTCATCGTATGATGATGATGATGATGATGATGATG 809  
DB 1554 SerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeuGlnArgGlyIle 1573  
QY 810 AAGACAGAAAGAGCGTGGAGCATGTATGGCCAGCTGACCTGCATGCGATCAACAGAGAAC 869  
DB 1574 LysHisGlyLysThrValAspIleTyrrGlyHisValIleThrLeuMetArgAlaGlnArgAsn 1593  
QY 870 TACATGGTGCAGAGGAGGACCATGAGTCTTTCATCGATGAGCGGCTGTGAGGCTGCC 929  
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DB 1594 TyrMetValGlnThrGluAspGlnTyrrIlePheIleHisAspAlaLeuGlnAlaVal 1613  
QY 930 AGCTGCGGCGACACAGAGAGTGGCTGCCCAACTGTATGCCACATCCAGAGCTGGCG 989  
DB 1614 ThrCysGlyAsnThrGluValProAlaArgAsnLeuTyrrAlaTyrrIleGlnLysLeuThr 1633  
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DB 1634 GlnIleGluThrGlyGluAsnValThrGlyMetGluLeuGluPheLysArgLeuAlaSer 1653  
QY 1050 TCCAAAGGCCACAGCGTCCCGCTTCATCCAGCGGCAACCTCCCTGCAACAGTTCAAAGAC 1109  
DB 1654 SerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLysAsn 1673  
QY 1110 CGGCTGTGAACATGATGCGCTTACGAATTGACCCCTGTGTCTGCACGCCATCCGTGGT 1169  
DB 1674 ArgLeuValAsnIleMetProTyrrGlnSerThrArgValCysLeuGlnProIleArgGly 1693  
QY 1170 GTGAGGCGCTGACTATCATATGCCAGCTTCTGGATGTTATAGACAGAGAGGCC 1229  
DB 1694 ValGluGlySerAspTyrrIleAsnAlaSerPheIleAspGlyTyrrArgGlnGlnLysAla 1713  
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QY 1710 CAGACCGTGAAGACCTTGCCTGACAGCGCTGCTGCATGCTGTCACAGAGAGACAGATAT 1769  
DB 1874 GlnThrValLysMetLeuArgThrGlnArgProAlaMetValGlnThrGlnLysPheGln 1893  
QY 1770 CAGCTGTGCTACCGTGGCGCGCTGTGAGTACCTGCGAGCTTGGACCATATGACAG 1826  
DB 1894 GlnPheSerTyrrArgAlaIleValLeuGlnTyrrLeuGlnLysPheAspHisTyrrAlaThr 1912

RESULT 3  
LAR\_DROME STANDARD: PRT: 2029 AA.  
AC PI6621:  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Protein-tyrosine phosphatase Lar precursor (EC 3.1.3.48) (Protein-tyrosine-phosphate phosphohydrolase) (DLAR).  
GN Lar.  
OS Drosophila melanogaster (Fruit fly).

CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxId=7227;  
RN [1]  
RP MEDLINE=90046860; PubMed=2554325;  
RX Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;  
RA "A family of receptor-linked protein tyrosine phosphatases in humans  
RT and Drosophila.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Cañton-S;  
RX MEDLINE=96178473; PubMed=8598047;  
RA Krueger N.X., Van Vactor D., Wan H.I., Gelbart W.M., Goodman C.S.,  
RT Saito H.;  
RT "The transmembrane tyrosine phosphatase DLAR controls motor axon  
RT guidance in Drosophila.";  
RL Cell 84:511-622(1996).  
CC -I- FUNCTION: IT IS POSSIBLE THAT DLAR IS A CELL ADHESION RECEPTOR.  
CC IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY  
CC (PTPASE). IT CONTROLS MOTOR AXON GUIDANCE.  
CC -I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
CC tyrosine + phosphate.  
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -I- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED IN A SUBSET OF AXONS AND  
CC PLURIPUR NEURONS IN THE EMBRYO.  
CC -I- SIMILARITY: CONTAINS 9 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
CC -I- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.  
CC -I- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
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CC EMBL: M27700; AAA28668.1; -;  
CC EMBL: U36857; AAC47002.1; -;  
CC EMBL: U36849; AAC47002.1; JOINED.  
CC EMBL: U36850; AAC47002.1; JOINED.  
CC EMBL: U36851; AAC47002.1; JOINED.  
CC EMBL: U36852; AAC47002.1; JOINED.  
CC EMBL: U36853; AAC47002.1; JOINED.  
CC EMBL: U36854; AAC47002.1; JOINED.  
CC EMBL: U36855; AAC47002.1; JOINED.  
CC EMBL: U36856; AAC47002.1; JOINED.  
CC PIR: A36182; TDFELK.  
CC HSSP: P28827; IRPM.  
CC FLYBase: FBgn00000464; lar.  
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CC InterPro: IPR004086; FN\_III\_repeat.  
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CC InterPro: IPR004104; FN\_III\_repeat.  
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CC InterPro: IPR004106; FN\_III\_repeat.  
CC InterPro: IPR004107; FN\_III\_repeat.  
CC InterPro: IPR004108; FN\_III\_repeat.  
CC InterPro: IPR004109; FN\_III\_repeat.  
CC InterPro: IPR004110; FN\_III\_repeat.  
CC InterPro: I

FT	CHAIN	33	2029	PROTEIN-TYROSINE PHOSPHATASE LAR.
FT	DOMAIN	33	1377	POTENTIAL.
FT	DOMAIN	1378	1402	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	1403	2029	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	50	118	IG-LIKE C2-TYPE DOMAIN 1.
FT	DOMAIN	154	216	IG-LIKE C2-TYPE DOMAIN 2.
FT	DOMAIN	249	308	IG-LIKE C2-TYPE DOMAIN 3.
FT	DOMAIN	320	417	FIBRONECTIN TYPE-III 1.
FT	DOMAIN	418	512	FIBRONECTIN TYPE-III 2.
FT	DOMAIN	513	607	FIBRONECTIN TYPE-III 3.
FT	DOMAIN	608	706	FIBRONECTIN TYPE-III 4.
FT	DOMAIN	707	809	FIBRONECTIN TYPE-III 5.
FT	DOMAIN	810	906	FIBRONECTIN TYPE-III 6.
FT	DOMAIN	907	1007	FIBRONECTIN TYPE-III 7.
FT	DOMAIN	1008	1102	FIBRONECTIN TYPE-III 8.
FT	DOMAIN	1103	1207	FIBRONECTIN TYPE-III 9.
FT	DOMAIN	1492	1738	PROTEIN-TYROSINE PHOSPHATASE 1.
FT	DOMAIN	1781	2029	PROTEIN-TYROSINE PHOSPHATASE 2.
FT	ACT_SITE	1670	1670	BY SIMILARITY.
FT	ACT_SITE	1961	1961	POTENTIAL.
FT	DISULFID	57	111	POTENTIAL.
FT	DISULFID	161	209	POTENTIAL.
FT	DISULFID	256	301	POTENTIAL.
FT	CARBOHYD	176	176	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	253	253	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	298	298	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	553	553	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	616	616	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	666	666	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	721	721	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	774	774	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	915	915	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	962	962	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1183	1183	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1304	1304	N-LINKED (GLCNAC. .) (POTENTIAL).
SQ	SEQUENCE	2029	AA: 229027	MF: 536A0C794D3D800 CRC64:

Alignment Scores:

Pred. No.:	1,28e142	Length:	2029
Score:	2503.00	Matches:	447
Percent Similarity:	88.24	Conservative:	78
Best Local Similarity:	75.13	Mismatches:	70
Query Match:	38.848	Indels:	0
DB:	1	Gaps:	0

US-09-743-492-1 (1-3467) x LAR\_DROME (1-2029)

QY	36	TCGACCTGTGGAGATGGCGGAGGCTTA	CTACCTACCAAGCCCAAGTGTGGCAAC	CCACCA	95
Db	1433	SetisprproValAspMetAdgAdgLeuAsnPrbGlnThrProDilYmetLeuSerHisPro			1455
QY	96	CCCATCCCAATACCGACCTGGCGGAGCAACATCGACGGCTCCAAAGCCAAACATGGGCTC			155
Db	1453	ProIleProIleSerGluPheMetAlaAsnHisIleGluAdgLeuYSerHisPsrnsnGln			1473
QY	156	AAGTTTCCCAAGAGTATGATCCATCGACCCCTGGACACAGACTTCACTGCGGAATTCA			215
Db	1473	LysPheSerGlnGluTyrGlnSerIleGluProGlnYglnGlnPheThrTrpAspSer			1493
QY	216	AACTGGGGGAGCAACGACCCCAAGACCCGATGGCAATGTCAATGCCCTACGACACACT			275
Db	1493	AsnLeuGlnHisAsnYsSerLysAsnAdgTyrAlaAsnValThrAlaTyrAspHisSer			1512
QY	276	CGAGTCATCCTTACCTTATTCATGCATGGCGTCCCGGAGTAGCTACTCAATGCCAATAC			335
Db	1513	ArgValAlaGlnLeuProAlaValGlnGluYValAlaGlySerAspTyrIleAsnAlaSer			1533
QY	336	ATGCATGGCTACCGCAGGACGCAAGTAAGCTCAATATGCCACGACGAGGCCCTGTGCCAGACC			395
Db	1533	CysAspGluTyrAdgYsHisAsnAlaTyrValAlaIleThrGlnGluYProLeuGlnGlnThr			1555
QY	396	ATGGGCATTTCTCGAACAATGTGTGGGAACACGACGCGCACTGTGCTCATGTATGCA			455



Db 1553 PheValAspPheThrArgMetCysTrpLeuLysThrAlaThrIleValMetMetThr 1572  
 QY 456 CGGGTGGAGAGAAATCCCGGGTAAATGTGATCAGTACTGGCCAGCCCTGGACCCAG 515  
 Db 1573 ArgLeuGluGluArgThrArgIleLysCysAspGlnTrpProThrArgGlyThrGlu 1592  
 QY 516 ACCTGTGGCCCTTATTCAGGTGACCCCTGTGGACACAGTGGACCTGGCCACATACACTGTG 575  
 Db 1593 ThrTrpGlyGlnIlePheValThrIleThrGlnIleThrGlnIleValAlaThrTyrSerIle 1612  
 QY 576 CGCACCTTCGGACCCACAGAGTGGCTCCAGTGGAGAGCGGAGCTCCGTCAGTTTAG 635  
 Db 1613 ArgThrPheGlnIleCysArgGlnIlePheAsnAspArgGluIleLysGlnLeuGln 1632  
 QY 636 TTCATGGCTGGCCAGACCATGAGTTCCTGATGATCCACATCCCATCTGGCTTCCTTA 695  
 Db 1653 PheThrAlaTrpProAspHisGlyAlaProAsnHisProAlaProPheLeuGlnPheLeu 1652  
 QY 696 CGAGCGGTCAAGGCTCCAGACCCCTAGACGAGGCGCCATGGGTGGTCCACTGACGGCG 755  
 Db 1653 ArgArgCysArgAlaLeuThrProProGluSerGlyProValIleValHisCysSerAla 1672  
 QY 756 GGGCGGGGGCCGACCGGCTGTCATGCTGATGATGATGATGATGATGATGATGATGATGAT 815  
 Db 1673 GlyValGlyArgThrGlyCysTrpIleValIleAspSerMetLeuGluArgMetLysHis 1692  
 QY 816 GAGAAGAGCGTGGACATGATGAGCCAGCTGACATGATGATGATGATGATGATGATGATGAT 875  
 Db 1693 GluLysIleIleAspIleTyrGlyHisValThrCysLeuArgAlaGlnArgAsnTyrMet 1712  
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 QY 1416 GAGTACAAATGCCCCAGTATATCTGCGTGAAGTTCAGATGATGATGATGATGATGATGATGAT 1475  
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 QY 1476 CAGTCAAGGACAAATCCGGCACTTCAGTTCACAGACTGGCCAGAGCGGCTGGCCACAG 1535  
 Db 1913 SerSerArgThrValArgGlnPheGlnIleAspTrpProGlnGlnGlyValProLys 1932

QY 1536 ACAGCGAGGGATTCATTGACTTTCATCGGCGAGTGCATTAAGACCCAGAGCGATTGGA 1595  
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 QY 1596 CAGCATGGCCCTATACGCTGACCTGACAGTGTGCTGGCGCGCCGACCGGGGTTCATC 1655  
 Db 1953 GlnAspGlyProIleThrValHisCysSerAlaGlyValGlyArgSerGlyValPheIle 1972  
 QY 1656 ACTGTGACATGCTGCTGGAGCGCATGCGCTATGAGGGCGGTGTCGACATGTTTCAGACC 1715  
 Db 1973 ThrLeuSerIleValIleLeuGluTrpMetGlnTyrGlnGlyValLeuAspValPheGlnThr 1992  
 QY 1716 GTGAAGACCTGCGTACACAGCGCTCCGATGTCAGACAGACAGACAGACAGTTCAGCTG 1775  
 Db 1993 ValArgIleLeuArgSerGlnArgProAlaMetValGlnThrGlnAspGlnTyrHisPhe 2012  
 QY 1776 TGCTACCGTGGCGCCCTGGAGTACTCGGCGACCTTGACCACTAT 1820  
 Db 2013 CysTyrArgAlaAlaIleuGluLysIleuGlySerPheAspAsnTyr 2027  
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 PTR\_A\_HUMAN STANDARD: PRT: 802 AA.  
 AC P18433; Q14513;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Protein-tyrosine phosphatase alpha precursor (EC 3.1.3.48) (R-PTP-  
 alpha)  
 GN PTR\_A OR PTR\_A.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90349565; PubMed=2166945;  
 RA Sap J., D'Eustachio P., Givol D., Schlessinger J.;  
 RT "Cloning and expression of a widely expressed receptor tyrosine  
 phosphatase";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6112-6116(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90384936; PubMed=2169617;  
 RA Kaplan R., Morse B., Huebner K., Croce C., Hawk R., Ravera M.,  
 RA Ricca G., Jaye M., Schlessinger J.;  
 RT "Cloning of three human tyrosine phosphatases reveals a multigene  
 family of receptor-linked protein-tyrosine-phosphatases expressed in  
 brain";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7000-7004(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91006018; PubMed=2170109;  
 RA Krueger N.X., Streuli W., Saito H.;  
 RT "Structural diversity and evolution of human receptor-like protein  
 tyrosine phosphatases";  
 RL EMBO J. 9:3241-3252(1990).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Kidney;  
 MEDLINE=91088320; PubMed=2175890;  
 RA Ohagi S., Nishi M., Steiner D.F.;  
 RT "Sequence of a cDNA encoding human LRP (Leukocyte common antigen-  
 related peptide).";  
 RL Nucleic Acids Res. 18:7159-7159(1990).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91032191; PubMed=2172030;  
 RA Jirik F.R., Janzen N.M., Melhado I.G., Harder K.W.;  
 RT "Cloning and chromosomal assignment of a widely expressed human  
 receptor-like protein-tyrosine phosphatase.";  
 RL FEBS Lett. 273:239-242(1990).



Db 436 GlyAlaIleValIleHisCysSerAlaGlyValGlyArgThrGlyThrPheValValIle 455  
 QY 789 GATGCCATGTGGAGCGGATGAAGCAGAGAGAGAGAGAGAGATGATGAGCAGCTGAC 848  
 Db 456 AsplAmLeuAspMetMetHisThrGluArgLysValAspValThrGlyPheValSer 475  
 QY 849 TGCATGCATACAG 908  
 Db 476 ArgIleArgAlaGlnArgCysGlnMetValGlnThrAspMetGlnThrValPheIleArg 495  
 QY 909 GAGGCGGTGGAGCGGTGGAGCGGTGGAGCGGTGGAGCGGTGGAGCGGTGGAGCGGT 968  
 Db 496 GlnAlaLeuLeuGlnHisThrLeuThrLeuThrGlnLeuValThrSerLeuGln 515  
 QY 969 GCCACATCATCAG 1028  
 Db 516 ThrHisLeuGlnLysIleThrAsnLysIleProGlyThrSerAsnAsnGlnLysLeu 535  
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 Db 536 GluPheLysLysLeuThrSerIleLysIleGlnAsnAspLysMetArgThrGlyAsnLeu 555  
 QY 1089 CCGTCGACAG 1148  
 Db 556 ProAlaSerMetLysLysAsnArgValLeuGlnIleIleProGlyThrPheAsnArgVal 575  
 QY 1149 TGCTGCGAGCCATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1208  
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 QY 1209 GGTATATACAGCAG 1268  
 Db 596 GlyThrArgGlnLysAspSerThrIleAlaSerGlnGlyProLeuLeuHisThrIleGln 615  
 QY 1269 GACTTGGCGGAG 1328  
 Db 616 AspPheThrArgMetIleThrPheLysLysGlnLysGlnLysGlnLysGlnLys 635  
 QY 1329 CGGAG 1388  
 Db 636 GluGluArgGlnLysGlnLysGlnLysGlnLysGlnLysGlnLysGlnLys 655  
 QY 1389 CAGTACTTGTGTTGACCCGATGCTGATGATGATGATGATGATGATGATGATGAT 1448  
 Db 656 GlyAspIleThrValGlnLeuLysLysGlnLysGlnLysGlnLysGlnLys 675  
 QY 1449 TTCAAGGTCAG 1508  
 Db 676 LeuLeuValThrAspThrArgGlnLysLysSerArgGlnIleArgGlnPheHisPheHis 695  
 QY 1509 GACTGCGCAG 1568  
 Db 696 GlyThrProGlnValGlyIleProSerAspLysGlnLysGlnLysGlnLys 715  
 QY 1569 GTGCATATAGACCAAG 1628  
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 QY 1629 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1688  
 Db 735 GlyAlaGlyArgThrGlyThrPheCysAlaLeuSerThrValLeuGlnArgValLysAla 754  
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 QY 1749 GTGCAG 1808  
 Db 775 ValGlnThrLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 794  
 QY 1809 TTTCAGCAGATGCA 1823  
 Db 795 PheSerAspThrAla 799

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 AC 003348:  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Protein-tyrosine phosphatase alpha precursor (EC 3.1.3.48) (R-PTP-  
 alpha).  
 GN PRPRA OR LRP.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=93038682; PubMed=1417854;  
 RA Moriyama T., Fujiwara Y., Imai E., Takenaka M., Kawanishi S.,  
 RT Inoue T., Noguchi T., Tanaka T., Kamada T., Ueda N.;  
 RT "cDNA cloning of rat LRP, a receptor like protein tyrosine  
 RT phosphatase, and evidence for its gene regulation in cultured rat  
 RT mesangial cells.";  
 RL Biochem. Biophys. Res. Commun. 188:34-39(1992).  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.  
 CC  
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 CC  
 CC EMBL: L01702; AAA1983.1; -;  
 DR HSSP: P18052; IYPO.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR InterPro: IPR000242; TYR\_PP.  
 DR Pfam: PF00102; Y-phosphatase; 2.  
 DR PRINTS: PR00700; PRTPHPTASE.  
 DR SMART: SM00194; PTPC; 2.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE: PS00555; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Glycoprotein; Transmembrane; Hydrolase; Phosphorylation; Repeat;  
 KW Signal.  
 FT SIGNAL. 1 19  
 FT CHAIN 20 796  
 FT DOMAIN 20 145  
 FT TRANSMEM 146 169  
 FT DOMAIN 170 796  
 FT DOMAIN 234 494  
 FT DOMAIN 495 796  
 FT ACT\_SITE 436 436  
 FT ACT\_SITE 726 726  
 FT CARBOHYD 20 20  
 FT CARBOHYD 21 21  
 FT CARBOHYD 47 47  
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Alignment Scores: 6,66e-84 Length: 796  
 Pred. No.: 1522.00 Matches: 294  
 Score:





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QY 801 GAGGGATGAAAGCAGACAGAGGCTGGACATCTATGGCCAGCGTGCATGGCATCA 860
Db 487 AspmethcHissergluArgLysValAlaSprValTyrGlyPheValSerArgLLeuAla 506
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Db 507 GlnArgGysGlnMetValGlnThrAspMetGlnTyrValPheLleTyrGlnAlaLeu 526
QY 921 GAGCTGCCAGCTGGCCGACACAGAGGTGCTGCCGACCTGTATGCCCATTCAG 980
Db 527 GlnHisTyrLeuTyrGlnAspThrGlnLeuGlnValThrSerLeuGlnThrHisLeuGln 546
QY 981 AAGCTGGGCGCAAGTCCCTCCAGGGGAGAGTGTGACCGCCATGGACCTGAGTCAAGTTG 1040
Db 547 LysLleTyrAsnLysLleProGlyThrSerAsnAsnGlyLeuGlnGlnPheLysLys 566
QY 1041 CTGGCCAGCTCCAGAGCCGACACAGCTCCGCTTCATCAGCCGACCTCCCTGCAACAG 1100
Db 567 LeuThrSerLleLysLleGlnAsnAspLysMetArgThrGlyAsnLeuProAlaAsnMet 586
QY 1101 TTCAGAACCGGCTGGTGACATCATGCGCTACAGATTGACCGCTGTCTGTCGAGCC 1160
Db 587 LysLysAsnArgValLeuGlnLleLeuProTyrGlnPheAsnArgValLleLeuProVal 606
QY 1161 ATCGGTGTGTGGAGGGCTGACTACATCATGCGCTTCCTGGATGGTTATGACAG 1220
Db 607 LysArgGlyGlnGlnAsnThrAspTyrValAsnAlaSerPheLleAspLleTyrArgL 626
QY 1221 CAGAGAGCGCTACATAGCTACAGAGGCGCTGCGACAGACAGCGAGACTTCTGGAGC 1280
Db 627 LysAspSerTyrLleAlaSerGlnGlyProLeuLeuHisThrLleGlnAspPheThrArg 646
QY 1281 ATGCTAGGAGACAAATTCACATCATGCTGATGCTGACCAAGCTTGGAGATGGGC 1340
Db 647 MetLleArgLleTyrLysSerCysSerLleValMetLeuThrGlnLeuGlnArgLys 666
QY 1341 AGGGAAGATGCCACCGCTACTGAGCGGACAGAGCGCTGCTGCTGCTACAGACTTGT 1400
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QY 1461 GATGCCGGGATGGGAGCTCAAGGACAAATCCGCGAGCTTCAGTTCACAGACTGGCCAGAG 1520
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QY 1521 CAGGGCGTGGCCCAAGACAGAGGAGGATTCATGACTTCAGCGGCGAGCTGATCAAGACC 1580
Db 727 ValGlyLleProSerAspLysGlnMetLleAsnLleLleAlaValAlaGlnLysGln 746
QY 1581 AAGGAGCAGTTTGGACAGAGATGGGCTATCAACGCTGACAGTGCAGTGGCGGGCGC 1640
Db 747 GlnGlnGlnInsery---AsnHisProLleThrValHisCysSerAlaGlyAlaGlyArg 765
QY 1641 ACCGGGGTTCATCATCTATCAGCATGCTGCTGAGAGCCGATGAGGCGCTGGCTG 1700
Db 766 ThrLysThrPheCysAlaLeuSerThrValLeuGlnArgValLysAlaGlnGlyLleLeu 785
QY 1701 GACATGTTTGGACGAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1760
Db 786 AspValPheGlnThrValLysSerLeuArgLeuGlnArgProHisMetValGlnThrLeu 805
QY 1761 GACCAAGTATCACTGTGCTACCGTGGCGGCGCTGAGTACCTGCGAGCTTTCACCACTAT 1820
Db 806 GlnGlnTyrGlnPheCysTyrLysValValGlnGlnTyrTTrLeuAspAlaPheSerAspTyr 825
QY 1821 GCA 1823
Db 826 Ala 826

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RESULT 7
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ID PRPE_HUMAN STANDARD: PRT: 700 AA.
AC P23469.
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase epsilon precursor (EC 3.1.3.48) (R-PTP-
DE epsilon).
GN PRPE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=9106018; PubMed=2170109;
RA Krueger N.X., Streuli M., Saito H.;
RT "Structural diversity and evolution of human receptor-like protein
RT tyrosine phosphatases."
RL EMBL J. 9:3241-3252(1990).
CC -1 CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1 SUBCELLULAR LOCATION: Type I membrane protein.
CC -1 SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
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DR EMBL: X54134; CAA38069.1; -.
DR PIR: S12053; S12053.
DR HSSP: P18052; 1YRO.
DR GeneW: HGNC:9669; PTPRE.
DR MIM: 600926; -.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00102; Y_phosphatase.
DR PRINTS: PR00700; PTPPHPTASE.
DR SMART: SM00194; PTPc: 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Transmembrane; Hydrolase; Phosphorylation; Repeat;
KW signal.
FT SIGNAL 1..19
FT CHAIN 20..700 POTENTIAL.
FT DOMAIN 20..46 PROTEIN-TYROSINE PHOSPHATASE EPSILON.
FT DOMAIN 47..69 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 70..700 POTENTIAL.
FT DOMAIN 154..393 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 394..700 PROTEIN-TYROSINE PHOSPHATASE 1.
FT DOMAIN 335..335 PROTEIN-TYROSINE PHOSPHATASE 2.
FT ACT_SITE 630..630 BY SIMILARITY.
FT ACT_SITE 23..23 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 30..30 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 30..30 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 700 AA; 80641 MW; D096BDADEA5708 CnC64;
Alignment Scores:
Pred. No.: 2,44e-78 Length: 700
Score: 1429.00 Matches: 284
Percent Similarity: 64.82% Conservative: 103
Best Local Similarity: 47.57% Mismatches: 200
Query Match: 22.18% Indels: 10
DB: 1 Gaps: 5
US-09-743-492-1 (1-3467) x PRPE_HUMAN (1-700)

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RL	Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN-C57BL/6; TISSUE=Brain, and Lung;
RA	Hou E.W., Li S.L.;
RL	submitted (JUN-1996) to the EMBL/Genbank/DDBJ databases.
RN	[4]
RP	*SEQUENCE OF 224-332 FROM N.A.
RC	STRAIN-BALB/c; TISSUE=Brain;
RX	MEDLINE=93086603; PubMed=1454056;
RA	Schepens J., Zeeuwen P., Wieringa B., Hendriks W.;
RT	"Identification and typing of members of the protein-tyrosine phosphatase gene family expressed in mouse brain.";
RL	Mol. Biol. Rep. 16:241-248(1992).
RN	[5]
RP	SEQUENCE OF 224-332 FROM N.A.
RC	STRAIN-BALB/c; TISSUE=Brain;
RX	MEDLINE=95134232; PubMed=7832766;
RA	Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.;
RT	"A novel receptor-type protein tyrosine phosphatase with a single catalytic domain is specifically expressed in mouse brain.";
RL	Biochem. J. 305:499-504(1995).
CC	-I CATALYTIC ACTIVITY: protein tyrosine phosphate + H(2O) = protein tyrosine + phosphate.
CC	-I SUBCELLULAR LOCATION: Type I membrane protein.
CC	-I SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
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CC	-----
DR	EMBL; U35368; AAC52281.1; -
DR	EMBL; D83484; BA011927.1; -
DR	EMBL; U62387; AAB04553.1; -
DR	EMBL; Z23052; CAAB0587.1; -
DR	EMBL; Z23053; CAAB0588.1; -
DR	HSSP; P18052; LYFO.
DR	MGI; MGI:97813; Ptprc.
DR	InterPro; IPRO00387; TYR_phosphatase.
DR	InterPro; IPRO00242; TYR_PP.
DR	Pfam; PF00102; Y_phosphatase; 2.
DR	PRINTS; PR00700; PTYPHPHPTASE.
DR	SMART; SM00194; PTRC; 2.
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR	PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR	PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW	Glycoprotein; Transmembrane; Hydrolase; Phosphorylation; Repeat; Signal.
FT	SIGNAL 1 19 POTENTIAL.
FT	CHAIN 20 699 PROTEIN-TYROSINE PHOSPHATASE EPSILON.
FT	DOMAIN 20 45 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 46 68 POTENTIAL.
FT	DOMAIN 69 699 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 153 392 PROTEIN-TYROSINE PHOSPHATASE 1.
FT	DOMAIN 393 699 PROTEIN-TYROSINE PHOSPHATASE 2.
FT	ACT_SITE 334 334 BY SIMILARITY.
FT	ACT_SITE 629 629 BY SIMILARITY.
FT	CARBOHYD 23 23 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD 31 31 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CONFLICT 500 500 G -> A (IN REF. 2).
FT	CONFLICT 506 506 G -> V (IN REF. 2).
FT	CONFLICT 521 522 IV -> ML (IN REF. 2).
FT	CONFLICT 606 606 M -> I (IN REF. 1).
SO	SEQUENCE 699 AA; 80645 MW; 4D04467438017FEBCRC64;
Alignment Scores:	
Pred. No.:	7.35e-78 Length: 699
Score:	1421.00 Matches: 281
Percent Similarity:	64.49% Conservative: 104

Best Local Similarity:	47.07%	Mismatches:	202
Query Match:	22.05%	Indels:	10
Dr:	1	Gaps:	4
US-09-743-492-1 (1-3467) x PTPF_MOUSE (1-699)			
QY	60	CTCAACATACCAAGACCCCGATATGCGAGACACCCACCCATCCCATCCACGACCTTGGCG	119
Db	101	LeuSerArgSerProSerGlyProLysLysPhePheProIleProValGluHisLeuGlu	120
QY	120	GACAAACATCGAGCCGCTTAAGACCAACAGATGGCTCAAGTTCTCCAGAGATGTAGCTCC	179
Db	121	GluGluIleArgValArgSerAlaAspAspLysArgPheArgGluGluPheAsnSer	140
QY	180	ATCGACCCCTGGACAG---CAGTTACGCGGGAGAAATTCAAACCTGGAGGAGCAAGACCC	236
Db	141	LeuProSerGlyHisIleGlnGlyThrPheGluLeuValAsnLysGluGluAsnArgGlu	160
QY	237	AAGAACCGCTATGGCATATGTCATGCGCTACGACACCTCTGAGTCATCCTTACCTTATC	296
Db	161	LysAsnArgTyrProAsnIleLeuProAsnAspHisCysArgValIleLeuSerGlnVal	180
QY	297	GATGGCGTCCCCGGAGAGTACTATCAATGCCAACTACATCATGGCTACCCGACAGAC	356
Db	181	AspGlyIleProCysSerAspTyrIleAsnAlaSerTyrIleAspGlyTyrLysGluLys	200
QY	357	AATGCTCATATCGCCACGACGAGGCGCCCTGCGCCAGACACCATGGCGCATTCGTGAGAAATG	416
Db	201	AsnLysPheIleAlaIleGlnGlyProLysGlnIleThrValAsnAspPheTrrArgMet	220
QY	417	GTTGGGAAACAGCCGACGCGCCATCTGTGTCATGATGACACGCGCTGAGAGAAATCCCG	476
Db	221	ValTrpGluGlnArgSerAlaThrIleValMetLeuThrAsnLeuLysGluArgLysGlu	240
QY	477	GTAATATGTACTACTACTGGCCGACCCCGTGGACCCAGACACTGTGGCTTATTACAGTG	536
Db	241	GluLysCysTyrGlnTyrTrrProAspIleGlyCysTrrPheTyrGluAsnIleArgVal	260
QY	537	ACCGTGTGGACACAGCTGGACCTGGCCACATACACTGTGGCGACCTTGGACTCCAC---	593
Db	261	CysValIleLysAspCysValValLeuValAspTyrThrIleArgLysPheCysIleHisPro	280
QY	594	-----AAGAGTGGCTCCAGTAGAGAAAGCTGAGCTGCGCAGTTTCAGTTCATAGGCTGG	647
Db	281	GlnLeuProAspSerCysLysAlaProArgLeuValSerGlnLeuHisPheThrSerTrr	300
QY	648	CCAGACCATGAGACTTCTGAGTACCACCACTCCATCTGGCTTCTTACAGCGGTCAAG	707
Db	301	ProAspPheGlyValProPheThrProIleGlyMetLeuLysPheLeuLysValLys	320
QY	708	GCGTCACACCCCGTACGAGCGAGGCGCCATGGTGTGTGACAGCGAGCGGCGTGGGCGCG	767
Db	321	ThrLeuAsnProSerHisAlaGlyProIleValValHisCysSerAlaGlyValGlyArg	340
QY	768	ACCGGCTCTTCATCGTATGTATGATCCATGTGTGGAGCGAGTGAAGCAAGAAAGAGTG	827
Db	341	ThrGlyThrPheIleValIleAspAlaMetMetAspMetIleHisSerGluGlnLysVal	360
QY	828	GACATCTATGGCCACGTCAGCTGCAGTACACAGAGAACTACATGCTGCAGACGGAG	887
Db	361	AspValPheGluPheValSerArgIleArgAsnGlnArgProGlnMetValGlnTrrAsp	380
QY	888	GACCACTGACGTTCATCATCAGAGGCGCTGTGAGAGGCTCGACAGTCCGCGCCACAGAG	947
Db	381	ValGlnTyrThrPheIleTyrGlnIleLeuGlnLysIleTyrIleuTyrGlnAspThrGlu	400
QY	948	GTCGCTGCCACCACTGTATGACCCACATCCAGAAAGCTGGGCGCAAGTCCCTCCAGGGAG	1007
Db	401	LeuAspValSerSerLeuGlnIleArgHisLeuGlnIleThrLeuHisSerThrIleAlaThrHisPhe	420
QY	1008	ACTGTGACCCGACATGAGCTCGAATTAAGTCTGTGGCCAGCTCCAGAGCCACAGCTCC	1067
Db	421	AspLysIleGlyLeuGluGluGluPheArgLysLeuThrAsnValArgIleMetLysGlu	440

QY	1068	CGCTTCATCAGCCGACCTGCGCCCTGACAGTCAAGTCAAGAGCCGGTGGTGAACATCAATG	1127
Db	441	AsnMetArgThrGlyAsnLeuProAlaAsnMetLysLysAlaArgValIleIleIleIle	460
QY	1128	CCCTACGAAATTGACCCGTGTGTGTCTGACAGCCCATCCGTGTGTGTGGAGGCTGTGATAC	1187
Db	461	ProArgAspPheAsnAlaValIleLeuSerMetLysArgGlyGlnGluIlePheThrAspArg	480
QY	1188	ATCAATGCCACCTTCCGTGATGGTTATAGACACACAAAGAGCTACATAGTACACAGGG	1247
Db	481	IleAsnAlaSerPheIleAspArgLysLysArgGlnLysAspArgPheMetAlaThrGlnLys	500
QY	1248	CCCTGGCAGACAGACACAGGAGCACTTGGCGGATGCTGTATGGAGACACAAATCCACATC	1307
Db	501	ProLeuAlaHisThrGlyGlnAspPheIleArgMetValIleProIleThrLysSerHisThr	520
QY	1308	ATCGTCACTGTGACCAAGCTTCCGGGAGATGGGAGGAGGAAATGCCACCACTATGAGCA	1367
Db	521	IleValMetLeuThrGlnValGlnGlnIleArgGlnGlnAspLysCysGlyGlnIleThrPro	540
QY	1368	GCAAGCGCCCTGCTGCTCCCTACAGACTTGTGTGTGTGACCCGATGGCTGTAGTCAACATG	1427
Db	541	ThrIleGlySerValIleThrHisGlyAspIleThrIleGluIleLysSerAspThrLeuSer	560
QY	1428	CCCCAGTATATCCGCTGAGTTCAGAGTCACG-----GATGCCGGAGT	1472
Db	561	GlnAlaIleSerValAlaArgAspPheLeuValIleThrPheLysGlnProLeuAlaArgGlnIle	580
QY	1473	GGGAGTCAAGACATATCCGACAGTCCAGTCCAGTCAACAGACTGGCCACAGAGGCGCTGCC	1532
Db	581	GluIleValAlaArgMetValAlaArgGlnPheHisGlyTyrProGlnIleValIlePro	600
QY	1533	AAGACAGCGGAGGATCATGTGACTTCATCGGGCAGGTGCATATAAGCAAGAGGACAGTT	1592
Db	601	AlaGluGlyLysGluMetLysAspLeuIleAlaValGlnLysGlnIleGlnIleIleThr	620
QY	1593	GGACAGAGTGGGCTTATCAGAGTGCATCGTGCAGTGTGGGCTGGGCGCACCGGGGTGTT	1652
Db	621	Gly---AsnHisProIleThrIleThrValHisCysSerAlaGlyAlaGlyLysArgIleThrPhe	639
QY	1653	ATCAGCTGTAGACATCTGCTCGTGGAGCGCATGCGCTATGAGAGCGGTGTGTGACATGTTT	1712
Db	640	IleAlaLeuSerAsnIleLeuGlnIleArgValLysAlaGlnGlyLysLeuAspValPheGln	659
QY	1713	ACCGTGAAGACCCCTGCTACACAGCGCCGATGCTGATGCTGACAGAGAGACCATGATGAG	1772
Db	660	AlaLysSerLeuAlaGluGlnIleAlaArgProHisMetValGlnIleThrLysGlnIleGlnIle	679
QY	1773	CTGTGCTACCGTGGCGCCCTGGAGTACCTCGGACGCTTGTGACCCACTATGCA	1823
Db	680	PheCysThrLysValValGlnAspPheIleAspIlePheSerAspTyrAla	696
RESULT 9			
TPM_MOUSE	STANDARD:	PRT:	1452 AA.
ID	PRIM_MOUSE		
AC	P28828;		
DT	01-DEC-1992 (Rel. 24, Created)		
DT	01-DEC-1992 (Rel. 24, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Protein-tyrosine phosphatase W0 precursor (BC 3.1.3.48) (R-PTP-MU).		
GN	PTPM.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lung;		
RX	MEDLINE=92008644; PubMed=1655529;		
RA	Geibnik M.F.B.G., van Etten I., Hebeero G., Suijkerbuijk R.,		
RA	Beijersbergen R., Geurts van Kessel A., Moolenaar W.H.;		
RT	"Cloning," expression and chromosomal localization of a new putative		

RT	receptor-like protein tyrosine phosphatase."	
RL	FEES left:290:123-130(1991).	
CC	- FUNCTION: MAY PLAY A KEY ROLE IN SIGNAL TRANSDUCTION AND GROWTH CONTROL.	
CC	- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.	
CC	- SUBCELLULAR LOCATION: Type I membrane protein.	
CC	- TISSUE SPECIFICITY: MOST ABUNDANT IN LUNG, LESS IN BRAIN AND HEART.	
CC	- SIMILARITY: CONTAINS 1 MAM DOMAIN.	
CC	- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.	
CC	- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.	
CC	- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.	
CC	-----	
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CC	-----	
DR	EMBL: X58287; CAA41225.1; -.	
DR	PIR: S17670; S17670.	
DR	HSSP: P28627; IRPM.	
DR	MGD: MGI:102694; Ptpm.	
DR	Interpro: IPR0003961; FN_III.	
DR	Interpro: IPR003962; FN.III_repeat.	
DR	Interpro: IPR003599; Ig.	
DR	Interpro: IPR003006; Ig_MHC.	
DR	Interpro: IPR000998; MAM_domain.	
DR	Interpro: IPR000387; TYR_phosphatase.	
DR	Interpro: IPR000242; TYR_PP.	
DR	Pfam: PF00047; Ig; 1.	
DR	Pfam: PF00102; X_phosphatase; 2.	
DR	Pfam: PF00629; MAM; 1	
DR	PRINTS: PR00014; ENTPEIII.	
DR	PRINTS: PR00020; MAMDOMAIN.	
DR	PRINTS: PR00700; PRTYPPHPTASE.	
DR	SMART: SM00060; FN3; 2.	
DR	SMART: SM00409; IG; 1.	
DR	SMART: SM00137; MAM; 1.	
DR	SMART: SM00194; PTPc; 2.	
DR	PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.	
DR	PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.	
DR	PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.	
DR	PROSITE: PS00740; MAM_1; 1.	
DR	PROSITE: PS50060; MAM_2; 1.	
KW	Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;	
KW	Immunoglobulin domain; Repeat.	
FT	SIGNAL	1 20
FT	CHAIN	21 1452
FT	DOMAIN	21 742
FT	TRANSMEM	743 764
FT	DOMAIN	765 1452
FT	DOMAIN	22 184
FT	DOMAIN	199 267
FT	DOMAIN	287 374
FT	DOMAIN	383 466
FT	DOMAIN	486 571
FT	DOMAIN	589 671
FT	DOMAIN	923 1153
FT	DOMAIN	1213 1447
FT	ACT_SITE	1095 1095
FT	ACT_SITE	1389 1389
FT	DISULF	206 260
FT	CARBOHYD	72 72
FT	CARBOHYD	92 92
FT	CARBOHYD	131 131
FT	CARBOHYD	249 249
FT	CARBOHYD	406 406
FT	CARBOHYD	414 414





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Db 1015 AsptHgluileTyrLysAspIleLeuValThrLeuIleGluThrGluLeuLeuAlaGlu 1034
QY 567 TACACGTGGCGACCTTGGACATCCACAAGACTGGCTCCAGTAGAAGCGTAGCGCT 626
Db 1035 TyrValIleArgThrPheAlaValIleGluYsArgGlyValHisGluIleArgGluIleArg 1054
QY 627 CAGTTTCATTCATGGCTGGCCAGACCATGGAGTTCCCTGAGTTCACCAACCTCCATCCG 686
Db 1055 GlnPheHisPheThrGlyTyrProAspHisGlyValProTyrHisAlaThrGlyLeuLeu 1074
QY 687 GCCTTCCTACGACGGGTGAAGGCTCAACCCCTAGACGACGGGCCATGGTGGTGCAC 746
Db 1075 GlyPheValArgGlnValLysSerLysSerProProSerAlaGlyProLeuValAlaHis 1094
QY 747 TGCACGGGGGGGTGGCCGACCGCGCTTCATCGTGATTCATGCCATGTGGACGG 806
Db 1095 CysSerAlaGlyAlaGlyArgThrGlyCysPheIleValIleAspIleMetLeuAspMet 1114
QY 807 ATGAAGCAGAGAGACGATGATGCGACGACGACCTGCATGCATGACACAGAG 866
Db 1115 AlaGluArgGluGlyValValAspIleTyrAsnGlyValArgGluLeuArgSerArgArg 1134
QY 867 AACTACATGATGTCAGACGAGGACCATGATGTCATCATGACGCGCTGGAGGCT 926
Db 1135 ValAsnMetValGlnThrGluGluGlnIleTyrValPheIleHisAspAlaIleLeuGluAla 1154
QY 927 GCCACGTGGCGGCACACAGAGGTGCTGCC-----CGCACCTGTATGCCACATC 977
Db 1155 CysLeuGlyAspThrSerValProAlaSerGlnValArgSerLeuTyrArgAspMet 1174
QY 978 CAGAAAGTCGGGGCAGAGTCCCTCCAGGGAGAGTGTGCGCCATGAGACTGACGTCAAG 1037
Db 1175 AsnLysLeu-----AspProGlnThrAsnSerSerGlnIleGluGluIleThrArg 1191
QY 1038 TTGCTG-----GCCAGCTCCAGAGGCCACAGTCCCGCTTCATGAGGCGCAACCTGCC 1091
Db 1192 ThrLeuAsnMetValThrProThrLeuArgValGluAspCysSerIleAlaLeuLeuPro 1211
QY 1092 TGCACACAGTTCACAGACCGGCTGTGACATCATGCCCCCTACGAATTGACCCGTGTGT 1151
Db 1212 ArgAsnHisGluLysAsnArgCysMetAspIleLeuProProAspArgCysLeuProPhe 1231
QY 1152 CTGCAGCCCATCGGTGGTGGAGGGCTGTGACTACATCATGCCCCGCTCCGTGGATGGT 1211
Db 1232 LeuIleThrIleAspGly---GluSerSerAsnTyrIleAsnAlaIleLeuMetLysPhe 1250
QY 1212 TATACAGACGAGAAAGCCTACATGCTACACAGGGGCTGTGGCAGAGACCGAGGAC 1271
Db 1251 TyrLysGlnProSerAlaPheIleValThrGlnHisProLeuProAsnThrValLysAsp 1270
QY 1272 TTCTGGCCCATGCTATGGGAGACAAATTCACCATCATCGTCATGCTGACCAAGCTTGG 1331
Db 1271 PheThrPArgLeuValLeuAspLysThrHisCysThrSerValValMetLeuAsnAspValAsp 1290
QY 1332 GAGATGGCGAGGAGAAATGCGACCATGACTGGCCA-----GCAGAGGGCTCTGCT 1382
Db 1291 Pro-----AlaGlnLeuGlyProGlnTyrTrpProGluAsnGlyValHisIleArgHisGly 1308
QY 1383 CGTACACAGTACTGTGTGTGTGACCCGATGGCTGATGATCAACATGCCAGATATTCCTG 1442
Db 1309 ProIleGlnValGluPheValSerAlaAspLeuGluGluAlaIleSerArgIlePhe 1328
QY 1443 CGTGAAGTTCAGAGGTACCGGATGCCGAGTGGGACGTCAAGACATCCGGCAGTTCCAG 1502
Db 1329 ArgIleTyrAsnAlaAlaIleArgProGlnAspGlyTyr---ArgMetValGlnGlnPheGln 1347
QY 1503 TTCACAGATGGCCA---GAGACGGGGCTGCCCAAGACGAGGAGGATTCATGACTTC 1559
Db 1348 PheLeuGlyTyrProMetTyrArgAspThrProValSerLysArgSerPheLeuLysLeu 1367
QY 1560 ATCGGGCAGGTGATACCAAGGAGGAGGAGTT---GGACAGGAGTGGCTATCACGGGTG 1616
Db 1368 IleArgGlnValAspLysTyrPheGlnGluGlnLysArgHisGlyGlyProThrValVal 1387

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QY 1617 CACTGCAGTGTGGCGTGGGCCGACACGGGGGTTCATCATCTGTGACATGCTCTGGAG 1676
Db 1388 HisCysLeuAsnGlyGlyValArgSerGlyThrPheCysAlaIleSerIleValCysGlu 1407
QY 1677 CGCATGCGGTATGAGGGCGGTGCGACATGTTTCAGACCGTGAAGACCTGGCTACAG 1736
Db 1408 MetLeuArgHisGlnArgThrValAspValPheHisAlaValLysThrLeuArgAsnAsn 1427
QY 1737 CGTCTGCCATGTCAGACAGAGGACGATGACGCTGTACCGTGGCGGCTGGAG 1796
Db 1428 LysProAsnMetValAspLeuLeuAspGlnTyrLysPheCysTyrGluValAlaLeuGlu 1447
QY 1797 TACCTGGCAGC 1808
Db 1448 TyrLeuAsnSer 1451

RESULT 11
PTPK_HUMAN
ID PTPK_HUMAN STANDARD: PRT: 1439 AA.
AC Q15262; Q14763;
DT 01-NOV-1997 (Rel. 35, Created)
DI 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein-tyrosine phosphatase kappa precursor (EC 3.1.3.48) (R-PTP-
DE kappa).
GN PTPRK OR PTPK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96279245; PubMed=8663237;
RX Fuchs M., Mueller T., Lerch M., Ullrich A.;
RT "Association of human protein-tyrosine phosphatase kappa with members
RT of the armadillo family."
RL J. Biol. Chem. 271:16712-16719(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Foreskin;
RX MEDLINE=97199372; PubMed=9047348;
RA Yang Y., Gil M.C., Choi E.Y., Park S.H., Pyun K.H., Ha H.;
RT "Molecular cloning and chromosomal localization of a human gene
RT homologous to the murine R-PTP-kappa, a receptor-type protein
RT tyrosine phosphatase."
RL Gene 186:77-82(1997).
CC -!- FUNCTION: REGULATION OF PROCESSES INVOLVING CELL CONTACT AND
CC ADHESION SUCH AS GROWTH CONTROL, TUMOR INVASION, AND METASTASIS.
CC FORMS COMPLEXES WITH BETA-CATENIN AND GAMMA-CATENIN/PLAKOGLOBIN.
CC BETA-CATENIN MAY BE A SUBSTRATE FOR THE CATALYTIC ACTIVITY OF PTP-
CC KAPPA.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN; AT ADHERENS
CC JUNCTIONS.
CC -!- TISSUE SPECIFICITY: HIGH LEVELS IN LUNG, BRAIN AND COLON; LESS IN
CC LIVER, PANCREAS, STOMACH, KIDNEY, PLACENTA AND MAMMARY CARCINOMA.
CC -!- PTM: THIS PROTEIN UNDERGOES PROTEOLYTIC PROCESSING.
CC -!- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; 270660; CAA94519.1; -.

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DR EMBL: L77886; AAC37599.1; -.  
 DR HSSP: P28827; IRPM.  
 DR Genew: HGNC:9674; PTPRK.  
 DR MIM: 602545; -.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR003962; FNIII\_repeat.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR000998; MAM\_domain.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR InterPro: IPR000242; Tyr\_PP.  
 DR Pfam: PF00041; fn3; 2.  
 DR Pfam: PF00047; Ig; 1.  
 DR Pfam: PF00102; Y\_phosphatase; 2.  
 DR Pfam: PF00629; MAM; 1.  
 DR PRINTS: PR00014; FNTYPEIII.  
 DR PRINTS: PR00020; MAMDOMAIN.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SM00060; FN3; 2.  
 DR SMART: SM00409; IG; 1.  
 DR SMART: SM00137; MAM; 1.  
 DR SMART: SM00194; PTPC; 2.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE: PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PP; 2.  
 DR PROSITE: PS500740; MAM\_1; 1.  
 DR PROSITE: PS50060; MAM\_2; 1.  
 DR KEGG: Hydroxylase: Receptor: Glycoprotein; Signal; Transmembrane;  
 KM Immunoglobulin domain: Repeat.  
 FT SIGNAL 1 26  
 FT CHAIN 27 1439  
 FT DOMAIN 27 752  
 FT TRANSLEM 753 774  
 FT DOMAIN 775 1439  
 FT DOMAIN 31 194  
 FT DOMAIN 209 277  
 FT DOMAIN 297 384  
 FT DOMAIN 393 474  
 FT DOMAIN 494 579  
 FT DOMAIN 597 680  
 FT DOMAIN 910 1141  
 FT DOMAIN 1200 1433  
 FT ACT\_SITE 1082 1082  
 FT ACT\_SITE 1376 1376  
 FT DISULFID 216 270  
 FT SITE 641 644  
 FT CARBOHYD 101 101  
 FT CARBOHYD 140 140  
 FT CARBOHYD 211 211  
 FT CARBOHYD 416 416  
 FT CARBOHYD 424 424  
 FT CARBOHYD 436 436  
 FT CARBOHYD 462 462  
 FT CARBOHYD 552 552  
 FT CARBOHYD 586 586  
 FT CARBOHYD 590 590  
 FT CARBOHYD 607 607  
 FT CARBOHYD 690 690  
 FT CONFLICT 9 9  
 FT CONFLICT 158 158  
 FT CONFLICT 284 284  
 FT CONFLICT 422 422  
 FT CONFLICT 672 674  
 FT CONFLICT 715 715  
 FT CONFLICT 732 732  
 FT CONFLICT 1366 1366  
 SQ SEQUENCE 1439 AA; 162087 MW; EED529AF7C9F4451 CRC64;

## Alignment Scores:

Pred. No.: 7 45e-68  
 Score: 1255.00  
 Percent Similarity: 62.59%  
 Best Local Similarity: 44.22%

Length: 1439  
 Matches: 260  
 Conservative: 108  
 Mismatches: 206

Query Match: 19.48% Indels: 14  
 DB: 1 Gaps: 9  
 US-09-743-492-1 (1-3467) x PTPK\_HUMAN (1-1439)  
 QY 66 TACCAGACCCAGGTATGCGAGACACCCACATCCCATCCAGGACCTGGGACAC 125  
 DB |||||  
 DB 858 TyrGlnThrGlnGlnLeu-----HisProAlaIleArgAlaAlaAspGlnGlnHis 875  
 QY 126 ATGACGGCCCTCAAGGCAAGCATGAGGCGCTCAAGTTCCTCCGAGGATGAGTCCATGCATG 185  
 DB |||  
 DB 876 IleAsnLeuMetLysThrSerAspSerTyrGlyPheLysGlnGlyTyrGlySerPhePhe 895  
 QY 186 CCTGACGACGATTCACGTGCGAGCAATCAACCTGAGAGTGGACCAAGCCCAAGACACCGC 245  
 DB |||||  
 DB 896 GluGlyGlnSerAlaSerThrPaspValAlaLysLysAspGlnAsnAlaAlaLysAsnArg 915  
 QY 246 TATGCGAATGTATCGCTACGACACCACTGCTGAGTATCTTACCTGTATGATGCGCTC 305  
 DB |||  
 DB 916 TyrGlnAsnIleIleAlaTyrAspHisSerArgValIleLeuGlnProValGluAspAsp 935  
 QY 306 CCCGGAGGTGATCAATCAATGACATGACATGATGCTACCGGACCAAGACAGATGCTTAC 365  
 DB |||  
 DB 936 ProSerSerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrGlnAlaArgProSerHisTyr 955  
 QY 366 ATGCGACGACGAGGCCCCCTCCGACGACATGGGCGCATTTCTGAGAAATGCTGGGAA 425  
 DB |||||  
 DB 956 IleAlaThrGlnGlnProValHisGlnThrValTyrAspPheThrArgGlyMetIleTyrPhe 975  
 QY 426 CAGGCGACGCGACCTGTGCTATGATGACACGCGCTGCGAGGAAAGTCCCGGTAATGT 485  
 DB |||||  
 DB 976 GluGlnSerAlaLysIleValIleMetValThrAsnLeuValGluValGluValLysLys 995  
 QY 486 GATGAGTACGTGCGACGCGCGCTGGGACGACCTGTGCGCTTATTCAGTACGCTGCTG 545  
 DB |||||  
 DB 996 TyrIleTyrTyrPro---AspAspThrGluValIleTyrGlyAspPheLysValThrCysVal 1014  
 QY 546 GACAGACGTGAGTGGCCACATACATCTGTGCGACCTGCGACCTGCGACGAGTGGCTCC 605  
 DB |||||  
 DB 1015 GluMetGluProLeuAlaGluTyrValValAlaArgThrPheThrLeuGlnAlaArgGlyTyr 1034  
 QY 606 AGTGAAGACGTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 665  
 DB |||||  
 DB 1035 AsnGluIleArgGluValLysGlnPheHisPheThrGlyTyrProAsnHisGlyValPro 1054  
 QY 666 GAGTACCCATCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 725  
 DB |||||  
 DB 1055 TyrHisAlaThrGlnGlyLeuLeuSerPheIleArgTyrValLysLeuSerAsnProSer 1074  
 QY 726 GCAGGCGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 785  
 DB |||||  
 DB 1075 AlaGlyProIleValIleValHisCysSerIleAlaGlyAlaGlyThrGlyCysTyrIleVal 1094  
 QY 786 ATTCATGCCATCTGGAGCGGATGAGCAGAGAGACGCTGACATCTATGCGACGCTG 845  
 DB |||||  
 DB 1095 IleAspIleMetLysLeuAspMetAlaGluArgGluValValAlaPheIleTyrAsnLysVal 1114  
 QY 846 ACCTGATGCGATGACAGAGAGATACATGCTGCGAGCGGAGCGACCTAGTGTGATC 905  
 DB |||||  
 DB 1115 LysAlaLeuAlaGlySerAlaGlyAlaIleAsnMetValGlnThrGlnGluGlnTyrIlePheIle 1134  
 QY 906 CATGAGCGCTGCTGAGGCTGCGACGCTGCGGCGCCACAGAGTGTGCTGCGCGCAACCTG 965  
 DB |||||  
 DB 1135 HisAspAlaIleLeuGlnAlaCysLeuLysGlnGluThrAlaIleProValCysGluPhe 1154  
 QY 966 TATGCCCATCATCGAAGACCTGGCGCAAGTGCCTCAGGAGGAGTGTGACCGCATGAGAG 1025  
 DB |||  
 DB 1155 LysAlaIleAlaTyrPheAspMetIleArgIleAspSerGlnThrAsnSerHisLeuLys 1174  
 QY 1026 CTCGAGTTCAAGTGTGCTGCGCAGC-----TCAAGGCGCCACAGTCCCGCTTATCAGC 1079  
 DB |||||  
 DB 1175 AspIlePheGlnThrLeuAsnSerValThrProArgLeuGlnAlaGluAspCysSerIle 1194





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FT ACT_SITE 1394 1394 BY SIMILARITY.
FT DISULFID 215 269 POTENTIAL.
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 415 415 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 551 551 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 585 585 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 589 589 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 689 689 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1457 AA; 164185 MW; 19D4B99B7E0CB605 CRC64;

Alignment Scores:
Pred. No.: 3 91e-67 Length: 1457
Score: 1243.00 Matches: 261
Percent Similarity: 61.95% Conservative: 107
Best Local Similarity: 43.94% Mismatches: 206
Query Match: 19.29% Indels: 20
DB: 1 Gaps: 10

US-09-743-492-1 (1-3467) x PTPK_MOUSE (1-1457)
QY 66 TACGACACCCGAGTATCGAGACCCACCACCATCCCATCCGAGCGGAGACAAC 125
DB 870 TyrglnThrGlnGlnLeu-----HisProAlaIleArgValAlaAspLeuGlnHis 887
QY 126 ATCGAGCCCTCAAGCCACGATGGCCTCAAGTTCTCCGAGAGTATGATCGATCGAC 185
DB 888 IleasnLeuMetIlysthrSerAspSerTyrGlnPheIytsGlnGlnTyrGlnSerPhe 907
QY 186 COTGACACGAGTCCGAGGAGAAATCAACCTGAGGAGTGAACAGCCGACGACGAC 245
DB 908 GlnGlnGlnSerAlaSerThrProAlaIlysthrAspGlnAsnArgAlaIlysthr 927
QY 246 TATGCGAATGTCATCGCTACGACGACCTCTGAGTATCTTACCTTATCGATGCGCGTC 305
DB 928 TyrglnAsnIleIleAlaTyrAspHisSerArgValIleLeuGlnProValGlnAsp 947
QY 306 CCCGGAGTACTACATCAATGCGACATACATC-----GATGGCTAC 347
DB 948 ProSerSerAspTyrIleAsnAlaAsnTyrIleAspIleTyrPheTyrArgAspIly 967
QY 348 CGGACGAGAAATGCTTACATCGCCGACGAGGCGCCCTGCGGAGACCATGGCGATTC 407
DB 968 GlnArgProSerHisTyrIleAlaThrGlnGlnProValHisGlnIlythrValTyrAsp 987
QY 408 TGGAGAAATGCTGGGAGACAGCGGACGACCTGTGATGATGACAGCGCTGGAGAG 467
DB 988 TrpArgMetValTyrGlnGlnIlythrAspIleValMetValThrAsnLeuValGln 1007
QY 468 AAGTCCGGGTTAAATGTCATGACTGCGGACCGCTGGACCGGACGACCTGGCTT 527
DB 1008 ValGlnArgValIlysthrCysTyrIlythrPro---AspAspThrGlnValTyrIly 1026
QY 528 ATTGAGGACCTGCTGTGAGACAGTGGAGCGGACATACATGCTGGCGGACCTTGGCA 587
DB 1027 PheIysValIlythrCysValGlnMetIlythrProLeuAlaGlnTyrValAlaThrPhe 1046
QY 588 CTCGACAGAGTGGCTCCAGTGAAGAGCGTACGCTCAAGTTTCAGTTTCATGGCGCTG 647
DB 1047 LeuGlnArgValGlnTyrAsnGlnIlythrValGlnValIlysthrPheHisThr 1066
QY 648 CCAAGCATGAGATTCCTGAGTACCAACTCCATCTGCGCTTCTGACAGCGGCTGAC 707
DB 1067 ProAspHisGlnValIlythrHisAlaThrGlnLeuLeuSerPheIleAlaArgValIly 1086
QY 708 GCGTCGACACCGCCATGACGAGCGGCGGTCGACCTGAGGCGGCGGCGGCGCGC 767
DB 1087 LeuSerAsnProProSerAlaGlnIlyProIleValIlyHisCysSerAlaGlnIly 1106

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QY 768 ACCGCGCTGCTCATCGTGTGATGATGCCATGTTGAGCGGATGACGACGACGAGCGTG 827
DB 1107 ThrGlnCysTyrIleValIleAsnIleMetLeuAspMetAlaGlnArgGlnIlyValVal 1126
QY 828 GACATCTATAGGCGACGTCGATCGCATGCGATCACAGAGAACTACATGCTGCGACGCGAG 887
DB 1127 AspIlyThrAsnCysValIlysthrAlaLeuArgSerArgValIleAsnMetValGlnThrGln 1146
QY 888 GACGAGTACGTTGATCCATGAGCGGCTGTGAGAGCGGCCGACGCGGCGGACGACGAG 947
DB 1147 GlnGlnIlyThrIlePheIleHisAspAlaIleLeuGlnAlaCysLeuGlnIlythrAla 1166
QY 948 GTGCGTCCCGGACACCTGTATGCCACATCCAGAAAGCTGGGCGCAAGTCCCTCAGCGGAG 1007
DB 1167 IleProValCysGlnPheIlysthrAlaIlyThrPheAspMetIleArgIleAspSerGlnThr 1186
QY 1008 AGTGTGACCGCCATGAGAGCTCGATTCGAAGTTGCTGGCCAGC-----TCCAGGCGCCAC 1061
DB 1187 AsnSerSerHisLeuIlysthrAspGlnPheGlnIlythrLeuAsnSerValIlyThrProArgLeuGln 1206
QY 1062 ACGTCCCGCTTCATCAGCGCCCAACCTCGCCCTGCAACAAGTTCAAGACCGGCTGGTGAAC 1121
DB 1207 AlaGlnAspCysSerIleAlaCysLeuProArgAsnHisAspIlysthrPheMetIly 1226
QY 1122 ATCATGCGCCCTACGAATTCACCCGCTGTGTCTGACAGCCCATCCGTGTGTGAGGCGCTCT 1181
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QY 1182 GACTCATCATGATGCCAGCTTCTGTGATGTTTATAGACGACAGAGCGCTACATACCTACA 1241
DB 1246 AsnTyrIleAsnAlaIleLeuMetAspSerTyrArgGlnProAlaAlaPheIleValIly 1265
QY 1242 CAGGGGCGCTGTGCGACGAGACGACGAGTCTGTGGCGCATGTTGAGGACACAATTTC 1301
DB 1266 GlnTyrProLeuProAsnThrValIlysthrAspPheThrPheValIlyThrAspIlyCys 1285
QY 1302 ACCATCATGCTCATGCTGACCAAGCTTGGGAGATGGGCGGAGAGAAATGCCACGATAC 1361
DB 1286 ThrSerIleValMetLeuAsnGlnIlyValAspLeu-----SerGlnGlnCysProGlnTyr 1303
QY 1362 TGGCCAGCAGAGCGCTGCTGCTGCTACCAAGTACTTTGTTGATGCCCGATGGCT----- 1415
DB 1304 TrpProGlnGlnGlnIlyMetLeuArgTyrGlnProIleGlnValGlnCysMetSerCys 1323
QY 1416 ---GAGTACAAACATGCCCGAGTATCCGCTGAGTTCAGATGACGATGCCCGGAT 1472
DB 1324 MetAspCysAspValIleAsnArgIlePheArgIleCysAsnLeuThrArgProGlnGln 1343
QY 1473 GGGCAGTCAAGAGACATCCGCGAGTTCCAGTTCCAGACTGG---CGAGACGAGGCGGTG 1529
DB 1344 GlnTyr---LeuMetValGlnGlnPheGlnIlyThrAlaSerHisArgGlnVal 1362
QY 1530 CCCAGACAGGCGGAGGATTCATTCATTCATTCGCGGACGTCATTAAGACCAAGACGACG 1589
DB 1363 ProGlnSerIlysthrArgSerPheLeuIlysthrLeuGlnValGlnIlysthrPheGln 1382
QY 1590 TTTGAGCAG---GATGGCGCTATCACGCGTCAAGTCAAGTGGCGGCGGCGGCGGAC 1646
DB 1383 CysGlnGlnGlnIlyGlnIlyArgThrIleIleHisCysLeuAsnGlnIlyGlnArgSerIly 1402
QY 1647 GTTTCATCATCTGAGCATGCTCTGTGAGACGCGATCCGCTATGAGGCGGCTGTGACATG 1706
DB 1403 MetPheCysAlaIleGlnIlyleValValGlnMetValIlysthrArgGlnAsnValIlyAsp 1422
QY 1707 TTTGACACCGTGAAGACCTGCGTACACAGCGTCTGCGCATGCTGTCACAGACGACGAC 1766
DB 1423 PheHisAlaValIlysthrLeuArgAsnSerIlysthrProAsnMetValGlnAlaProGln 1442
QY 1767 TATCAGCTGTGCTACCGTGGCGGCGCTGAGTACCTCGGAGAC 1808
DB 1443 TyrArgPheCysTyrAspValAlaLeuGlnIlyThrLeuGlnSer 1456

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RESULT 13
PRPG_HUMAN STANDARD; PRT; 1445 AA.
AC P23470; Q15623;
DT 01-JUN-1991 (Rel. 20, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase gamma precursor (EC 3.1.3.48) (R-PRP-
DE gamma).
GN PRPG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID:9606;
RN RN
RP MEDLINE-93180796; PubMed-8382771;
RX MEDLINE-96425999; PubMed-8833149;
RA Krusty K., Ohta M., Lasota J., Moir D., Dorman T., Laforgia S.,
RA Drack T., Huebner K.;
RT "Structure of the human receptor tyrosine phosphatase gamma gene
RT (PTPK) and relation to the familial RCC t(3;8) chromosome
RT translocation.";
RL Genomics 32:225-235(1996).
RN RN
RP SEQUENCE OF 836-1445 FROM N.A.
RX MEDLINE-91006018; PubMed-21701019;
RA Krueger N.X., Streuli M., Saito H.;
RT "Structural diversity and evolution of human receptor-like protein
RT tyrosine phosphatases.";
RL EMBJ J. 9:3241-3252(1990).
RN RN
RP [4]
RP SEQUENCE OF 874-1118 AND 1175-1409 FROM N.A.
RC TISSUE-Brain;
RX MEDLINE-90384936; PubMed-2169617;
RA Kaplan R., Morse B., Huebner K., Croce C., Hawk R., Ravera M.,
RA Ricca G., Jaye M., Schlessinger J.;
RT "Cloning of three human tyrosine phosphatases reveals a multigene
RT family of receptor-linked protein-tyrosine-phosphatases expressed in
RT brain.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:7000-7004(1990).
CC CC
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC CC
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC CC
CC -1- TISSUE SPECIFICITY: FOUND IN A VARIETY OF TISSUES. IT IS
CC DEVELOPMENTALLY REGULATED IN THE BRAIN (BY SIMILARITY).
CC CC
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE EUKARYOTIC-
CC TYPE CARBONIC ANHYDRASE FAMILY.
CC CC
CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
CC CC
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC CC
DR EMBL; L09347; AAA60224.1; -
DR EMBL; U46116; AAC50439.1; -
DR EMBL; U46089; AAC50439.1; JOINED.
DR EMBL; U46090; AAC50439.1; JOINED.

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DR	EMBL	U46091	AAC50439.1	JOINED	
DR	EMBL	U46092	AAC50439.1	JOINED	
DR	EMBL	U46093	AAC50439.1	JOINED	
DR	EMBL	U46094	AAC50439.1	JOINED	
DR	EMBL	U46095	AAC50439.1	JOINED	
DR	EMBL	U46096	AAC50439.1	JOINED	
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DR	EMBL	U46099	AAC50439.1	JOINED	
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DR	EMBL	U46101	AAC50439.1	JOINED	
DR	EMBL	U46102	AAC50439.1	JOINED	
DR	EMBL	U46103	AAC50439.1	JOINED	
DR	EMBL	U46104	AAC50439.1	JOINED	
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DR	EMBL	U46110	AAC50439.1	JOINED	
DR	EMBL	U46111	AAC50439.1	JOINED	
DR	EMBL	U46112	AAC50439.1	JOINED	
DR	EMBL	U46113	AAC50439.1	JOINED	
DR	EMBL	U46114	AAC50439.1	JOINED	
DR	EMBL	U46115	AAC50439.1	JOINED	
DR	EMBL	X54132	CAA38067.1	..	
DR	PIR	S12051	S12051		
DR	HSSP	P18052	LYFO		
DR	Genew	HGNC:9671	PTPBG		
DR	MM	176886	..		
DR	InterPro	IPR001148	Euk_Coanhd.		
DR	InterPro	IPR003961	FN_III		
DR	InterPro	IPR000387	Tyr_phosphatase		
DR	InterPro	IPR000242	Tyr_Pp		
DR	Pfam	PF00041	Tn3_1		
DR	Pfam	PF00102	Y_phosphatase_2		
DR	Pfam	PF00194	carb_anhydase_1		
DR	PRINTS	PR00700	PRTPHPTASR		
DR	PRODOM	PD000865	Euk_Coanhd_1		
DR	SMART	SM00060	FN3_1		
DR	SMART	SM00194	PTPC_2		
DR	PROSITE	PS00383	Tyr_PHSPPHATASE_1; 1		
DR	PROSITE	PS50056	Tyr_PHSPPHATASE_2; 2		
DR	PROSITE	PS50055	Tyr_PHSPPHATASE_PTP; 2		
KW	Glycoprotein; Transmembrane; Hydrolase; Phosphorylation; Repeat;				
FT	Signal.				
FT	CHAIN	1	19		
FT	DOMAIN	20	1445		
FT	DOMAIN	20	736		
FT	TRANSMEM	737	762		
FT	DOMAIN	763	1445		
FT	DOMAIN	56	322		
FT	DOMAIN	347	441		
FT	DOMAIN	869	1125		
FT	DOMAIN	1126	1445		
FT	ACI_SITE	1060	1060		
FT	SITE	1351	1351		
FT	CARBOHYD	109	109		
FT	CARBOHYD	113	113		
FT	CARBOHYD	156	156		
FT	CARBOHYD	359	359		
FT	CARBOHYD	444	444		
FT	CARBOHYD	619	619		
FT	CARBOHYD	631	631		
FT	CARBOHYD	722	722		
FT	CONFLICT	80	80		
FT	CONFLICT	92	92		
FT	CONFLICT	549	549		
FT	CONFLICT	756	756		
FT	CONFLICT	1407	1407		
3Q	SEQUENCE 1445 AA: 162058 MM: 350F990CC94E80BD CRC64;				

Alignment Scores:



RA B      G. Silvennoinen O., Shaan B., Honegger A.M., Canoll P.D.,  
 RA D'Eustachio P., Morse B., Levy J.B., Latorfa S., Huebner K.,  
 RA Musacchio J.M., Sap J., Schlessinger J.:  
 RT "Identification of a carbonic anhydrase-like domain in the  
 RT extracellular region of RPTP gamma defines a new subfamily of receptor  
 RT tyrosine phosphatases".  
 RL Mol. Cell. Biol. 13:1497-1506(1993).  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
 CC -1- TISSUE SPECIFICITY: DETECTED IN BRAIN, LUNG, KIDNEY, HEART, LIVER,  
 CC SKELETAL MUSCLE, SPLEEN AND TESTES. IT IS DEVELOPMENTALLY  
 CC REGULATED IN THE BRAIN.  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE EUKARYOTIC-  
 CC TYPE CARBONIC ANHYDRASE FAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.  
 CC  
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 CC -----  
 DR EMBL: L09562; AAA40022.1; -.  
 DR PIR: B48148; B48148.  
 DR HSSP: P18052; IYFO.  
 DR MGD: MGI:97814; Ptpyg.  
 DR InterPro: IPR001148; Euk\_Coanhd.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR000387; Tyr\_phosphatase.  
 DR InterPro: IPR000242; Tyr\_Pp.  
 DR Pfam: PF00041; fn3\_1.  
 DR Pfam: PF00102; Y\_phosphatase; 2.  
 DR Pfam: PF00194; carb\_anhydrase; 1.  
 DR PRINTS: PR00700; PTPYPPHPTASE.  
 DR ProDom: PD000865; Euk\_Coanhd; 1.  
 DR SMART: SM00060; FN3; 1.  
 DR SMART: SM00194; PTPc; 2.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Glycoprotein; Transmembrane; Hydrolyse; Repeat; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 1 19  
 FT DOMAIN 20 1442  
 FT TRANSSEM 734 733  
 FT DOMAIN 734 759  
 FT DOMAIN 1442 1442  
 FT DOMAIN 56 322  
 FT DOMAIN 347 441  
 FT DOMAIN 866 1122  
 FT DOMAIN 1123 1442  
 FT DOMAIN 1057 1057  
 FT ACT\_SITE 1057 1348  
 FT SITE 1057 1348  
 FT CARBOHYD 109 109  
 FT CARBOHYD 113 113  
 FT CARBOHYD 156 156  
 FT CARBOHYD 359 359  
 FT CARBOHYD 444 444  
 FT CARBOHYD 719 719  
 SO SEQUENCE 1442 AA; 161242 MW; 5887715568FBEC08 CRC64;

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OY	147	GATGCCTCCAAATGTCTCCAGGAGATGATGATCCATCCGAC-----CCTGCACGCGAG	197
Dd	841	SerGIlnHisGLyPheSerOtlusPrPheGLUGlUvalGlInArGcystHrILasPmetLan	860
OY	136	TTCACGTGGGAGAATTCAAACCTGGAGGCTGAACAACGCCCAAGACCCSTATCGGAATGTC	257
Dd	861	IleThrAlaGLInHisSerAsnHisProAsPasnLysHisLysAsnArGlyrILeAsnIle	880
OY	258	ATCCGGCTACGACCACTCTGGATGCATCTTACTCTGTATGAGCTCCAGCTCCCGGG-----	311
Dd	881	LeuAlaTyraSPhisSerILeArgValLysLysLeuAlaGrProLeuPrOGlLylusAsPserLysHis	900
OY	312	AGTGACATACATCAATGCCAATACATCGATGGCTACCGCACGACAGATGCTATACATCGCC	371
Dd	901	SerAsPtyrILeAsnAlaSnThyValaSPryLYrAsnLysAlaLysAlaTyrlleAla	920
OY	372	ACGCAGGGCCCCCTGCCGACGACATGGSCGAAATTTCTGGAGAATGCTGGCAACGGCC	431
Dd	921	ThrgInGLyProLeuLysSerThrPheGLuAsPheTrArgMetIlePrpGLUGlnAsn	940
OY	432	ACGGCCACATGTGTATGATGACAGCGCGTGGAGAGAAATCCCGGATAAATGTATGACG	491
Dd	941	ThrgLylleIleIleMetIleThrAsnLeuValGLInLysGLyArGargLysCysAsprGLIn	960
OY	492	TACTGCCCACGCCGTGGCCAGCAGACCTGTGCGCTTATTCAAGTGACCCCTGTGGACACA	551
Dd	961	TyrTrpProthrGLInAsnThrGLInGLInLylLysAsnIleIleValThrLeuLysSerThr	980
OY	552	GTGGAGCTGGCCACATACACTGTGGCGACCTTGCGACCTCCACAGAAGT-----	599
Dd	981	LysValHisAlaCysTryrThrValArGLeUsenSerValArGsnHrLysValLysLys	1000
OY	600	-----GGCTCCAGATGAGAAAGCTGACCTGCCTGCATGTTCCAGTTC	638
Dd	1001	GLInLysGLyAsnProLysGLyArGLInAsnGLInArGThrValILeInLynHisTYr	1020
OY	639	ATGCGCTGGCCACGACCATGGAATCTCTAGTACCCACATCCCATCTCTGGCCTTCCACGA	698
Dd	1021	ThrgInTProAsPmetGLyAlaProGLInLylLalaLeuPrOGlValThrPheValArg	1040
OY	699	CGGGTCAAGAGCCTGGAAACCCCTTAGACGCGAGGGCCCATGCTGGTGCATCGACGGCGGC	758
Dd	1041	ArgSerSerAlaAlaArgMetProAsPmetGLyProValLeuValHisCysSerAlaGLy	1060
OY	759	GTGGGCGCGACCGCTCTTCATCGTATGATATGCCATGTGGAGCGGATGAACGACGAG	818
Dd	1061	ValGLyArGThrgLylThrTYrILeValILeAsPserMetLeuGLInLyleLysAsPLys	1080
OY	819	AAGAGGTGGAGATCTATGGCGCCACGAGNACCTGCATCCGATCAAGAGAGACTACATCGTG	878
Dd	1081	SerTrnValAsnValLeuGLyPheLeuLysHisLIleArgThrgInLynAsnTYrLeuVal	1100
OY	879	CAGACGGAGGACAGTACCTGTTTCATCCATGAGAGCGCTCTGGAGGCTCCACGTGCGGC	938
Dd	1101	GLInThrgInGLInGLInTYrILePheIleHisAsPalaLeuLenglnValaILeLengLys	1120
OY	939	CACACAGAGTGCTCCGCCGACAACTGTATGCCACATCCAGAAAGCTGGGCGCAATGCTCT	998
Dd	1121	GLInTrnAlaValaSerSerSerGLInLeuHisSerTYrValaLsnSerIle--LeuILEPro	1139
OY	999	CCAGGGAGAGTGTACCCGACCGCATGAGCGCGAGTTTCGACATCTCCGCCACGTCAAGCG	1058
Dd	1140	GLyValaGLyGLyLysThrArgLenglnLysGLInPheLysLeuIleThrOlnCysAsnAla	1159
OY	1059	CACAGCTCCCGCTTATCAGCGCCCAACCTGCCCTGCACAAAGTTCACAGAACCGGCTGTG	1118
Dd	1160	LysTYrValaGLInCysPheSerILeAGlnLysGLInCysAsnLysGLyLysAsnTrArgnsSer	1179





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GenCore version 5.1.3  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 17, 2003, 09:56:39 ; Search time 213.5 Seconds

(without alignments)  
6591.947 Million cell updates/sec

Title: US-09-743-492-1

Perfect score: 6444  
Sequence: 1 gatccgagctgaagagctcc.....attgataataatcagattctt 3467

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_n2p.model -DEV=xlp  
-O=/cgn2.1/USPTO\_spool/US09743492/rnat.17012003.093836.11532/app-query.fasta-1.3655  
-DB=SPTRMBL.21 -OPEN=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human0.cdf -LIST=45  
-OCALIGN=200 -THR.SCORE=pcr -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTER=fto -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09743492@cgn.1.1.321@rnat.17012003.093836.11532 -NCPU=6 -ICPU=3  
-NO\_XLPHY -NO\_MAP -LARGEQUERY -NEG.SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120  
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTRMBL.21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3192	49.5	1887	11 Q9QW67	Q9QW67 rattus sp.

2	3175	49.3	1898	11 Q9EQ17	Q9EQ17 mus musculus
3	3172	49.2	1898	11 Q64604	Q64604 r protein-t
4	3057	47.5	1788	13 Q91A00	Q91A00 xenopus lae
5	3057	47.4	582	11 Q64696	Q64696 mus musculus
6	2938	45.6	749	11 Q8R169	Q8R169 mus musculus
7	2938	45.6	1254	11 Q8R169	Q8R169 mus musculus
8	2922	45.3	1896	13 Q91A01	Q91A01 xenopus lae
9	2880	44.7	1502	4 Q9QW81	Q9QW81 homo sapien
10	2868	44.5	615	13 Q91A18	Q91A18 xenopus lae
11	2867.5	44.5	1499	13 Q90815	Q90815 gallus gall
12	2862	44.4	857	13 Q90Y14	Q90Y14 brachydantio
13	2856	44.3	1948	4 Q13332	Q13332 homo sapien
14	2850	44.2	1501	11 Q9QW00	Q9QW00 rattus sp.
15	2850	44.2	1663	11 Q64605	Q64605 rattus norv
16	2823.5	43.8	1904	11 Q64699	Q64699 mus musculus
17	2752.5	42.7	1894	11 Q64487	Q64487 mus musculus
18	2746	42.6	1399	4 Q75870	Q75870 homo sapien
19	2574	39.9	508	13 Q90Y15	Q90Y15 brachydantio
20	2509	38.9	1231	5 Q17024	Q17024 anopheles g
21	2503	38.8	1597	5 Q660M3	Q660M3 drosophila
22	2503	38.8	2037	5 Q9V1S8	Q9V1S8 drosophila
23	2450.5	38.0	1437	5 Q44329	Q44329 hirudo medi
24	2413	37.4	460	11 Q62917	Q62917 rattus norv
25	2377	36.9	2051	5 Q43328	Q43328 hirudo medi
26	2364	36.7	468	13 Q91BA5	Q91BA5 potamoxygo
27	2290	35.5	468	13 Q91BA2	Q91BA2 potamoxygo
28	2263	35.1	468	13 Q91BA0	Q91BA0 potamoxygo
29	2251	34.9	469	5 Q9N1L1	Q9N1L1 branchiosto
30	2188.5	34.0	469	13 Q9N1L8	Q9N1L8 eptaretus
31	2068	32.1	468	13 Q9N1L6	Q9N1L6 eptaretus
32	1869	29.0	398	11 Q62604	Q62604 rattus norv
33	1836.5	28.5	2200	5 Q9B8N8	Q9B8N8 caenorhabdi
34	1633	25.3	472	13 Q9N1L2	Q9N1L2 eptaretus
35	1551	24.1	793	3 Q91V35	Q91V35 mus musculus
36	1551	24.1	802	4 Q96FD9	Q96FD9 homo sapien
37	1524	23.6	822	13 Q91556	Q91556 xenopus lae
38	1509	23.4	833	13 Q9PES7	Q9PES7 brachydantio
39	1464.5	22.7	807	13 Q91969	Q91969 gallus gall
40	1426	22.1	642	4 Q96K06	Q96K06 homo sapien
41	1423	22.1	699	11 Q61042	Q61042 mus musculus
42	1421	22.1	642	11 Q60986	Q60986 mus musculus
43	1415	22.0	659	11 Q63477	Q63477 rattus norv
44	1247.5	19.4	1444	11 Q9J1Z1	Q9J1Z1 mus musculus
45	1245.5	19.3	1435	11 Q9J1Z2	Q9J1Z2 mus musculus

## ALIGNMENTS

### RESULT 1

ID	Q9QW67	PRELIMINARY:	PRT:	1887 AA.
AC	Q9QW67			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	LAR, leukocyte common antigen-related PROTEIN=TRANSMEMBRANE receptor			
DE	phosphotyrosine phosphatase.			
OS	Rattus sp.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Rattus.			
OX	NCBI_TaxId=10118;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92278755; PubMed=1317540;			
RA	Yu Q., Lenardo T., Weinberg R.A.;			
RT	"The N-terminal and C-terminal domains of a receptor tyrosine			
RT	phosphatase are associated by non-covalent linkage.";			
RL	Oncogene 7:1051-1057(1992).			
DR	HSSP: P18052; IYFO.			
DR	InterPro: IPR003962; FNIII_repeat.			
DR	InterPro: IPR003961; FN_III.			
DR	InterPro: IPR003598; IG_c2.			
DR	InterPro: IPR003600; Ig_like.			

DR InterPro: IPR003006; IQ\_MHC.  
 DR InterPro: IPR001005; Myb\_DNA\_binding.  
 DR InterPro: IPR000387; Tyr\_phosphatase.  
 DR InterPro: IPR000242; Tyr\_PP.  
 DR Pfam: PF00041; fn3; 7.  
 DR Pfam: PF00047; Ig; 3.  
 DR Pfam: PF00102; Y\_phosphatase; 2.  
 DR PRINTS: PR00014; ENTPEPIT.  
 DR PRINTS: PR00700; PRTPHPHPTASE.  
 DR SMART: SM00060; FN3; 6.  
 DR SMART: SM00408; IGC2; 2.  
 DR SMART: SM00410; IG\_Like; 1.  
 DR SMART: SM00194; PTPC; 2.  
 DR PROSITE: PS00037; MYB\_1; UNKNOWN\_1.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PP; 2.  
 KW Hydroxylase; Immunoglobulin domain; Repeat.  
 SQ SEQUENCE 1887 AA; 210453 MW; B84B33E7E4E70281 CRC64;

## Alignment Scores:

Pred. No.:	1.23e-242	Length:	1887
Score:	3192.00	Matches:	599
Percent Similarity:	99.34%	Conservative:	4
Best Local Similarity:	98.68%	Mismatches:	0
Query Match:	49.53%	Gaps:	0

US-09-743-492-1 (1-3467) x Q9QW67 (1-1887)

QY 6 GCATCGAAGGAGCTCTTGGTGGCCCACTCTTGACCTGTGGAGATGGGAGGCTCAAC 65  
 Db 1281 GlyleuLysASPserLeuLahLisSerAspProValGluMetArgArgLeuAsn 1300  
 QY 66 TACGAGCCCAAGGATGAGAGACACCCACCCATCCCATCCAGGAGCTGGGAGACAC 125  
 Db 1301 TyrglntrProGluMetArgAspHisProProLleProLlethAspLeuLahAspSn 1320  
 QY 126 ATCGAGCCCTCAAGGACCAAGCATGAGCTCAAGTTCTCCAGAGATGATGCTCATGAC 185  
 Db 1321 lIegluArgleuLysAlahAsnAspGlyLeuLysPheSerGlnGluTyrGluSerlIeAsp 1340  
 QY 186 CCTGACACGACGTTACGTTGGGAGAAATTCAAACCTGGAGGTAAACAGCCCAAGACCC 245  
 Db 1341 ProGlyGlnGlnPheThrTrpLuhAsnSerAsnSerGluValAsnLysProLysAsnArg 1360  
 QY 246 TATGCGATGTCATGCGCTACAGACACACTCTGAGTCATGCTTACCTATGATGCGCTAC 305  
 Db 1361 TyrAlahAsnValIleAlaTyrAspHisSerArgValLeuLeuThrSerlIeAspLysAl 1380  
 QY 306 CCCGGAGTGCATACATGCAATGCGCAATGATGCTTACCGGACAGCAATGCGCTAC 365  
 Db 1381 ProGlySerAspTyrIleAsnAlahAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 1400  
 QY 366 ATGCGCAGGACGAGGCCCCCTGGCCAGACATGGGCGATTTTGGAGATGGTGTGGAA 425  
 Db 1401 lIeAlaTrpGlnGlyProLeuMetProGluThrMetGlyAspPheTrpArgMetValTrpGlu 1420  
 QY 426 CAGCCACAGGCGCACTGTGTCATGATGACAGCGCTGGAGAGAAATCCCGGTAATAATGT 485  
 Db 1421 GlnArgTrpAlahThrValValMetMetThrArgLeuGluGlyLysSerArgValLysCys 1440  
 QY 486 GATGAGTACTGGCCAGCCCGTGGACACGAGACCTGTGGCTTATTCAGGTGACCTGTGG 545  
 Db 1441 AspGlnTyrTrpProAlahArgGlyThrGluTrpGlyLeuIleGlnValThrIleVal 1460  
 QY 546 GACACAGTGGAGCTGGCCACATACCTGTGGCAGCTTGGCAGCTGCACADAAGTGGCTGC 605  
 Db 1461 AspTrpValGluLeuAlahThrTyrThrMetArgTrpPheAlaLeuAlahLysSerGlySer 1480  
 QY 606 AGTGAAGCGGTGAGCTGCGTCAAGTTTCAGTTCATGCGCTGGCCGAGACCATGCTTGC 665  
 Db 1481 SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 1500

QY 666 GAGTACCAACTCCCATCTGCGCTTCTACGACGGGTCAAGGCTCAAGCCCTAGAC 725  
 Db 1501 GluTyrProThrProThrIleuLahPheLeuArgArgValLysAlahLysAsnProLeuAsp 1520  
 QY 726 GCAGGCGCCATGCTGTGATGATGCTGACGCGCGGCGTGGCCGACCGGCTTCATGCTG 785  
 Db 1521 AlaGlyProMetValValahLysSerAlahGlyValGlyArgThrGlyLysPheIleVal 1540  
 QY 786 ATTGATGCCATGTGAGCGGATGAAGACGAGAAACGCTGGACATCATGGCCACGCG 845  
 Db 1541 lIeAspAlahMetLeuGlnLuhArgMetLysGlnLysTrpValAspLleThrGlnLysVal 1560  
 QY 846 AACTGCATGCGATCAGACAGCACTACATGATGTCAGACAGGAGACCATGATGCTTCATC 905  
 Db 1561 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGlnAspLleThrValPheIle 1580  
 QY 906 CATGAGGCGCTCTGGAGGCTGCCACGTCGCGCCACACAGAGGTGCTGCCGCAACTG 965  
 Db 1581 HisGluAlahLeuLeuGlnLuhAlahMetCysGlnHisThrGluValLeuLahArgAsnLeu 1600  
 QY 966 TATGCCCATCAGACAGCTGGGCGCAAGTGCCTCCAGGGGAGAGTGAACGCGCATGGAG 1025  
 Db 1601 TyrAlahHisIleGlnLysLeuGlnValProProGlyGlySerValThrAlahMetGlu 1620  
 QY 1026 CTCGAGTTCAGTTCCTGGCCAGCTCCAGAGCCACACAGCTCCGCTTCATCAGCGCCAC 1085  
 Db 1621 LeuGluPheLysLeuLeuLahAsnSerLysAlahHisThrSerArgPheIleSerAlahAsn 1640  
 QY 1086 CTGCCCTGCACACAGTTCAAGAACCGGCTGTGAACATATGCTTCAGAAATGACCGCT 1145  
 Db 1641 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 1660  
 QY 1146 GTGTGTCGACCCCATCGCTGTGGAGGCGCTGACTATGATCAATGCAAGCTTCGCG 1205  
 Db 1661 ValCysLeuGlnProLleArgGlyValGlnGlySerAspTyrIleAsnAlahSerPheLeu 1680  
 QY 1206 GATGCTTATAGACAGACAGAGGCTCATATAGCTTACACAGAGGCTCTGGACAGAGACAC 1265  
 Db 1681 AspGlyTyrArgGlnGlnLysAlahTyrIleAlahThrGlnGlyProLeuAlahLysThr 1700  
 QY 1266 GAGGACTTGTGGCGCATGCTATGGGAGACACAAATTCACCATATGCTCATGCTGACACAG 1325  
 Db 1701 GluhAspPheTrpArgMetLeuTrpGlnHisAsnSerThrIleAlahMetLeuThrLys 1720  
 QY 1326 CTTCGAGATGAGGCGAGGAAATGCCACAGTACTGGCCGACAGAGGCTCTGCTGCC 1385  
 Db 1721 LeuArgGluMetGlyArgGlyLysCysHisGlnTyrTrpProAlahLuhArgSerAlahArg 1740  
 QY 1386 TACGACTTTTGTGTGACCCGATGCTGAGTACAAACATGCCCCAGTATATCTGCGT 1445  
 Db 1741 TyrGlnTyrPheValValahAspProMetAlahGluTyrAsnMetProGlnTyrIleLeuArg 1760  
 QY 1446 GAGTTCAGAGTACAGGATGCCCGGAGATGGGACGTCAGAGCAATCCGAGTTCAGATTCC 1505  
 Db 1761 GluhPheLysValThrAspAlahArgAspGlyGlnSerAlahTyrIleArgGlnPheGlnPhe 1780  
 QY 1506 ACAGACTGGCCAGACAGGCGCTGCCCAAGACAGGCGAGAGGATTCATTCATTCATCGGG 1565  
 Db 1781 ThrAspTrpProGlnGlnLysAlahProLysThrGlnGlyGlnPheIleAspPheIleGly 1800  
 QY 1566 CAGGTGCATTAAGACCAAGAGAGAGCTTGGACAGATGGGCTTATCAGGCTGCATGCACT 1625  
 Db 1801 GlnValahLysLysThrLysGlnLuhPheGlnLysAspGlyProLleThrValahLysCysSer 1820  
 QY 1626 GCTGCGCTGGGCGGACCGGAGGTTCATCACTGTGAGCATGCTCTGGAGCGCATGGCC 1685  
 Db 1821 AlaGlyValGlyArgThrGlyValPheIleThrLysSerIleValahLeuGlnLuhArgMetArg 1840  
 QY 1686 TATGAGGCGGTGCGACATGTTTCAGACCGGAGAGACCTTCGTAACACAGGCTCTGCC 1745  
 Db 1841 TyrGlnGlyValahValahAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAlah 1860

Oy	1746	ATGTCGAGACAGAGCAGCGACTTTCACGTGGCCCTGAGATCACTGCAC	1809
Dd	1861	MetvalGlnThrGluAspGlnTrpGlnLeuCysTryrAlaGalaIleuGlnIuTrpLeuGly	1860
Oy	1806	AGCTTGACCACATATGCAACG	1826
Dd	1881	SerheapshtsITyrAlaIthr	1887
RESULT 2			
O9EQ17			
ID	O9EQ17	PRELIMINARY;	PRT; 1898 AA.
AC	O9EQ17:		
DT	01-MAR-2001 (TREMBLEl. 16, Created)		
DT	01-MAR-2001 (TREMBLEl. 16, Last sequence update)		
DT	01-JUN-2002 (TREMBLEl. 21, last annotation update)		
DE	Tyrosine phosphatase IAR.		
GN	ptprf.		
OC	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCHI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=THYMUS;		
KX	MEDLINE=21135493; PubMed=11241288;		
RA	Terszowski G., Dankowski A., Hendriks W.J.A.J., Rolink A.G.,		
RA	Kisielow P.;		
RT	"Within the hemopoietic system, IAR phosphatase is a T cell lineage-		
RT	specific adhesion receptor-like protein whose phosphatase activity		
RT	appears dispensable for T cell development, repertoire selection and		
RT	function."		
RL	Eur. J. Immunol. 31:832-840(2001).		
DR	HSMB; AF300943; AAC40194.1; -		
DR	HSP; P18052; 1YFO.		
DR	InterPro: IPRO03962; FNIII_repeat.		
DR	InterPro: IPRO03961; FN_III.		
DR	InterPro: IPRO03599; Ig.		
DR	InterPro: IPRO03598; Ig_C2.		
DR	InterPro: IPRO03600; Ig_Like.		
DR	InterPro: IPRO03006; Ig_MHC.		
DR	InterPro: IPRO03595; pTPC_motif.		
DR	InterPro: IPRO00387; TYR_phosphatase.		
DR	InterPro: IPRO00242; Tyr_PP.		
DR	pTiam; PF00041; fn3; 7.		
DR	pTiam; PF00047; Ig; 3.		
DR	pTiam; PF00102; Y-phosphatase; 2.		
DR	PRINTS: PRO0014; ENTPEPIL.		
DR	PRINTS: PRO0700; PRTRYPHPTASE.		
DR	SMART: SM00060; FN3; 6.		
DR	SMART: SM00409; IG; 3.		
DR	SMART: SM00408; IGC2; 3.		
DR	SMART: SM00410; IG_Like; 2.		
DR	SMART: SM00194; pTPC; 2.		
DR	SMART: SM00404; pTPC_motif; 2.		
DR	PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.		
DR	PROSITE: PSS0056; TYR_PHOSPHATASE_2; 2.		
DR	PROSITE: PSS0055; TYR_PHOSPHATASE_PTP; 2.		
KW	Hydrolase; Immunoglobulin domain; Repeat		
SO	SEQUENCE	1898 AA; 211504 MW; EPD4BDJ1IB532A4A CRC64;	
Alignment Scores:			
Pred. No.:	2,7e+241	Length:	1898
Score:	3175.00	Matches:	595
Percent Similarity:	99.01%	Conservative:	6
Best Local Similarity:	98.02%	Mismatches:	6
Query Match:	49.27%	Indels:	0
DB:	11	Gaps:	0
US-09-743-492-1 (1-3467) x O9EQ17 (1-1898)			
Oy	6	GCATGTAAGAGCATCTTCGTCGCCACATCTCTGACACCTGTGAGATGCGAGAGCTCAAC	65
Dd	1292	GlllleuuuyspsSerleuauaiAhIsSerAspPrIvaGlImetrGrgrgleuSn	1311

QY	66	TACAGACCCAGGATATGGAGACACACACCCATCCCATACGAGCTGGCGGACAC	125
Db	1312	TyrGlnThrProGlyMetAlaGlnHisProProIlePheTolIenHisAspLeuAlaAspHis	1331
QY	126	ATCAGAGCGCTCAAGAGCAACGATGGCGCTCCAGTTCTCCAGAGTATGATGATCCATC	185
Db	1332	IleGluThrGluLeuLysAlaIleAsnAspGlyLeuLysPheSerGlnGluTyrGlnSerIleAsp	1351
QY	186	CCTGGACAGCAGTTCCACGTGGGAGAAATTCAAACCTGGAGAGTAAACAAGCCCAAGACCC	245
Db	1352	ProGlyAlaGlnPheThrTrpGluAsnSerAsnSerGluValAlaHisLysProLysAsnArg	1371
QY	246	TATGCAATGTCATCGGCTACGACCACTCCGAGTATCTCTTACCTATGATGAGGCTCC	305
Db	1372	TyrIleAspValIleAlaTyrAlaPheHisSerArgValIleLeuThrSerIleAspGlyVal	1391
QY	306	CCGCGAGTGAATCATCAATGCCAATCATGATGAGTACCGGACAGAAATGCTGAGAA	425
Db	1412	IleAlaThrGlnGlyProLeuProGluThrMetGlnLysPheTrpArgMetValTrpIle	1431
QY	426	CAGCGACGGCCACTGTGGTCATGATGACACGGCTGGAGAAATCCCGGGTAAAAAGT	485
Db	1432	GlnArgThrAlaThrValValMetMetThrArgLeuGlnGluLysSerArgAlaLysGly	1451
QY	486	GATCAGTACTGGCCACCGCTGGCACCCGAGACCTGTGGCTTATTCAGTGACCTGTGG	545
Db	1452	AspIleThrTrpProValAlaArgGlyThrGlnThrTyrGlnIleGlnValAlaThrIleuVal	1471
QY	546	GACACAGTGGAGCTGGCCACATACACTGAGGCGGACCTTGACACTCCACAAGATGGCTCC	605
Db	1472	AspThrValGluLeuAlaThrTyrTrpMetArgThrPheAlaIleuHisLysSerGlySer	1491
QY	606	AGTGAAGCGTGAAGCTGCCTCAGTTTCAGTTTCATGGCTGACCAAGCATGAGATTCCT	665
Db	1492	SerGluLysArgGluLeuAlaArgGlnPheGlnPheMetAlaTrpProAspIleGlyAlaPro	1511
QY	666	GAGTACCCACTCCCATCCCTGGGCTTCCTCAACAGCGGCTCAAGGCTGCAACCCCTTAAC	725
Db	1512	GluThrProThrProIleLeuAlaPheLeuAlaGluValLysAlaCysAsnProLeuAsp	1531
QY	726	GCAGGCGCCATGTGTGTGCTGCTGACACGCGGCGGTGGCGGACCGGCTTTCATCTGTG	785
Db	1532	AlaGlyProMetValValHisCysSerAlaGlyValGlyAlaArgThrGlyCysPheIleVal	1551
QY	786	ATTATGCGCATGTGGAGGCGGATGAAAGCACAGAAAGCGGTGACATCTATGGCCACGTG	845
Db	1552	IleAspAlaMetLeuGluAlaGluMetLysHisGluLysGlyThrValAspIleTyrGluVal	1571
QY	846	ACTGCATCGGATACACAGAGAGCACTCATGAGTGCACACGAGGACACAGACTGTTCATC	905
Db	1572	ThrCysMetArgSerGlnAlaGlnAsnTyrMetValGlnThrGlnAspGlnTyrValPheIle	1591
QY	906	CATGAGCGCTGTGAGAGCTGCGCACGTGCGGACACAGAGAGTGCCTGCGCGCAACTG	965
Db	1592	HisGlnAlaIleuLeuGlnAlaIleAlaIleMetCysGlyHisThrGlnValIleuAlaArgAsnLeu	1611
QY	966	TATGCCCAATCCAGAAAGCTGGGGCCAAAGTGCCTCCACGGGGAAGAAGTGTACCGGCATGAG	1025
Db	1612	TyrAlaHisIleGlnLysLeuGlnValProProGlyLysSerValThrAlaIleTleu	1631
QY	1026	CTCAGATTCAAGTTGGTGGGCGCCACTCCAAAGGCCACACACTCCCGCTTACAGCCCAAC	1085
Db	1632	LeuGluThrLysLeuLeuAlaAsnSerLysAlaHisThrSerArgPheValSerIleAsn	1651
QY	1086	CTGCGCTGCACAAGTTCAAGAAACGGGTGGTGAACATGATGCTCCATGCAATGACCGCT	1145
Db	1652	LeuProCysAsnLysPheLysAsnAlaGluValAsnIleMetProTyrGlnIleuThrArg	1671

Qy	1086	CTCCCTCTGCAACAAGTTCAAGAACCCGGCTGGACATCATGCCCCTACGAATTGACCCCGT	1145
Db	1652	LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg	1671





Db 1772 GlubhelysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1791  
 QY 1506 ACAGACTGGCCAGACAGAGCGGCGTGGCCCAAGACAGCGAGGATTCATTGACTTCATCGG 1565  
 Db 1792 ThrAspTrpProGlnGlnGlyValProIlysrThrGlyGlnGlyPheIleAspPheIleGly 1811  
 QY 1566 CAGGTGCATTAAGACCAAGAGAGCAGTGTGGACAGATGGGCGCTATACAGGTGCAGTGCAGT 1625  
 Db 1812 GlnValHisLysThrLysGlnGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1831  
 QY 1626 GCTGGCCGGGGCCGACGCGGGGGTGTTCATCACTGTCAGCATCGTCGTCGAGCGGCGTGGCG 1685  
 Db 1832 AlaGlyValGlyArgThrGlyValPheIleThrLysSerIleValLeuGlnArgMetLys 1851  
 QY 1686 TATGAGGCGTGTGCAGCATGTTTCAGACGCTGAAGACCTGCGTACACAGCGTCTGCC 1745  
 Db 1852 TyrGlnGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 1871  
 QY 1746 ATGTGCGACAGACAGAGCAGCAGTATCAGTGTGCTACCGTGGCGCGCTGAGTACCTGGCG 1805  
 Db 1872 MetValGlnThrGlnAspGlnTyrGlnLeuGlyTyrArgAlaAlaLeuGlnTyrLeuGly 1891  
 QY 1806 AGCTTGACCACTATGCAACG 1826  
 Db 1892 SerPheAspHisTyrAlaThr 1898  
 RESULT 4  
 Q9IAJ0 PRELIMINARY: PRT: 1788 AA.  
 ID Q9IAJ0  
 AC Q9IAJ0  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Receptor protein tyrosine phosphatase LAR.  
 GN XPRP-LAR.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-20193505; PubMed-10727868;  
 RA Johnson K.G., Holt C.E.;  
 RT "Expression of CRYP-alpha, LAR, PTP-delta, and PTP-rho in the  
 RT developing xenopus visual system.";  
 RL Mech. Dev. 92:291-294(2000).  
 DR HSP; Pf0052; AAF43606.1; -  
 DR HSP; Pf0052; IYFO.  
 DR InterPro: IPR003962; FNIII\_repeat.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR003598; Ig\_c2.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR InterPro: IPR000242; TYR\_PP.  
 DR Pfam: PF00041; fn3; 7.  
 DR Pfam: PF00047; Ig; 3.  
 DR Pfam: PF00102; Y\_phosphatase; 2.  
 DR PRINTS: PR00014; FNTYPEIIT.  
 DR PRINTS: PR00700; PRTYPRHPTASE.  
 DR SMART: SM00060; FN3; 7.  
 DR SMART: SM00408; IGC2; 3.  
 DR SMART: SM00194; PTPC; 2.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE: PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE: PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Hydroxylase; Immunoglobulin domain; Repeat.  
 SQ SEQUENCE 1788 AA; 200271 MW; AB1925498669067 CRC64;

Alignment Scores: Pred. No.: 3.68e-232 Length: 1788  
 Score: 3059.00 Matches: 567  
 Percent Similarity: 97.53% Conservative: 25

Best Local Similarity: 93.41% Mismatches: 15  
 Query Match: 47.47% Indels: 0  
 DB: 13 Gaps: 0  
 US-09-743-492-1 (1-3467) x Q9IAJ0 (1-1788)  
 QY 6 GGAAGTAAAGAGACTCTTCTGCTGGCCCACTGCTGACCTGTGGAGATGCGGAGGCTCAAC 65  
 Db 1182 GlyLeuLysAspCysLeuLeuAlaHisSerSerAspProValGlnMetArgLeuAsn 1201  
 QY 66 TACCGAGCCCAAGATGCGAGACACCCACCACCCATCCCATCCAGCTGGCGGACAC 125  
 Db 1202 TyrGlnThrProGlyMetArgGlnHisProProIleProIleSerAspLeuAlaAspAsn 1221  
 QY 126 ATCGAGCCCTCAAGACCAAGATGCGCTCAAGTCTCCAGAGATGATGCTCATC 185  
 Db 1222 IleGlnArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGlnTyrGlnSerIleAsp 1241  
 QY 186 CTTGACAGCAGATTTCAGCTGGGAGAAATTCAACTGTGAGGTGACACAGCCCAAGACCGC 245  
 Db 1242 ProGlyGlnGlnPheThrTrpGlnAsnSerAsnLeuGlnValAsnLysProLysAsnArg 1261  
 QY 246 TATGGCAATGTCATCGCCTACGACACCACTGAGTCATCCTTACTATGATGCGCTC 305  
 Db 1262 TyrAlaAsnValIleAlaIleArgAspHisSerArgValIleLeuThrSerValAspAlaVal 1281  
 QY 306 CCCGAGTACTACATCAATGCAACTACATCATGAGTACCCGACCAAGACCAATGCTTAC 365  
 Db 1282 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 1301  
 QY 366 ATCGCCACGACAGGCGCCCTGCGCCGACACCATGGGCGATTTCTGGAGAAATGCTGGGAA 425  
 Db 1302 IleAlaThrGlnGlyProLeuProGlnThrIleThrAspMetArgMetMetTrpLys 1321  
 QY 426 CAGCGCAGCGGCACATGCTGATGATGACAGCGCGTGAGAGAAATGCCGGTAAATGT 485  
 Db 1322 GlnArgThrAlaThrIleValMetMetThrArgLeuGlnGlyLysSerArgValLysCys 1341  
 QY 486 GATCAGTACTGCGCCAGCCGCTGCGACCGAGACTGTGCGCTTATTCAGTACACCTGTG 545  
 Db 1342 AspGlnTyrTrpProSerArgGlySerGlnThrArgLysMetIleGlnValThrLeuMet 1361  
 QY 546 GACACAGTGAAGCTGGCCACATACACTGTGCGACCTTGCGACTTCACACAGATGGCTCC 605  
 Db 1362 AspThrValGlnLeuAlaThrTyrThrValArgThrPheThrValTyrLysAsnGlySer 1381  
 QY 606 AGTGAAGCGGTGAGCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 665  
 Db 1382 AsnGlnLysArgAspValArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 1401  
 QY 666 GAGTACCCCAACTCCCATCTGCGCTTCTTACAGACGGGTCAAGGCGCTGCACACCCCTGAC 725  
 Db 1402 GlnTyrProThrProIleLeuGlyPheLeuArgValLysAlaCysAsnProProAsp 1421  
 QY 726 GCAGGCGCCATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 785  
 Db 1422 AlaGlyPrometPheValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 1441  
 QY 786 ATGTATGCGCATGTGGAGCGGATGAGACAGACAGAGAGAGGTGGACATGATGCGCACCTG 845  
 Db 1442 IleAspAlaMetLeuGlnArgValLysLeuGlnLysThrValAspIleTyrGlyHisVal 1461  
 QY 846 ACCTGCATGCGATGCACAGACAGACATGATGTCAGAGAGGAGACCATGATGCTTCATC 905  
 Db 1462 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGlnAspGlnTyrIlePheIle 1481  
 QY 906 CATGAGGCGCTGTGGAGGCTGCGACGTGCGGACACACAGAGGTGCTGCCGCAACCTG 965  
 Db 1482 HisGlnAlaLeuLeuGlnAlaValMetCysGlyValThrGlnValProAlaArgSerLeu 1501  
 QY 966 TATGCCCCATTCACAGAGCTGGCCCAAGTGCCTCAGAGGAGAGGTGATACCGCCATGGAG 1025  
 Db 1502 TyrAlaHisIleGlnLysLeuSerGlnValProProGlyGlnSerValThrSerMetGln 1521

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OY 1026 CTCGAGTTCAAGTTGGTGGCCAGCTCCAAAGCCCAACGTCGCCGTTTCATCAGGCCAAC 1085
    |||
Db 1522 LeGIuPhelYsLeuEuAlaAsnSerLySaIhIstHSerTrpPheIIeSeAlaAsn 1341
OY 1086 CTGCCCCGCAACAAGTTCAAGAACCGGCTGTGTAGACATCATGCGCTTACGAATGACCCGT 1145
    |||
Db 1542 LeuProCysAsnLysPheYsAsnArgLeuValAsnIleMetProTrpArgIuLeuSerArg 1361
OY 1146 GTGTGCTCTGAGCCCATCCGTGGTGTGGAGGGCTGTGACTACATCATGCGCAGCTTCG 1205
    |||
Db 1562 ValSerLeuGIuPhelArgIleArgGlyValGIuGIYSerAspTrpIleAsnAlaSerPheIIe 1381
OY 1206 GATGGTTATAGACAGAGAAGGAGGCTCATATGCTACACAGAGGGGCTGTGGAGAGACACC 1265
    |||
Db 1582 AspGIYTYrArgGIuInGInLysGIYrIleAlaThrGInGInLysProLeuAlaGIuTrpThr 1601
OY 1266 GAGGACTTCTGGCGCATGCGATGGAGACAAATTCACATCATGCTCATGAGCCAAAG 1325
    |||
Db 1602 GIuAspPheTrpArgMetLeuTrpGIuIhIsAsnSerThrIleValIaMetLeuThrLys 1621
OY 1326 CTTCGGGAGATGGGCAAGGAGAAATGCCACCACTACTGGCCAGACAGCGCTGCTCGC 1385
    |||
Db 1622 LeuArgGIuMetGIYrArgGIuLysCysHIsGIYrTrpProAlaGIuArgSerAlaArg 1641
OY 1386 TACCAGTACTTGTGTGTGACCCGATGCGTGAATACACATGCGCCAGTATATCTGCGT 1445
    |||
Db 1642 TYrGIuTrpPheValIaIaAspPheAlaGIuTrpAsnMetProGIuTrpIleLeuArg 1661
OY 1446 GAGTTCAAGGTACAGGATGCCCGGATGGGACAGTCAAGCAATCCGGCAGTTCCAGTTG 1505
    |||
Db 1662 GIuPhelYsValIhAspAlaArgAspGIuInSerArgThrIleArgInPheGIuInPhe 1681
OY 1506 ACAAGTGGCCAGACAGAGGCGCTGCCCAAGACAGCGAGGAGTTCATGACTTCATCGGG 1565
    |||
Db 1682 ThrAspTrpProGIuInGInLysValProLysThrGIYGIuIhLeuAspPheIIeGIY 1701
OY 1566 CAGGTGCATTAAGACCAAGGAGGAGTGTGGACAGATGGGCTTCACGCGGACCTCGAGT 1625
    |||
Db 1702 GIuValhIstLysThrLysGIuInPheGIuInAspGIYProIleThrValhIstCysSer 1721
OY 1626 GCTGGCGTGGCGCCAGCCGGGGTGTTCATCATCTGATCAGCATCGCTCTGGAGCCAGCGC 1685
    |||
Db 1722 AlaGIYValGIYrArgThrGIYrValPheIleThrLeuSerIleValLeuGIuArgMetArg 1741
OY 1686 TATGAGGGCGTGTGCATGTTTCAGACCGGTAAAGACCCCTGGTACACAGCGTCTGCC 1745
    |||
Db 1742 TYrGIuGIYValIaIaAspMetPheGIuInThrValLysThrLeuArgThrGIuArgProAla 1761
OY 1746 ATGGTGCACAGACAGAGACCAAGTATCAGCTGTGCTACCGTGGCGCCCTGGAGTACCTCGC 1805
    |||
Db 1762 MetValGIuInThrGIuInAspGIuInTYrGIuInLeuCysTYrArgIaIaLeuGIuTrpLeuGIY 1781
OY 1806 AGCTTTGACCACATATCAACAG 1826
    |||
Db 1782 SerPheAspHIsTrpIaThr 1788

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RESULT 5

064696 PRELIMINARY; PRT; 582 AA.

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AC 064696;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Protein-tyrosine phosphatase, receptor-type, F polypeptide
DE (EC 3.1.3.48) (LAR protein) (Leukocyte antigen related) (Fragment).
OS PTPRF OR LAR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-BALB/C; TISSUE-BRAIN;
RX MEDLINE=95394448; PubMed=7665159;
RA Schaapveld R.Q.J., Van den Maadenberg A.M.J.M., Schepens J.T.G.,
RA Weghuis D.O., van Kessel A.G., Wieringa B., Hendriks W.J.A.J.;
RT "The mouse gene Ptpfr encoding the leukocyte common antigen-related
RT molecule LAR: cloning, characterization, and chromosomal
RT localization.";
RL Genomics 27:124-130(1995).
RN [2]
RP SEQUENCE OF 116-221 AND 405-512 FROM N.A.
RC STRAIN-BALB/C; TISSUE-BRAIN;
RX MEDLINE=93086603; PubMed=1454056;
RA Schepens J., Zeeuwen P., Wieringa B., Hendriks W.;
RT "Identification and typing of members of the protein-tyrosine
RT phosphatase gene family expressed in mouse brain.";
RL Mol. Biol. Rep. 16:241-248(1992).
RN [3]
RP SEQUENCE OF 116-221 FROM N.A.
RC STRAIN-BALB/C; TISSUE-BRAIN;
RX MEDLINE=95134232; PubMed=7832766;
RA Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.;
RT "A novel receptor-type protein tyrosine phosphatase with a single
RT catalytic domain is specifically expressed in mouse brain.";
RL Biochem. J. 305:499-504(1995).
CC -1- FUNCTION: IT IS POSSIBLE THAT LAR IS A CELL ADHESION RECEPTOR. IT
CC POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY
CC (PTPASE) (BY SIMILARITY).
CC -1- FUNCTION: THE FIRST PTPASE DOMAIN HAS ENZYMTIC ACTIVITY, WHILE
CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
CC THE FIRST ONE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN
CC TYROSINE + PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: EXTRACELLULAR REGION TYPE OF A CAM FAMILY (3 IG-LIKE
CC DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS), AND A
CC CYTOPLASMIC REGION COMPOSED OF TWO PTPASE DOMAINS.
CC -1- SIMILARITY: NO DPTP AND TO LAR.
DR EMBL: Z37988; CAA86070.1; -
DR EMBL: Z23061; CAA80596.1; -
DR EMBL: Z23049; CAA80584.1; -
DR HSSP: P18052; LYFO.
DR MGD: MGI:102695; Ptpfr.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PF00102; Y-phosphatase; 2.
DR PRINTS: PR00700; PTPYPHPTASE.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase; Receptor; Glycoprotein; Transmembrane; Cell adhesion;
KW Immunoglobulin domain.
FT NON_TER 1
FT DOMAIN <1 582 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 45 291 PROTEIN-TYROSINE PHOSPHATASE.
FT DOMAIN 334 582 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 223 BY SIMILARITY.
FT ACT_SITE 514 BY SIMILARITY.
SQ SEQUENCE 582 AA; 66965 MW; 933C3C08536342FE CRC64;

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Alignment Scores:

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pred. No.: 3,57e-232 Length: 582
Score: 3057.00 Matches: 572
Percent Similarity: 99.14% Conservative: 5
Best Local Similarity: 98.28% Mismatches: 5
Query Match: 47.44% Indels: 0
DB: 11 Gaps: 0

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US-09-743-492-1 (1-3467) x 064696 (1-582)

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OY 81 ATCGAGACCCACCACCATCCCATCCAGCTGCGGAGCAACATCGAGCGCTCAAA 140
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Db 1 MetArgAspHIsTrpProIleThrAspLeuAlaAspAsnIleGIuArgLeuLys 20

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OY 141 GCCAAGCATGGCCTCAAGTTCTTCCACGAGATATGAGTCCATGCAACCCCTGGACGACGATTTC 200
    |||
Db 21 AIAAsnAspGlyLeuLysPheSerGlnGluTyrGlnSerIleAspProGlyGlnGlnPhe 40
OY 201 ACGTGGGGAATTCACAACTCGAGGTGAGACAGCCCAACAGCCGCTATGCGAATGTCATC 260
    |||
Db 41 TTTTTPGluAsnSerAsnSerGlnValAsnLysProLysAsnArgTyrIleAsnValIle 60
OY 261 GCGTACGACACCTCTGAGTCACTCTTACCTATATGAGAGGCGTCCCGAGAGTCACTAC 320
    |||
Db 61 AlaTyrAspHisSerArgValLeuLeuThrSerIleAspGlyValProGlySerAspTyr 80
OY 321 ATCAATGCCAACTACATGCGATGCGTACCGCAAGACAGAAATGCGCTACATGCGCACGAGGC 380
    |||
Db 81 IleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGly 100
OY 381 CCCCGGCCGAGACCATGGGCGCATTTCTGGAGAAATGCGTGGGAGACGCGGCGCACT 440
    |||
Db 101 ProLeuProGluThrMetLysAspPheTyrArgMetValTyrPgluGlnArgThrAlaThr 120
OY 441 GTGTCTATGATGACACGCGCTGGAGAGAAATCCCGGTAAATGTGATGATGATGAGCA 500
    |||
Db 121 ValValMetMetThrArgLeuGlnGluTyrSerArgValLysCysAspGlnTyrTrpPro 140
OY 501 GCCCGTGGCAGCAGACCTGTGGCCTTATTCAGGTGACCGCTGTGGACACAGTGAAGCTG 560
    |||
Db 141 ValArgGlyThrGluThrGlyGluLeuIleGlnValThrLeuValAspThrValGluLeu 160
OY 561 GCCAATACACCTGTGGACCTTCCGACCTCCACAGAGTGGCTCCAGTGAAGAGCTGAG 620
    |||
Db 161 AlaThrTyrThrMetArgThrPheAlaLeuHisLysSerGlySerSerLysLysArgGlu 180
OY 621 CTGCGTCAAGTTTCAGTTATGCGTGGCCAGACCATGAGATGCGTCTGAGTACCACTGCC 680
    |||
Db 181 LeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValArgProGluTyrProThrPro 200
OY 681 ATCTGGCCTTCTCTAGCAGCGGGTCAAGGCGCTGCAACCCCGCTGAGACGAGCGCCATGCTG 740
    |||
Db 201 IleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAspAlaGlyProMetVal 220
OY 741 GTGCACTGCGAGCGGGGCTGGGCGGCAACCGGCTGCTTCACTGATGATGATGATGCTGG 800
    |||
Db 221 ValHisCysSerAlaGlyValGlyValGlyThrGlyCysPheIleValIleAspAlaMetLeu 240
OY 801 GAGCGATGAAGCAGACGAGACGAGTGCATCTATGCGCAGCTGATGCGATGCGATCA 860
    |||
Db 241 GluArgMetLysHisGlyLysThrValAspIleTyrGlnHisValThrCysMetArgSer 260
OY 861 CAGAGCAACTACATGCTGCGACGAGACGAGACAGACAGTACGTGTTGATGAGCGCTGCTG 920
    |||
Db 261 GlnArgAsnTyrMetValGlnThrGlnAspGlnTyrValPheIleHisGlnAlaLeuLeu 280
OY 921 GAGGCTGCGACGCTGGGCGGACACAGAGTGGCTGCGGCGCAACCTGATGCGCCACATCCAG 980
    |||
Db 281 GlnAlaAlaMetCysGlyHisThrGlnValLeuAlaArgAsnLeuTyrAlaHisIleGln 300
OY 981 AAGCTGGCGCAAGTGCCTCCACAGGAGAGTGCAGCGCATGAGCTGAGTTCAGTTCAAGTTG 1040
    |||
Db 301 LysLeuGlnGlnValProProGluLysIleSerValThrAlaMetGlnLeuGlnPheLysLeu 320
OY 1041 CTGGCCAGCTCCCAAGGCCACACAGTCCGCTTCATCAGCGGCCAACCTGCGCTGCAACAG 1100
    |||
Db 321 LeuAlaAsnSerLysAlaHisThrSerArgPheValSerAlaAsnLeuProCysAsnLys 340
OY 1101 TTCAGAAACCGGCTGGTGAACATCATGCCCTACGAATTGACCCGCTGTGTGTGACAGCC 1160
    |||
Db 341 PheLysAsnArgLeuValAsnIleMetProTyrGlnLeuThrArgValCysLeuGlnPro 360
OY 1161 ATCCGTGTGTGGAGGCTGTGACTACATCAATGCGACGTTCTGTGAGGTATATGACAG 1220
    |||
Db 361 IleArgGlyValGlnGlySerAspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGln 380

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OY 1221 CAGAAAGCCTACATAGCTACACAGGGGCGCTGTGGCAGAGACGAGGACGTTCTGGCGC 1280
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Db 381 GlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGlnSerThrGlnAspPheTrpArg 400
OY 1281 ATGCTATGGGACACAAATCCCAACATCATGCTCATGCTTACCAAGCTTGGGAGATGGCC 1340
    |||
Db 401 MetLeuThrGlnHisAsnSerThrIleIleValMetLeuThrLysLeuArgGlnMetGly 420
OY 1341 ACGGAGAAATGCCACACAGTACTGGCCACAGACGCGCTGTGCTGCGTACAGTACTTTGTT 1400
    |||
Db 421 ArgGlnLysCysHisGlnTyrTrpProAlaGlnArgSerAlaArgTyrGlnThrPheVal 440
OY 1401 GTTGACCGCATGGCTGAGTACAAACATGCCCAAGTATATCTCGTGGTGAAGTTCACAG 1460
    |||
Db 441 ValAspProMetAlaGlnTyrTrpAsnMetProGlnTyrIleLeuArgGlnPheLysValThr 460
OY 1461 GATGCCCGGAGATGGGACAGCAGACGAAATCCGGCAGTTTCCACTTTCACAGACTGGCCAG 1520
    |||
Db 461 AspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPheThrAspTrpProGlu 480
OY 1521 CAGGCGTCCCAAGACAGGAGGAGGATTCATTGACTTTCATGCGGAGAGTACATGAACC 1580
    |||
Db 481 GlnGlyValProLysThrGlnGlnGlyPheIleAspPheIleGlyGlnValHisLysThr 500
OY 1581 AAGAGCAGTTTGAACAGGATGGGCTTATCAGCGTGCACGTGACGTGCTGGCGCGCC 1640
    |||
Db 501 LysGlnGlnPheGlyGlnAspGlyProIleThrValHisCysSerAlaGlyValGlyArg 520
OY 1641 ACCGGGGTGTATCATCTTGAGCATGCTGCTGGAGCGGATGCGGTATGAGGGCTGGTC 1700
    |||
Db 521 ThrGlyValPheIleThrLeuSerIleValIleGlnArgMetArgTyrGlnIleValVal 540
OY 1701 GACATGTTTCAGACCGGTGAAGACCTGCGTACACAGCGTCCGCAATGGTGGCAGACAG 1760
    |||
Db 541 AspMetPheGlnThrValLysThrLeuArgThrGlnArgProAlaMetValGlnThrGln 560
OY 1761 GACCAATACAGCTGTGCTACCGTGGCGGCTGGAAGTACCTTGGGACGTTTGACCACTAT 1820
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Db 561 AspGlnTyrGlnLeuCysTyrArgAlaIleLeuGlnTyrLeuGlySerPheAspHisTyr 580
OY 1821 GCAAGC 1826
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Db 581 AlaThr 582

RESULT 6
OBR169 PRELIMINARY: PRT: 749 AA.
ID OBR169
AC OBR169-
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 86.1 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025145; AAH25145.1; -
KW Hypothetical protein.
SQ SEQUENCE 749 AA; 86082 MW; 421FC6B9B50C959E CRC64;

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Alignment Scores:

Pred. No.:	9,36e-223	Length:	749
Score:	2938.00	Matches:	540
Percent Similarity:	96.16%	Conservative:	36
Best Local Similarity:	90.15%	Mismatches:	23
Query Match:	45.59%	Indels:	0
DB:	11	Gaps:	0

US-09-743-492-1 (1-3467) x Q8R169 (1-749)

QY	30	CACHTCSTCTACACCTGTGGAGATGCGGAGGCTTAACCTACCAGACCCCAAGTATGCGAGAC	89
		: : : : :	
Db	151	HISProthraspProValIGlutineArgIleuAsnPhelGlnProGlyMetIaSer	170
QY	90	CACCACCACATCCCAATCACCGACCTGGCGGACAAACATGAGAGCGGCTCAACACCAACAT	149
		: : : : :	
Db	171	HISProProIleProIleIleuGluIleuAlaAspHisIleGluArgIleuLysIaAsnSP	190
QY	150	GGCCTCAAGTTCTCCACAGAGTATGAGTCCATGACCCCTGGACAGCACTTCACGTGGAG	209
		: : : : :	
Db	191	AsnIleuLysPheSerGlnGluTyrGluSerIleAspProGlyGlnGlnPheThrTyrPglu	210
QY	210	AATTCACAAACCGGAGGAGGAACAGCCCAAGACCGCTATGCGAATGTCATGCGCTACAGAC	269
		: : : : :	
Db	211	HISserAsnIleuGluValAsnLysProLysAsnArgTyrAlaAsnAlaIleIleIaTyrSP	230
QY	270	CACHTCGAGTCACTTACCTCTATGATGAGGCGGCTCCCGGAGAGTACATCAATACCC	329
		: : : : :	
Db	221	HISserArgValIleuIleuSerAlaIleGluGlyIleProGlySerAspTyrAlaAsnIa	250
QY	330	AACATACATCGATGGCTACCCGACAGCAGAATGCTACATGCTCCACGACGAGGCCCTCGCC	389
		: : : : :	
Db	251	AsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGlySerIlePro	270
QY	390	GAGACATGCGGCGATTTCTCGAGAAATGCTGTGGACACGCGACGCGCCACTGCTCATMG	449
		: : : : :	
Db	271	GluThrPheGlyAspPheThrPargMetIleTyrGluGlnArgSerAlaThrValIaMet	290
QY	450	ATGACACGCGCTGAGAGAGAAGTCCCGGCTAAATGTGATGACTACTGGCCACCGCTGAC	509
		: : : : :	
Db	291	MetThrLysIleuGlnGluArgSerArgValLysCysAspGlnTyrTyrProSerArgGly	310
QY	510	ACCGAGACSTGTGCGCTTATTCAGAGTACGACCTGTGGACAAACGTGACCTGGCCCAATAC	569
		: : : : :	
Db	311	ThrGluThrHisGlyIleuValGlnValThrIleuLysAspThrValGluIleuLysIaThrTyr	330
QY	570	ACTGTGGCACCTTCGCGACATCCACAGAGAGTGGCTCCAGAGAGAAGCGTAGCTGGCTAG	629
		: : : : :	
Db	331	CysValArgThrPheAlaIleuTyrLysAsnGlySerSerGluLysArgGluValaArgGln	350
QY	630	TTTACAGTTTACGGCTGGCCCAACACATGAGATTCCTGATACCCCAACTCCCTCGGCC	689
		: : : : :	
Db	351	PheGlnPheThrIleArgProAspHisGlyValIleProGlnIleProThrPheIleuLysIa	370
QY	690	TTTCTACGACGCGGTCAAGGCGCTCAACCGGCTTAGACGAGAGGCGCCATGGTGTGTCAGTGC	749
		: : : : :	
Db	371	PheIleuArgIleValLysThrCysAsnProIleAspIleGlyProMetValIaHisCys	390
QY	750	AGCGCGGCGGTGGCGCGCACCGGCTGCTTCATCGTGATTGATGATGATGATGGACGGATG	809
		: : : : :	
Db	391	SerIleArgValIleGlyArgThrGlyCysPheIleValIleAspAlaMetIleuGlnIaArgIle	410
QY	810	AAGACGAGGAAGGAGGTGGACATCTATGGCGACGCTGACCTGGATCGAATCAACAGAGAGAC	869
		: : : : :	
Db	411	LysHisGluLysThrValAspIleTyrGlyLysValThrIleuMetArgIaIleIaTrgAsn	430
QY	870	TACATGGTGCAGACGAGAGACAGTACAGCTGTTTCATCTCATGAGAGCGCTGCTGGAGGCTGCC	929
		: : : : :	
Db	431	TyrMetValGlnThrGlnAspGlnTyrIlePheIleHisAspAlaIleuIleuGlnIaVal	450
QY	930	ACGTGGCGGCGCACACAGAGTGGCTGGCGCGACCTGTATGGCCACATCCACAAGCTGGGC	989
		: : : : :	
Db	451	ThrCysGluAsnThrGluValProAlaArgAsnIleuTyrAlaTyrIleIleLysIleuThr	470
QY	990	CAATGGCTCCAGCGAGAGTGTGACCGGCGCATGAGCTGAGCTGCAATGATGCTGGCGACG	1049
		: : : : :	
Db	471	GlnIleGluThrGlyGluAsnValThrGlyMetGluIleuGlnIleuPheLysArgIleuIaSer	490
QY	1050	TCCAGAGCCACACGTCGCCGCTTCATACGCGCCCAACTCGCTCCGAACAATGTTCAAGAAC	1109
		: : : : :	
Db	491	SerLysAlaHisThrSerArgPheIleSerAlaAsnIleuProCysAsnLysPheLysAsn	510

QY	1110	CGGTCGGTGAACATCATATGCCCCCTACGAATTACACCCCTGTGTCTCTGACGCCATCCGTGTGT	1169
Db	511	ArgLeuValAsnIleMetProTyrGluSerThrArgValCysLeuGlnProIleArgGly	530
QY	1170	GTGGAGGGCTCTGACTCATCATATGCCAGCTTCTCTGTGATGGATTATGACAGCAAGAGGCC	1229
Db	531	ValGluGlySerAspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGlnMetIysAla	550
QY	1230	TACATAGCTACACAGGGGGCCCTTGCCAGAGAGACCCAGAGACTTCTGGCCATGCTATGG	1289
Db	551	TyrIleAlaThrGlnGlyProLeuAlaGluThrThrGlnAspPheThrPargMetLeuTyr	570
QY	1290	GAGCACATTCACCATCATCTGATCTGATGCTGACCAACTTCGGAGATGGCAGGAGAA	1349
Db	571	GluHisAsnSerThrIleValValMetLeuThrLysLeuAlaGluMetGlyArgGluLys	590
QY	1350	TGCCACCGTCTGCGCCAGAGAGACGGCTGCTGCGCTACAGACTTGTGTTTACCCG	1409
Db	591	CysHisGlnTyrTrpProAlaGluAlaArgSerAlaArgTyrGlnTyrPheValAlaAspPro	610
QY	1410	ATGGCTAGTACAACATGCCCCAGATATATCTGCTGCGAGTTCAAGTCAACGGATGCCGG	1469
Db	611	MetaIaGluTyrAsnMetProGlnTyrIleLeuAlaGluIupheLysValThrAspAlaArg	630
QY	1470	GATGGCAGTACAGAACATCCCGGCACTTCCACTTACACAGACTGGCCAGACGAGCGCTG	1529
Db	631	AspGlyGlnSerAlaArgThrValArgGlnPheGlnPheThrAspTrpProGluGlnIysAl	650
QY	1530	CCCAAGACAGCGCGAGGATTCATGACTTATGCTATGCGGCAGGTGCAATPAAGCAAGAGAG	1589
Db	651	ProLysSerGlyGluGlyPheIleAspPheIleGlyGlnValHisLysThrLysGluGln	670
QY	1590	TTTGACAGAGATGGGCGCTATCACGGTGCACATGCTGATGCGGTGGCGCCAGCGGGTG	1649
Db	671	PheGlyGlnAspGlyProIleSerValHisCysSerAlaGlyValGlyLysArgThrGlyAl	690
QY	1650	TTTCATCACTCTGACCATCTGCTGCTGAGACCGATCGCTAGTAGGGCGTGGTCACATGTT	1709
Db	691	PheIleThrLeuSerIleValIleGluAlaGlyMetArgTyrGlnGlyValValAspIlePhe	710
QY	1710	CAGACCGTGAAGACCTCTGCTATACAGACGCTGCTCCATGGTGCAGACAGAGAGCAGCAT	1769
Db	711	GlnThrValLysMetLeuAlaGlnThrGlnAlaArgProAlaMetValGlnThrGlnAspGlnTyr	730
QY	1770	CAGCTGTGCTACCGCTGGCGCCCTGGAGACTCTGGCAGCTTTGACCATATGCAACG	1826
Db	731	GlnPheCysTyrArgAlaAlaIleGluGlyTyrLeuGlySerPheAspHisTyrAlaThr	749
RESULT 7			
Q8BV0			
ID	Q8BV0	PRELIMINARY;	PRT; 1254 AA.
AC Q8BV0:			
DT	01-MAR-2002 (TREMBlrel. 20, Created)		
OC	01-MAR-2002 (TREMBlrel. 20, Last sequence update)		
DT	01-JUN-2002 (TREMBlrel. 21, last annotation update)		
DE	Protein tyrosine phosphatase, receptor type, delta A.		
GN	PTFRD.		
OS	Mus musculus (Mouse).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RM	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=DBA/2U, AND C57BL/6J; TISSUE=BRAIN;		
RA	Fehr C., Belknap J.K., Crabbe J.C., Buck K.J.;		
RT	"High resolution mapping of a quantitative trait locus for acute		
RT	ethanol withdrawal on mouse chromosome 4 and characterization of		
RT	potential candidate genes."		
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF326550; AL37406.1; -		
DR	EMBL; AF36559; AL37405.1; -		
DR	MGD; MGI:97812; Pfrd.		



Oy	1710	CANACCGTGAAGAACCCCTGCTATACACAGCGCTCCCATGTGGTCAGACAGAGACCAATGAT	1769
Db	1216	GlnfrhVallylsMetleuAagTrhgInaGrpAlaMeIvaIGlnThrGlubspelIntYr	12355
Oy	1770	CAGCTGCCTCACCCTGGCGGCCGCGAGGTACTCGTGACGCTTTGAGCACATGATCAACG	1826
Db	1236	GlnPhcygStrYarGalalalaLeuGIUTryLeuGIYSerPhnaspHisTrYtAlatr	1254
RESULT 8			
ID	091AJ1	PRELIMINARY;	PRT; 1896 AA.
AC	091AJ1;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	01-MAR-2002 (TrEMBLrel. 20, last annotation update)		
DE	Receptor protein tyrosine phosphatase delta.		
GN	XPPP-D.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;		
OC	Xenopodidae; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20193505; PubMed=10727868;		
RA	Johnson K.G., Holt C.E.,		
RT	"Expression of CrYP-alpha, LAR, PTP-delta, and PTP-rho in the		
RL	developing xenopus visual system."		
RM	Mech. Dev. 92:291-294(2000).		
DR	EMBL: AF197944; AAF43605.1; -.		
DR	HSSP: PI8052; IYFO.		
DR	InterPro: IPR003962; FNIII_repeat.		
DR	InterPro: IPR003961; FN_III.		
DR	InterPro: IPR003598; Ig_c2.		
DR	InterPro: IPR003006; Ig_MHC.		
DR	InterPro: IPR000387; TYR_phosphatase.		
DR	InterPro: IPR000242; Tyr_PP.		
DR	pfam: PF00041; fn3; 8.		
DR	pfam: PF00047; ig; 3.		
DR	pfam: PF00102; Y-phosphatase; 2.		
DR	PRINTS: PRO0014; ENTPPEII.		
DR	PRINTS: PR00700; PTPYPPHTASE.		
DR	SMART: SM00060; FN3; 8.		
DR	SMART: SM00408; IGc2; 3.		
DR	SMART: SM00194; PTPC; 2.		
DR	PROSITE: PS00383; TYR_PHOSPATASE_1; 2.		
DR	PROSITE: PSS0056; TYR_PHOSPATASE_2; 2.		
DR	PROSITE: PSS0055; TYR_PHOSPATASE_PTP; 2.		
KW	Hydrolase; Immunoglobulin domain; Repeat.		
SO	SEQUENCE 1896 AA; 213067 MW; 08AC9003034199NA CRC64;		
Alignment Scores:			
Fred. No.:	2.37e-221	Length:	1896
Score:	2922..00	Matches:	535
Percent Similarity:	96.31%	Conservative:	40
Best local Similarity:	89.61%	Mismatches:	22
Query Match:	45.34%	Indels:	0
DB:	13	Gaps:	0
US-09-743-492-1 (1-3467) x 091AJ1 (1-1896)			
OY	36	TCTGACCGCTTGAGATGCGGAGGCTCACTGACACGACCCGAGTATCGAGACCAACA	95
Db	1300	ThrsprrvralgluleuAtgaTgyldeuAsnpheginlThPrroGIYMeAlasnhisPro	1319
OY	96	CCCATCCCCATCACCGCATGTGGCGGACAACATCGAGCGGCTCAAAAGCCACGATGGCTC	155
Db	1320	ProtleorlleuGIuLeuGIuLeuGIuAspnhisileGIuArGIeUlyAlaAsnaSpmlen	1339
OY	156	AAGTTTCCCAGAGGATGATAGTGCATATCGACACCGCTGGACAGACATTGACTGGAGAAATTC	215
Db	1340	LysHserGerInguITryGIuSerIlleaSPrrroGIYngIngnlPheThTrPGlunHisSer	1359

QY	216	AACTGGAGGTGAACAAAGCCCAAGAACCCGCTATGCAATGTGCATGGCTACGACCACTCT	275
Db	1360	AsnLeuGlnValAsnLysProLysAsnArgTyrAlaAsnValIleLeuIleTyrAspHisSer	1379
QY	276	CGAGTCATCCTTACCTCTATGATGGGGTCCCCGGAGAGTACTACATCAATGCCAAATAC	335
Db	1380	ArgValIleuLeuSerAlaIleAspGlyIleProGlySerAspTyrIleAsnSerAsnTyr	1399
QY	336	ATCGATGGCTACCCGCAAGCAAGAAATGGCTCATGCGCCACGAGGGCCCCCTGGCCGAGAC	395
Db	1400	IleAspGlyTyrArgLysGlnAsnAlaTyrIleLeuIleGlnIleProLeuProIleuThr	1419
QY	396	ATGGGCGATTTCTGAGAAATGTGTGGGAACAGCGACGGCCACTGTGTGCATGATGACA	455
Db	1420	PheGlyAspPheThrArgMetMetTrrGlnArgSerAlaThrValValMetMetThr	1439
QY	456	CGGCTGGAGGAGAGTCCCCGGGTAAATGTGATCAGTACTGGCCAGCCCGTGGCAACGAG	515
Db	1440	LysMetGlnLysArgSerArgIleLysCysAspGlnTyrTrpProSerArgIleThrGlu	1459
QY	516	ACCTGTGGCTTTATTCAGGGAGGACCCCTTTGGACACAGTGAAGTGGCCCATACATACCTGG	575
Db	1460	ThrTyrGlyLeuIleGlnValThrLeuLeuAspThrValGluIleuAlaThrTyrThrVal	1479
QY	576	CGCACCTTCGACCTCCACAAAGAGTGGCTCAGTGAAGACGTGAAGCTGGCTCAGTTTCAAG	635
Db	1480	ArgThrPheIleAlaLeuTyrLysAsnGlySerSerGlnLysArgGluValArgGlnPheGln	1499
QY	636	TTTCATGGCTGGCCCAAGACATGGAAGTTCCGTGATACCCAACTCCATCTGGCTTCCCTGA	695
Db	1500	PheThrAlaTrpProAspHisGlyValArgGlnHisProThrProPheLeuAlaPheLeu	1519
QY	696	CGACGGCTCAAGGGCTCCCAACCCCGCTTAGACGACGAGGCCCATGGTGGTGCATGACGAGCCG	755
Db	1520	ArgArgValLysThrCysAsnProProAspAlaGlyProMetValValHisCysSerAla	1539
QY	756	GCGGTGGCGCACCGGCTGCTTCATGCTGATTTGATGCATGTTGAGCGGATGAAGAC	815
Db	1540	GlyValGlnArgThrGlnLysPheAsnValIleAspAlaMetLeuGlnArgIleArgHis	1559
QY	816	GAGAAAGCGGTGGACATCTATGGCCACGTGACCTGCATGCGATCACAGAGAACTACATG	875
Db	1560	GluLysThrValAspIleTyrGlnHisValThrLeuMetArgAlaGlnArgAsnTyrMet	1579
QY	876	GTGCGACGAGGACACAGTGCAGTTCATGCATGACAGGCGCTGTGGAGGCTCCGACGGC	935
Db	1580	ValGlnThrGlnAspGlnTyrIlePheIleHisAspAlaLeuLeuGlnAlaIleThrCys	1599
QY	936	GGCCACACAGAGTGCCTGCCCGCAACCTGTATGCCACATCCAGAAAGCTGGGCCCAAGTG	995
Db	1600	GlyAsnThrGlnValProAlaArgAsnLeuTyrAlaTyrIleGlnLysLeuThrGlnIle	1619
QY	996	CCTCCAGGGGAGAGTGTGACCCCATGAGAGCTGTGAAGTTCAAGTTGCTGGCCACGCTCCAG	1055
Db	1620	GluProGlyLysAsnValThrGlyMetGlnLeuGlnPheLysArgLeuAlaSerPheLys	1639
QY	1056	GCCCAACAGTCCGCTTCATCAGGGCCAACTCCCTGGCAACAAGTCAAGAACCGGCTG	1115
Db	1640	AlaHisThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLysAsnArgLeu	1659
QY	1116	GTGAACATCATGCCCTCAGAATTTGACCCCGTGTCTCTCACGCCCATCCGTGGTGTGAG	1175
Db	1660	ValAsnIleMetProTyrGlnUserThrArgValCysLeuGlnProIleArgGlyValGlu	1679
QY	1176	GGCTGTGACTACATCATGCCACGTTCTGTGATGGTTATAGACAGCAGAAGCCTACATA	1235
Db	1680	GlySerAspTyrIleAsnAlaSerPheIleAspGlyTyrArgGlnGlnLysAlaTyrIle	1699
QY	1236	GCTACACAGGGGCGCTGGGAGAGAGACAGCAGAGCAATCTTGGCGCATGCTAAGGAGAC	1295
Db	1700	AlaThrGlnLysProLeuAlaGluThrThrGlnAspPheThrArgMetLeuTrpIleHis	1719
QY	1296	AATTCCACACATCATGCTCATGCTGACCAGGCTTCGGGAANTGGCAGGAGAAATGCCAC	1355

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|||||
Db 1720 AsnSerThrIleValValMetLeuThrLysLeuArgIleMetGluValGluLysCysHis 1739
QY 1356 CAGTACTGGCCAGACAGACCCCTGCTGCTACAGACTTTGTTGACCCGATGGCT 1415
|||
Db 1740 GluTyrTrpProAlaGluValGlySerAlaArgTyrGlnTyrPheValValAspPheMetAla 1759
QY 1416 GAGTACAAATGCCCGCATATCTCGCTGAGTTCAGAGTACAGATGCCGAGATGGG 1475
|||
Db 1760 GluTyrAsnMetProGlnTyrIleLeuAlaGlnPheLysValIleAspAlaArgAspGly 1779
QY 1476 CAGCAAGCAATCCGGCGAGTTCAGTCAAGACGTCGACGAGCGGCGGTCGCCAAG 1535
|||
Db 1780 GluSerArgThrValAlaGlnPheGlnPheThrAspTrpProGluGlnGluValProLys 1799
QY 1536 ACAGGCGAGGATTCATTCATTCATCGGCGAGGTCGATAGACCAAGACGACTTTGGA 1595
|||
Db 1800 SecIylGluGlyPheIleAspPheIleGlyValAlaHisLysThrLysGluGlnPheGly 1819
QY 1596 CAGGATGGCCCTATCAGCGTGCTGCTGCACTGCTGCGTGGCGCCACCGGGGTTCATC 1655
|||
Db 1820 GluAspGlyProIleSerValHisCysSerAlaGlyValGlyArgThrGlyValPheIle 1839
QY 1656 ACCTGAGCATGCTGCGTGGAGCGCATGCGATGAGGGCGGTCGACATGTTCCAGACC 1715
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Db 1840 ThrLeuSerIleValIleGluValArgMetArgTyrGlnGluValValAspIlePheGlnThr 1859
QY 1716 GTGNAAGACCTGCGCTACACAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1775
|||
Db 1860 ValLysMetLeuArgThrGlnArgProAlaValAlaGlnThrGluAspGlnTyrGlnPhe 1879
QY 1776 TGCATCGGTCGCGCCCTGAGATCCTGCGCAGCTTTGACCACTATGCAACG 1826
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Db 1880 CysTyrArgAlaGlyLeuGluTyrLeuGlySerPheAspHisTyrAlaThr 1896
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RESULT 9
Q9UM81 PRELIMINARY: PRT: 1502 AA.
ID Q9UM81;
AC Q9UM81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE PpPsiGMA-(brain) precursor.
GN PpPsiGMA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
|||
RP SEQUENCE FROM N.A.
RA Endo N., Rutledge S.J., Opas E.E., Vogel R., Rodan G.A., Schmidt A.;
RT "Human protein tyrosine phosphatase-sigma: Alternative splicing and
RT inhibition by biophosphates.";
RL J. Bone Miner. Res. 0:0-0(1995).
DR EMBL: UAI1725; AAD09360.1; -.
DR HSSP: P18052; 1YFO.
DR InterPro: IPR003962; FNIII_repeat.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR000387; TYR_MHC.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00041; fn3; 4.
DR Pfam: PF00047; fn3; 4.
DR Pfam: PF00102; Y-phosphatase; 2.
DR PRINTS: PR00700; EMTYPHPTASE.
DR PRINTS: PR00700; EMTYPHPTASE.
DR SMART: SM00060; FN3; 4.
DR SMART: SM00408; IG_C2; 2.
DR SMART: SM00410; IG_Like; 1.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
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DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50053; TYR_PHOSPHATASE_PP; 2.
KW HydroLase; Immunoglobulin domain; Repeat; Signal.
FT SIGNAL 1 28 POTENTIAL.
SQ SEQUENCE 1502 AA; 168788 MW; AD6705AFEB0F3CFD CRC64;

Alignment Scores:
Pred. No.: 4,46e-218 Length: 1502
Score: 2880.00 Matches: 530
Percent Similarity: 94.32% Conservative: 35
Best Local Similarity: 88.48% Mismatches: 34
Query Match: 44.69% Indels: 0
DB: 4 Gaps: 0

US-09-743-492-1 (1-3467) x Q9UM81 (1-1502)
QY 30 CACTCTCTGTCGACCTGTGAGATGCGGAGGCTCACTACCAAGCCCGAGTATCGAGAC 89
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Db 904 HisProLysAspProValAlaGluMetAlaArgIleAsnPheGlnThrProGluMetLeuSer 923
QY 90 CACCCACCATCCCATCACCGACCTGGCGGACCAACATCGAGCGCTCAAGCCAGAT 149
|||
Db 924 HisProIleProIleAlaAspMetAlaGluHisThrGluArgLeuLysAlaAsnAsp 943
QY 150 GGCCTCAAGTTCTCCAGAGATATGATCCATGACCCCTGGACAGCACTTCACTGGAG 209
|||
Db 944 SerLeuLysLeuSerGlnGluTyrGluSerIleAspProGluGlnPheThrTrpGlu 963
QY 210 AATTCAACTCGAGGTGAGTGAACCAACCCAGAACCGTATGCGATGTCATGCTTACGAC 269
|||
Db 964 HisSerAsnLeuGluValAsnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAsp 983
QY 270 CACTCTGAGTCACTCTTACCTATGATGCGCTGCCCGGAGTGAATCAATGACC 329
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Db 984 HisSerArgValIleLeuGlnProIleGluGlyLeuMetGlySerAspTyrIleAsnAla 1003
QY 330 AACTACATCGATGCTACCGCAACAGAAATCCCTACATCGCCAGGAGGCCCTTCCG 389
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Db 1004 AsnTyrValAspGlyTyrArgArgGlnAsnAlaTyrIleAlaThrGlnGlyProLeuPro 1023
QY 390 GAGACCATGGCGGATTCCTGAGAAATGGTGGGAGACAGCGCACGCTGTGATG 449
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Db 1024 GluThrPheGlyAspPheTrpArgMetValTrpGlnArgSerAlaThrIleValMet 1043
QY 450 ATGACAGGCTGAGGAGAAATCCCGGTTAAATGTGATCATGTAAGTGGCCAGCCGCTGGC 509
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Db 1044 MethTrArgLeuGlnGluLysSerArgIleLysCysAspGlnTyrTrpProAsnArgGly 1063
QY 510 ACCGAGACCTGGCTTATTCAGTACGACCTGTGGACACAGTGGAGCTGGCCACATAC 569
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Db 1064 ThrIleThrTyrGlyPheIleGlnValThrLeuLysPheIleGluLeuAlaThrPhe 1083
QY 570 ACTGTGCGACCTTGGACATCCACAAAGTGGCTCCAGTGGAGAGCTGAGCTGCTGAG 629
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Db 1084 CysValAlaArgThrPheSerLeuHisLysAsnLysSerGlnLysValGluValAlaGln 1103
QY 630 TTTCAGTTTCATGGCTGGCCGACAGCATATGAGTTCCTGATCCACATCCCATCTGGCC 689
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Db 1104 PheGlnPheThrAlaTrpProAspHisGlyAlaProGluTyrProThrProPheLeuAla 1123
QY 690 TTTCATGAGCGGCTCAGAGCTGCAAGCCCTTAACAGCAGGAGGCCCAATGCTGCTGCTG 749
|||
Db 1124 PheLeuArgValLysTyrCysAsnProTAspArgIleGlyProIleValAlaHisCys 1143
QY 750 AGCGGCGGCTGGCGCCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 809
|||
Db 1144 SerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeuGluArgIle 1163
QY 810 AAGCAGCAAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 869
|||
Db 1164 LysProGluLysThrValAspValTyrGlyHisValThrLeuMetArgSerGlnArgAsn 1183
QY 870 TACATGCTGACAGACGAGGACCACTACGTGTTTCATGATGAGCGCTGCTGAGGCTGCC 929
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Db 1184 TyrtetvalglnthrgluaspdltyrserthelienhsiglualaleuGlualalval 1203
QY 930 ACGTGGCGCCACACAGAGGCTCTGCCGACACTGTATGCCACATCCAGAGCTGGGC 989
Db 1204 G1YcSglYsnthrgluvalProalAargSerleuTYralatYrlleGlInlyLeuvala 1223
QY 990 CAAGTGGCTCCAGGGAGAGTGTACCGCCATGGAGCTCGAGTTCAGTTCCTGCTGCCAGC 1049
Db 1224 GlnvalgluproglygluhsvalthrglymetoluleugluPhelysArgLeuAlasn 1243
QY 1050 TCCAGGCCACACAGCTCCGCTTCATGACGCGCAACCTGCCCTGACACAAATTCAGAAC 1109
Db 1244 SerlysalhsthrSeratrgPheleSerlalsnleuProCyslyslsPhelysasn 1263
QY 1110 CGGCTGTGAACATCATGCCCTACGAATTCAGCCGCTGTCTGTGCAGGCCATCCGTGT 1169
Db 1264 ArgLeuValasnIleMetProTyrGluSerThrArgValCysLeuGlnProIleArggly 1283
QY 1170 GTGGAGGGCTGTGACTACATCAATGCAGCTTCTGTGATGGTTATAGACAGCAAGGCC 1229
Db 1284 ValglulyserspTYrlleAsnalaserPheIleaspGlyTYrArgGlnInlysal 1303
QY 1230 TACATAGCTACACAGGGGCTCTGCGAGAGACCGAGACTCTGGCGCATGCTATGG 1289
Db 1304 TyrllealathrglnglyProleualagluthrthrGluaspPheTPrArgMetleuTPr 1323
QY 1290 GAGCACAATTCACCATCATGTCATGTCACCAAGCTTCGGAGATGGCGAGAGAGAA 1349
Db 1324 GluAsnAsnSerThrIleValIValMetleuThrIlysleuArgGluMetGlyArgGluLys 1343
QY 1350 TGGCACCAGTACTGGCCAGACAGAGCGCTGTCTGCTACCAAGTACTTTGTTGTGACCCG 1409
Db 1344 CysHisGlnTYrTPrProalagluArgSerIalArgTYrGlnTYrPheValIAspPro 1363
QY 1410 ATGGCTAGTACACAGCCCGCTATATCTGCTGCTGAGTTCAGAGTTCAGGAGATGCCGG 1469
Db 1364 MetIlealutyrAsnMetProGlnTYrIleleuArgGluPhelysValThrAspIalArg 1383
QY 1470 GATGGGACGTCAAGAGCAATCCGGCACTTCAGTTCACAGACTGCCAGAGAGCGCGTG 1539
Db 1384 AspIylGlnSeratrgThrValArgGlnPheGlnPheThrAspTPrProGluGlnGlyVal 1403
QY 1530 CCCAAGACAGGCGGAGTTCATGACTTCATCGGGCAGAGGTCATAGACCAAGAGCAG 1589
Db 1404 ProlysserGlygluGlyPheIleAspPheIleGlyGlnValHisLysThLysGlnGln 1423
QY 1590 TTGGAGACGATGGGCTATCATCAGGTGCACATGCTGCTGCGGGCGGCGAGCGGGTG 1649
Db 1424 PheGlyGlnaspGlyProIleSerValHisCysSerIalaglValGlyArgThGlyVal 1443
QY 1650 TTCATCATCTGACCATGCTCTGAGAGCGCATGCGCTATGAGAGGCGGTGTCAGATGTT 1709
Db 1444 PheIleThrIleuSerIleValIleuGluArgMetArgTYrGluGlyValIAspIlePhe 1463
QY 1710 CAGACCTGGAAGCCCTGCTACACAGCGTCTGCTGCGAGAGAGAGAGACAGATAT 1769
Db 1464 GlnThrValIysMetIleuArgThGlnArgProIalMetValGlnThrgluAspGlnTYr 1483
QY 1770 CAGCTGTGCTACGCTGGCGGCTGAGTACTGGCAGCTTGACCACTATGCAAGC 1826
Db 1484 GlnPheCysTYrGlnIalalaleuGlnTYrIleuGlySerPheAspHisTYrIalathr 1502

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OC Amphibia: Batrachia: Anura: Mesobatrachia: Pipoidae: Pipidae;
OC Xenopodidae: Xenopus.
OX NCBI_TaxID=8355;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=20193505; PubMed=10727868;
RA Johnson K.G., Holt C.E.;
RT "Expression of CRYP-alpha, LAR, PTP-delta, and PTP-rho in the
RT developing xenopus visual system.";
RL Mech. Dev. 92:291-294 (2000).
DR EMBL: AF198450; AAF43607.1; -.
DR HSSP: P18052; IYFO.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00102; Y-phosphatase; 2.
DR PRINTS: PR00700; PTPPHPTASE.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase.
FT NON_TER 1 1
FT SEQUENCE 615 AA; 70728 MW; 42593554887858AC CRC64;
SQ
Alignment Scores:
Pred. No.: 2.88e-217 Length: 615
Score: 2868.00 Matches: 528
Percent Similarity: 94.16% Conservative: 36
Best Local Similarity: 88.15% Mismatches: 35
Query Match: 44.51% Indels: 0
DB: 13 gaps: 0
US-09-743-492-1 (1-3467) x Q91A18 (1-615)
QY 30 CACTCTCTGTGACCCGTGTGAGATGGAGGCTCAACTACGACGCCAGTATGCGAGAC 89
Db 17 HisProthAspProValGlnMetIleArgAlaIleAsnPhelGlnThrProGlyMetleuAsn 36
QY 90 CACCCACCATCCCATCAGCAGCGCTGGGAGACAAATGCAGCGGCTCAAGCAAGCAT 149
Db 37 HisProIleProIleAlaIAspLeuIalGlnHisThrGlnHisLeuLysAlaIAsnAsp 56
QY 150 GGCCTCAAGTCTCCACAGAGTATGAGTCATCCAGCCTGGACAGACATTCACGGGGAG 209
Db 57 AsnLeuLysLeuSerGlnGlyIleValIleuSerValAspProGlyGlnGlnPheThrPdlu 76
QY 210 AATTCAAACCTGAGAGTGAACAACCCCAAGAACCGCTATGCAATGTCATCGCTACGAC 269
Db 77 HisSerAsnLeuGluValAsnLysAlaLysAsnArgTYrAlaAsnValIleIalatyAsp 96
QY 270 CACTCTGAGTATCTTACCTATATGATGATGATGATGATGATGATGATGATGATGATGAT 329
Db 97 HisSerArgValIleLeuLeuProValGlnGlyIleIleGlySerAspTYrIleAsnAla 116
QY 330 AACTACATCGATGGCTACCGAGACAGAAATGCCATCATCGCCAGCAGAGGCCCTGCCC 389
Db 117 AsnTYrIleAspGlyTYrArgLysGlnAsnAlaTYrIleAlaIArgGlnGlyAlaLeuPro 136
QY 390 GAGACCATGAGCGAATTCGTGAGATGGTGGGAACAGCGCCACGCGCATGTGCTGTCG 449
Db 137 GluthrPheGlyAspPheTPrArgMetValIleGlnIleArgSerIalathrValIalMet 156
QY 450 ATGACAGGCTGAGAGAGAACTCCCGGTAATGTGATGATGATGATGATGATGATGATGAT 509
Db 157 MetThrLysLeuGlnGluLysSerArgValLysCysAspArgIleTYrTPrProSerArggly 176
QY 510 ACCAGACCTTGCGCTTATTCAGGTGACCTGTGGACACAGTGGAGCTGGCCATAC 569
Db 177 ThrIleuThrTYrGlyMetIleGlnValThrIleuAspPrlIleGlnIleuAlaIathrPhe 196
QY 570 ACTGTGGCAGCTTCGCGCTCCACAAAGAGTGGCTCAGTATGAGAGCGGAGCTGGCTGAC 629
Db 197 CysValIalArgThrPheSerIleuHisLysSerGlySerSerGlyLysArgGluValArgGln 216

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QY 630 TTTCAGTTCATGGCCCTGGCCAGACATGGAGTTCTGAGTACCCCAATCCCATCTGGCC 689
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Db 217 PheGlnPheThrAlaTrpProAspHisGlyValProGluTrpProThrProPheLeuAla 236
QY 690 TTCTACGACGAGGCTCAAGGCTTCGAACCCCTTACAGCAGAGGCCCATGGTGTGACATGC 749
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 237 PheLeuAlaGlyValIleLysThrCysAsnProProAspAlaGlyProIleValIleHisCys 256
QY 750 AGCGGGGAGGGGGGGCCGCCCTGCTTCATGCTGATGGATTCGCAATGGTGGAGGGGATG 809
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 257 SerAlaGlyValIleGlyTrpThrGlyCysPheIleValIleAspAlaLeuGluValIle 276
QY 810 AAGCAGCAAGACGAGCTGACATCTATGGCCAGCAGTGCATCGCATCCAGACAGAGAAC 869
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 277 LysHisGluLysThrValAspIleTyrglyHisValThrLeuMetLysSerGlnAsn 296
QY 870 TACATGTCACAGCAGGAGACACAGTACGTGTTCCATCCATGAGCGCTGTCGAGCTGCC 929
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 297 TyrMetValGlnThrGluAspGlnTyrSerPheIleHisAspAlaLeuGluAlaVal 316
QY 930 AGCTGGGGCAGACAGAGGCTGCGCCGACATGCTGATCCCAATCCAGAACGTCGGGC 989
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Db 317 AlaCysGlyAsnThrGluValProAlaArgAsnLeuTyrThrTyrIleGlnAsnLeuAla 336
QY 990 CAAGTCCCTCCAGGGAGAGTGTGACCGCCATGAGCTCGAGTTCAAGTTCTGCGCCAGC 1049
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Db 337 GlnIleAspValGlyGluHisValIleGlyMetGluLeuGluPheLysArgLeuAlaAsn 356
QY 1050 TCCAGGCCCCACAGCTCCCGCTTCATCAGCGCCACCTCCCTGCACAAGTTCAAGAAC 1109
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 357 SerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLysAsn 376
QY 1110 CGGCTGTGACATCATGCCCTGACGAATGACCGTGTGTGTGTCGAGCCCATCCGGGT 1169
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Db 377 ArgLeuValAsnIleMetProTyrGluThrThrArgValCysLeuGlnProIleArgGly 396
QY 1170 GTGAGAGGCTGTGACTATACATCAATGCCAGCTTCCTGGATGTTATGACAGCAAGGCC 1229
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Db 397 ValGluGlySerAspTyrIleAsnAlaSerPheIleAspLysTyrArgGlnGlnLysAla 416
QY 1230 TACATAGCTACACAGGCGCTCTGGCAGAGACAGCAGGACCTTCGGCCATGCTATGG 1289
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Db 417 TyrIleAlaThrGlnIleProLeuAlaGluThrThrGluAspPheTrpArgMetLeuTyr 436
QY 1290 GAGCACAATTCACCATCATCGTCATGTCAGCAGCTTCGGAGATGGGACAGGAGAA 1349
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 437 GluAsnAsnSerThrIleValIleValMetLeuThrLysLeuArgGluMetGlyArgGluLys 456
QY 1350 TGGCACCAGTACTGCGCCAGCAGACGCTGTCTGCTACCACTACTTGTGTGACCCG 1409
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 457 CysHisGlnTyrTrpProAlaGluArgSerAlaArgTyrGlnTyrPheValIleAspPro 476
QY 1410 ATGGTGATATACAACTGCCCCAGTATATCTCTCGTAGATTCAAGGTACAGATGCCCGG 1469
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 477 MetAlaGlnTyrAsnMetProGlnTyrIleLeuArgGluPheLysValIleTrpAspAlaArg 496
QY 1470 GATGGCAGCAAGCAATCCGCGAGTTCGATTCACAGATCGGCGACAGGAGGGGCTG 1529
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 497 AspGlyGlnSerArgThrValArgGlnPheGlnPheThrAspTrpProGluGlnGlyVal 516
QY 1530 CCCAAGACGCGCAGGAGTTCATTCATTCATGCGGCGAGGTGATAGACCAAGAGAGCAG 1589
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 517 ProLysSerGlyGlnLysPheIleAspPheIleGlyGlnValHisLysThrLysGluGln 536
QY 1590 TTTCGACAGATGGCCCTATACGCTGACGTGCTGCTGGCGTGGCCGACCGGGGTG 1649
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Db 537 PheGlyGlnAspLysProIleSerValHisCysSerAlaGlyValGlyArgThrGlyVal 556
QY 1650 TTTCATACGTCGATCGCTGCTGAGGCGCATGCGCTATAGGGCGGTGCGCATGTTT 1709
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 557 PheIleThrLeuSerIleValIleGluArgMetArgTyrGlnIleValIleAspIlePhe 576

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QY 1710 CAGACCGTGAAGACCTCGCTACACAGCGTCTGCCATGTGTCGACAGACAGCACTAT 1769
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Db 577 GlnThrValLysMetLeuArgThrGlnArgProAlaMetValGlnThrGluAspGluTyr 596
QY 1770 CAGCTGTCTACCGCTGGCGCCCTGGAGTACTCTGGCAGCTTTGACCACTTTCGAAG 1826
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 597 GlnPheCysTyrGlnAlaAlaLeuGluTyrLeuGlySerPheAspHisTyrAlaThr 615

RESULT 11
Q90815
ID Q90815 PRELIMINARY; PRT; 1499 AA.
AC Q90815;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Protein-tyrosine phosphatase.
GN CRYPALPHAL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=95001563; PubMed=7918104;
RA Stoker A.W.;
RT "Isoforms of a novel cell adhesion molecule-like protein tyrosine
phosphatase are implicated in neural development.";
RL Mech. Dev. 46:201-217(1994).
DR EMBL; L32780; AA64460.1; -.
DR HSSP; P18052; 1YFO.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR00242; TYR_PP.
DR Pfam; PF00041; fn3; 4.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRYDHPRTASE.
DR SMART; SM00060; FN3; 4.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS0055; TYR_PHOSPHATASE_PTP; 2.
KW Hydroxylase; Immunoglobulin domain.
SQ SEQUENCE 1499 AA; 168570 MW; A1FBD6E3C2453F82 CRC64;

Alignment Scores:
Pred. No.: 4, 31e-217 Length: 1499
Score: 2667.50 Matches: 527
Percent Similarity: 94.328 Conservative: 38
Best Local Similarity: 87.988 Mismatches: 33
Query Match: 44,508 Indels: 1
DB: 13 Gaps: 1

US-09-743-492-1 (1-3467) x Q90815 (1-1499)
QY 30 CACTCTCTGACCCCTGTGGATGCGGAGCTCACTACAGACCCCGATATGCGAGAC 89
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Db 902 HisProLysAspProValGluMetArgArgIleAsnPheGlnThrProGluMetLeuSer 921
QY 90 CACCCACCCATCCCATCAGCAGCTGGCGGACAACTCGACGGCCCTCAAGCAAGCAAGAT 149
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 922 HisProProIleProValSerGluLeuAlaGluHisThrGluHisLysValAlaAsnAsp 941
QY 150 GGCCTCAAGTTCTCCGAGGATATGATGCATGCAGCCCTGAGACAGCTTACAGTGGAG 209
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 942 AsnLeuLysLeuSerGlnGluTyrGluSerIleAspProGlyGlnGlnPheThrTyrPglu 961
QY 210 AATTCAAACTGAGGTGAACAAGCCCAAGACCCGCTATGCGAATGTCATGCGCTACGAC 269

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Db 962 HisSerAsnLeuValAlaValnLysProLysAsnArgThrAlaValnValIleAlaTyrAsp 981
QY 270 CACTCTCGAGTACTCCTTACCTCTATCGATGGCTCCCGGAGTGAATCATATGCC 329
Db 982 HisSerArgValIleLeuLeuProIleGluGlyIleValGlySerAspTyrIleAsnAla 1001
QY 330 AACTATCATGATGGTACCGCAGAGAAATGCTTACATGCGCCACGAGGGCCCTGCCC 389
Db 1002 AsnArgTyrLeuSerLysThrArgLysGlnAsnAlaTyrIleAlaThrGlnGlyProLeuPro 1021
QY 390 GAGACCATGGGCGCATTTCTGGAGAAATGTTGGGAACAGCGACGCGCACTGTGTCATG 449
Db 1022 GluThrPheGlyAspPheThrArgMetValTyrGluGlnArgSerAlaThrIleValMet 1041
QY 450 ATGACACGGCTGGAGAGAAAGTCCCGGGTAAATGTGTATCAGTACTGGCCAGCCGTGGC 509
Db 1042 MetThrLysLeuGlnGlyLysSerArgIleLysCysAspGlnTyrTrpGluArgGly 1061
QY 510 ACCGAGACCTGTGGCTTATATCAGTGGACCTGTGGACAGTGGAGCTGGCCACATAC 569
Db 1062 ThrAspThrTyrGlyMetIleGlnValThrLeuLeuAspThrIleGluLeuAlaThrPhe 1081
QY 570 ACTGTGGCGACCTTGGACACTCCAGAGAGTGGCTCCAGTGAAGCGTGAAGCGTGGCAG 629
Db 1082 CysValAlaThrPheSerLeuHisLysAsnGlySerSerGluLysArgGluValArgGln 1101
QY 630 TTTCAGTTCATGGCTGGCGCAGACATGAGTTCGTAGTACCCAACTGCCATCTGGCC 689
Db 1102 PheGlnPheThrAlaThrProAspHisGlyValProGluTyrProThrProPheLeuAla 1121
QY 690 TTTCCTGAGACGGGTCAAGGCTGCAACCCCTGAGCGACAGGCGCCATGGTGGCTGCG 749
Db 1122 PheLeuAlaThrValLysThrCysAsnProProAspAlaGlyProIleValIleHisCys 1141
QY 750 AGCGCGGGGTGGCGCCGACCGGCTGTCATGCTGATGATGATGATGATGATGATGATGAT 809
Db 1142 SerAlaGlyValGlyLysThrArgLysPheIleValIleAspIleMetLeuGluArgGly 1161
QY 810 AAGCAGCAGAAAGAGCGGTGACATCTATGGCCAGCTGACCTGATGCGATGACAGAGAAC 869
Db 1162 LysHisGlyLysThrValAspIleTyrGlyLysValThrLeuMetArgSerGlnArgAsn 1181
QY 870 TACATGTCGAGCGAGGAGCGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 929
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Db 1202 AlaCysGlyAsnThrGluValProAlaArgAsnLeuTyrThrTyrIleGlnLysLeuAla 1221
QY 990 CAAGTCCCTCCAGGAGAGTGTGACCGCGCATGAGCTGAGTTCAGTTCAGTTCAGTTCAG 1049
Db 1222 GlnIleGlyValGlyLysThrValThrGlyMetGluLeuGlnPheLysArgLeuAlaAsn 1241
QY 1050 TCCAGAGCCCGACGCTCCGCTTCATCAGGCGCAACCTGCGCTGCGCAAGTTCAGAAC 1109
Db 1242 SerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLysAsn 1261
QY 1110 CGGCTGGTGAACATCATGCTGCTGCAATGACCGGTGTGTGTGTGTGTGTGTGTGTGTGT 1169
Db 1262 ArgLeuValAlaAsnIleMetProTyrGluThrThrArgValCysLeuGlnProIleArgGly 1281
QY 1170 GTGGAGGGCTGTGATCATCAATGCCAGGCTCTGTGGATGGTTATAGACAGCAGAACGCC 1229
Db 1282 ValGlnGlySerAspTyrIleAsnAlaSerPheIleAspTyrIleArgGlnGlnLysAla 1301
QY 1230 TACATGCTACACAGGGGCTGTGGCAGAGAGACCGAGAGACTTGTGGCCATGCTATAG 1289
Db 1302 TyrIleAlaThrGlnGlyProLeuAlaGlyThrThrGluAspPheThrArgMetLeuTyr 1321
QY 1290 GAGCAGAAATTCACATCATGCTGATGCTGACCAAGCTTCGGAGATGGCGAGGAGAAA 1349

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Db 1322 GluAsnAsnSerThrIleValIleValMetLeuThrLysLeuArgGluMetGlyArgGluLys 1341
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Db 1342 CysHisGlnTyrTrpProAlaGluArgSerAlaArgTyrGlnThrPheValIleAspPro 1361
QY 1410 ATGGCTGAGTACAAACAGCCCGCATATATCTGCTGAGTTCAGTTCAGGTCAGGATGCCCG 1469
Db 1362 MetAlaGluTyrAsnMetProGlnTyrIleLeuArgGluPheLysValThrAspAlaArg 1381
QY 1470 GATGGCGAGTCAAGAGCAATCCGCGACCTTCCAGTTCACAGACTGGCCAGAGAGCGGTG 1529
Db 1382 AspGlyGlnSerArgThrValArgGlnPheGlnPheThrAspTrpProGluGlnGlyVal 1401
QY 1530 CCCAAGACAGCGAGGAGTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 1589
Db 1402 ProLysSerGlyGlnGlyPheIleAspPheIleGlyLysValHisLysThrLysGluGln 1421
QY 1590 TTTCGACAGATGGGCGCTTATCAGCGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 1649
Db 1422 PheGlyGlnAspGlyProIleSerValHisCysSerAlaGlyValGlyArgThrGlyVal 1441
QY 1650 TTTCATCATCTGACATGCTGCTGAGCGCATGCGCATGAGGCGGTGCTGATGCTTT 1709
Db 1442 PheIleThrIleuSerIleValLeuGlnArgMetArgTyrGluGlyValIleAspIlePhe 1461
QY 1710 CAGACCGTGAAGACCTGCTACACAGCGTCTGCCATGCTGTCAGACAGAGACAGATAT 1769
Db 1462 GlnThrValLysMetLeuArgThrGln---ProAlaMetValGlnThrGluAspGluTyr 1480
QY 1770 CAGTGTGTCACCGTGGCGGCGCTGAGTACTGCGGACGTTTGACCACTATGACAG 1826
Db 1481 GlnPheCysTyrGlnAlaAlaLeuGluTyrLeuLysSerPheAspHisTyrAlaThr 1499

RESULT 12
ID 090YJ4 PRELIMINARY; PRT; 857 AA.
AC 090YJ4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Receptor protein-tyrosine phosphatase sigma (Fragment).
GN pPFRS OR RPPRSIGMA.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA van der Sar A., Betist M., de Fockert J., Overvoorde J., Zivkovic D.,
RA den Hertog J.;
RT "Expression of receptor protein-tyrosine phosphatase alpha, sigma and
RT LAR during development of the zebrafish embryo."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
EMBL: AJ311886; CAC44759.1; -.
ZFIN: ZDB-GENE-020107-3; pPFRS.
DR InterPro: IPR000387; Tyr_PP.
DR Pfam: PF00102; Y_phosphatase. 2.
DR PRINTS: PR00700; PTPYPHATASE.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; UNKNOWN_1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
FT NON_TER
FT SEQUENCE 857 AA; 97709 MW; 604A926BB08E81D8 CRC64;

Alignment Scores:
Pred. No.: 9,6e-217 Length: 857
Score: 2862.00 Matches: 524
Percent Similarity: 94.66% Conservative: 43
Best Local Similarity: 87.48% Mismatches: 32
Query Match: 44.41% Indels: 0

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DB: 13 Gaps: 0

US-09-743-492-1 (1-3467) x 090YJ4 (1-857)

QY 30 CACTCTCTGACCTGTGGAGATGGGAGGCTCACTACAGCCCGAGTATGGAGAC 89  
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DB 259 HisProthAspProValGluMetArgIleAsnPhenGlnThrProGlyMetLeuAsn 278  
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QY 90 CACCACCCATCCCATCAACGAGCTGGCGGAGCAACATGACGGCTCAACCAAGCAT 149  
 ||| ..... |||

DB 279 HisProProIleProIleSerGluLeuAlaGluHisThrGluLeuLeuYsAlaAsnAsp 298  
 ||| ..... |||

QY 150 GGCCTCAAGTCTCCAGAGATGATGATCCATGACCTGGACAGCATGTTCAAGTGGAG 209  
 ||| ..... |||

DB 299 AsnLeuYsLeuSerGlnIleuTyrgIserIleAspProGlyGlnGlnPhenThrTrpGlu 318  
 ||| ..... |||

QY 210 AATTCAAACCTGGAGGTGAGCAAGCCAGAACCGCTATGCGCAATGTCATGCGCTCGAC 269  
 ||| ..... |||

DB 319 HisSerAsnLeuGluValAsnYsProYsAsnArgTyAlaAsnValIleAlaTyAsp 338  
 ||| ..... |||

QY 270 CACTCTGAGTATCTTCACTCTATGATGGCGTCCCGGAGTGAATCAATCAATGCC 329  
 ||| ..... |||

DB 339 HisSerArgValIleLeuAlaProIleGluGlyIleThrGlySerAspTyrlleAsnSer 358  
 ||| ..... |||

QY 330 AACTACATGATGCTTACCCGAGCAAGAAATGCTTACATGCCACAGCGGCCCTGCC 389  
 ||| ..... |||

DB 359 AsnTyrlleAspGlyTyArgTyrgIsgIAsnAlaTyrlleAlaThrGlnGlyProLeuPro 378  
 ||| ..... |||

QY 390 GAGACCATGGCGGATTTCTGGAGATGGTGGGAACAGCGGACGCGCTGGTGCATG 449  
 ||| ..... |||

DB 379 GlnThrPhenGlyAspPhenThrArgMetValITrpGluGlnArgAlaAlaThrValAlaMet 398  
 ||| ..... |||

QY 450 ATGACACGGCTGGAGAGAAATCCCGGTAAATGATGATCACTAGTGGCCACCGCTGGC 509  
 ||| ..... |||

DB 399 MetThrArgLeuGluGluYsSerArgIleYsCysAspGlnTyrrProSerArgGly 418  
 ||| ..... |||

QY 510 ACCGAGACCTGTGGCTTATTCAGGTGACCTGTGGACACAGTGGAGCTGGCCACATAC 569  
 ||| ..... |||

DB 419 ThrGlnThrTyrgIleMetIleGlnValIThrLeuLeuAspThrIleGluLeuAlaThrPh 438  
 ||| ..... |||

QY 570 ACTGGCGGACCTTGGCACTCCAAAGAGTGGCTCCAGTGAAGAGCGTACGCTGGCTGAG 629  
 ||| ..... |||

DB 439 CysValAlaGlnThrPhenSerLeuHisYsAsnGlySerSerGluYsArgIleValArgGln 458  
 ||| ..... |||

QY 630 TTTCAGTTCATGCTGGCGGACAGCATGAGTTCCTGATACCCCACTCCATCTGGCGC 689  
 ||| ..... |||

DB 459 PheGlnPhenThrAlaThrProAspHisGlyValProGluTyrrProThrProPheLeuAla 478  
 ||| ..... |||

QY 650 TTCTTACGACGGGTCAAGGCTGCAACCCCTAGACGCGAGGCGCCATGGTGGTGCATGC 749  
 ||| ..... |||

DB 479 PheLeuArgArgValIlyThrCysAsnProProAspAlaGlyProIleIleAlaHisCys 498  
 ||| ..... |||

QY 750 AGCGGGGGGTGGGGCGGCGGCTTCATGCTGATGATGATGATGATGATGATGATGATG 809  
 ||| ..... |||

DB 499 SerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeuGluAlaGlyIle 518  
 ||| ..... |||

QY 810 AAGCAGAGAAAGACGCTGACATTCATGAGCAGCTGACCTGATGCGATCAGAGAGAAC 869  
 ||| ..... |||

DB 519 LysHisGluYsThrValAspIleTyrgIYsHisValIThrLeuMetArgSerGlnArgAsn 538  
 ||| ..... |||

QY 870 TACATGCTGACAGAGAGACCATGATGCTTCATTCATGAGAGCGCTGCTGGAGCTGCC 929  
 ||| ..... |||

DB 539 TyrlleValGlnIThrGluYsPrlnTyrrSerPheIleHisAspAlaLeuLeuGluAlaVal 558  
 ||| ..... |||

QY 930 AGCTGGCGGACACAGAGGTGGCTCCCGGACAGCTATGCGGACCATCCAGAAAGCTGGGC 989  
 ||| ..... |||

DB 559 AlaCysGlyAsnIThrGluValAlaAlaArgSerLeuPheSerTyrlleGlnYsLeuAla 578  
 ||| ..... |||

QY 990 TAAAGTCTCCAGGAGAGATGTCAGCCGACCATGAGATGTCAGATGTCAGCTGGCGCAC 1049  
 ||| ..... |||

DB 579 GlnValGluAlaGlyGluHisValSerGlyMetGluLeuGlnPheYsArgLeuAlaAsn 598  
 ||| ..... |||

QY 1050 TCCAAAGGCCACACAGCTCCCGCTTCATCAGCGCCAACTGGCTGCAACAAGTTCAAGAAC 1109  
 ||| ..... |||

DB 599 SerYsAlaHisIThrSerArgPheIleSerAlaAsnLeuProCysAsnYsPheYsAsn 618  
 ||| ..... |||

QY 1110 CGGCTGGTGAACATCATGCGCTTACGAATGACCCGGTGTGCTGGAGCCATCCCTGGT 1169  
 ||| ..... |||

DB 619 ArgLeuValAsnIleMetProTyrgIuThrIThrArgValCysLeuGlnProIleArgGly 638  
 ||| ..... |||

QY 1170 GTGGAGGCTGTGACTTACATCAATGCCACCTCTCGATGCTTATAGACAGCAAGAGCC 1229  
 ||| ..... |||

DB 639 LeuGluGlySerAspTyrlleAsnSerPheIleAspGlyTyrgArgGlnYsAla 658  
 ||| ..... |||

QY 1230 TACATGCTTACACAGGGGCTCTGGCAGAGAGACCGAGACTTCTGGCGCATGCTATGG 1289  
 ||| ..... |||

DB 659 TyrlleAlaThrGlnIleProLeuAlaGluIThrIThrGluAspPhenThrArgMetLeuTrp 678  
 ||| ..... |||

QY 1290 GAGCAATTCACACCATCATGCTGATCGACCAAGCTTCGGAGATGGGAGGAGAA 1349  
 ||| ..... |||

DB 679 GluAsnAsnSerIThrIThrValAlaMetLeuIThrYsLeuArgGluMetGlyArgGluYs 698  
 ||| ..... |||

QY 1350 TGCACACATGCTGGCCACAGAGCGCTGCTCGCTACCATGCTTGTGTGACCG 1409  
 ||| ..... |||

DB 699 CysHisGlnTyrrIThrProAlaGluArgSerAlaArgTyrgIuTyrrPheValAlaAspPro 718  
 ||| ..... |||

QY 1410 ATGGCTGATTAACAATGCCCCAGTATATCTGCTGATTCAGAGTCAAGTCCGATGCCG 1469  
 ||| ..... |||

DB 719 MetAlaGluITyrAsnMetProGlnITyrlleLeuArgGluPheYsValIThrAspAlaArg 738  
 ||| ..... |||

QY 1470 GATGGCGATTCAGAGCAATCATGCTGGCGGATTCAGTTCAGAGACTGGCCAGCGGCGTG 1529  
 ||| ..... |||

DB 739 AspGlyGlnSerArgIThrIThrValAlaGlnPheGlnPhenIThrAspIThrProGluGlnGlyVal 758  
 ||| ..... |||

QY 1530 CCCAAGACAGGCGAGGAGATTCATGATTCATCGGGCAGAGTGCATTAAGCAAGAGACAG 1589  
 ||| ..... |||

DB 759 ProYsSerGlyGluGlyPheIleAspPheIleGlyGlnValHisYsThrYsGluGln 778  
 ||| ..... |||

QY 1590 TTTCGACAGATGGGCTTATCAGGTGACCTGACAGTGCCTGGCGTGGCGGACCGGGG 1649  
 ||| ..... |||

DB 779 PheGlyGlnAspGlyProIleSerValHisCysSerAlaGlyValGlyITyrIThrGlyVal 798  
 ||| ..... |||

QY 1650 TTTCATCATCTGAGCATGCTGCTGGCGGCGCATGCGTATGAGAGGCGGTGGCGCATGTT 1709  
 ||| ..... |||

DB 799 PheIleIThrLeuSerIThrValLeuGluArgMetArgTyrgIuValAlaValAspIlePhe 818  
 ||| ..... |||

QY 1710 CAGACCGTGAAGACCTCGGTGATCACAGCGCTCTCCATGATGGTGCAGACAGACCATAT 1769  
 ||| ..... |||

DB 819 GlnIThrValYsMetLeuArgIThrGlnArgProAlaMetValGlnIThrGluAspGluTyrr 838  
 ||| ..... |||

QY 1770 CAGCTGCTACCGTGGCGCTGGAGTACCTGCGGAGCTTTGACCATATGCAACG 1826  
 ||| ..... |||

DB 839 GlnPheCysTyrgIuAlaAlaLeuGluITyrgIeGlySerPheAspHisITyrrAlaIThr 857  
 ||| ..... |||

RESULT 13

Q13332 PRELIMINARY: PRT: 1948 AA.

ID Q13332 Q15718: Q16341:

AC Q13332: Q15718: Q16341: 01, Created)

DT 01-NOV-1996 (TRMBLrel. 01, last sequence update)

DT 01-NOV-1996 (TRMBLrel. 01, last sequence update)

DE 01-MAR-2002 (TRMBLrel. 20, last annotation update)

DE Protein-tyrosine phosphatase, receptor-type, S precursor (EC 3.1.3.48)

GN (Protein-tyrosine phosphatase sigma) (R-PTP-sigma) (PTPRS).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=FETAL BRAIN;

TX MEDLINE=96102179; PubMed=8524829;

RA Pulido R., Serra-Pages C., Tang M., Streuli M.;

RT "The LAR/pnp delta/pnp sigma subfamily of transmembrane protein-tyrosine-phosphatases: multiple human LAR, PTP delta, and PTP sigma isoforms are expressed in a tissue-specific manner and associate with

RT the LAR-interacting protein LIP.1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:11686-11690(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9625038; PubMed=8992885;  
 RA Endo N., Rutledge S.J., Opas E.E., Vogel R., Rodan G.A., Schmidt A.;  
 RT "Human protein tyrosine phosphatase-sigma: alternative splicing and  
 inhibition by bisphosphonates.";  
 RL J. Bone Miner. Res. 11:535-543(1996).  
 RN [3]  
 RP SEQUENCE OF 1-126 FROM N.A.  
 RA Lamedin J.E., McCready P.M., Skowronski E., Viswanathan V.,  
 RA Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,  
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Gaines J.,  
 RA Dangnan L., Ertler A., Christensen M., Georgescu A., Avila J., Liu S.,  
 RA Attix C., Andreise T., Frankheim M., Amico-Keller G., Coefield J.,  
 RA Darelle S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,  
 RA Ariellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,  
 RA Olsen A.S., Carrano A.V.;  
 RT "Sequence analysis of a 2.5 Mb region in 19p13.3";  
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1503-1589 FROM N.A.  
 RX MEDLINE=92119637; PubMed=1370651;  
 RA Adachi M., Sekiya M., Arimura Y., Takekawa M., Itoh F., Hinoda Y.,  
 RA Imai K., Yachi A.;  
 RT "Protein-tyrosine phosphatase expression in pre-B cell NALM-6.";  
 RL Cancer Res. 52:737-740(1992).  
 CC CC -1- FUNCTION: INTERACTS WITH LAR-INTERACTING PROTEIN LIP.1.  
 CC CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN  
 CC CC TYROSINE + ORTHOPHOSPHATE.  
 CC CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC CC -1- ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS ARE FOUND IN DIFFERENT  
 CC CC TISSUES DUE TO ALTERNATIVE SPLICING.  
 CC CC -1- TISSUE SPECIFICITY: DETECTED IN ALL OF THE TISSUE TESTED EXCEPT  
 CC CC FOR PLACENTA AND LIVER.  
 CC CC -1- SIMILARITY: EXTRACELLULAR REGION TYPIC OF A CAM FAMILY (3 IG-LIKE  
 CC CC DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS), AND A  
 CC CC CYTOPLASMIC REGION COMPOSED OF TWO PTASE DOMAINS.  
 DR EMBL: U35234; AAC50299.1; -;  
 DR EMBL: U40311; AAC50567.1; -;  
 DR EMBL: AC005790; AAC62832.1; -;  
 DR HSSP: S78080; AAB21146.2; -;  
 DR HSSP: P18052; IYFO.  
 DR MIM: 601576; -;  
 DR InterPro: IPR003962; FNIII\_repeat.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR003598; Ig\_C2.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR InterPro: IPR000242; TYR\_PP.  
 DR Pfam: PF00041; fn3; 8.  
 DR Pfam: PF00047; Ig; 3.  
 DR Pfam: PF00102; Y\_phosphatase; 2.  
 DR PRINTS: PR00014; FNTPYFIII.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SM00060; FN3; 7.  
 DR SMART: SM00408; IgC2; 3.  
 DR SMART: SM00194; PTPc; 2.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; FALSE\_NEG.  
 DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
 DR Hydrobase: Receptor: Glycoprotein, Signal: Transmembrane;  
 KM Cell adhesion: Immunoglobulin domain; Duplication;  
 KM Alternative splicing: Repeat.  
 FT SIGNAL 1 29  
 FT CHAIN 30 1948  
 FT FT  
 FT DOMAIN 30 1282  
 FT TRANSMEM 1283 1303  
 FT DOMAIN 1304 1948  
 FT DOMAIN 32 124  
 FT DOMAIN 127 234  
 FT DOMAIN  
 IG-LIKE C2-TYPE DOMAIN.  
 IG-LIKE C2-TYPE DOMAIN.

FT DOMAIN 241 327  
 FT DOMAIN 329 423  
 FT DOMAIN 426 522  
 FT DOMAIN 525 615  
 FT DOMAIN 618 717  
 FT DOMAIN 720 831  
 FT DOMAIN 834 926  
 FT DOMAIN 928 1033  
 FT DOMAIN 1036 1151  
 FT DOMAIN 1411 1657  
 FT DOMAIN 1700 1948  
 FT DOMAIN 641 644  
 FT DISULFID 54 107  
 FT DISULFID 156 216  
 FT ACT\_SITE 266 311  
 FT ACT\_SITE 1589 1589  
 FT ACT\_SITE 1880 1880  
 FT CARBOHYD 263 263  
 FT CARBOHYD 308 308  
 FT CARBOHYD 733 733  
 FT CARBOHYD 940 940  
 FT CARBOHYD 190 198  
 FT VARSPLIC 236 239  
 FT VARSPLIC 617 1034  
 FT VARSPLIC 784 792  
 FT VARSPLIC 1035 1035  
 FT VARSPLIC 1350 1365  
 FT VARSPLIC 1366 1366  
 FT CONFLICT 309 310  
 FT CONFLICT 428 429  
 FT CONFLICT 742 745  
 FT CONFLICT 765 773  
 FT CONFLICT 910 910  
 FT CONFLICT 986 995  
 FT CONFLICT 1195 1196  
 FT CONFLICT 1431 1431  
 FT CONFLICT 1546 1546  
 FT CONFLICT 1587 1587  
 FT CONFLICT 1705 1705  
 SQ SEQUENCE 1948 AA: 217080 MW: 7DC049EC03171136 CRC64:  
 Alignment Scores:  
 Pred. No.: 3.81e-216  
 Score: 2856.00  
 Percent Similarity: 91.71%  
 Best Local Similarity: 86.02%  
 Query Match: 44.32%  
 DB: 4  
 Gaps: 1  
 US-09-743-492-1 (1-3467) x Q13332 (1-1948)  
 QY 30 CACTCTCTGTGACCTGTGAGATGCGGAGGCTCACTACAGACCCCA----- 77  
 DB 1334 HisProlyAspProValGluMetArgArgIleAsnPhgInThrProAspSerGlyLeu 1353  
 QY 78 -----GATATGCGAGACCAACCCATC 101  
 DB 1354 ArgSerProLeuArgGluProGlyPheHisPhgIleSerMetLeuSerHisProPile 1373  
 QY 102 CCCATCACCGCATGCGGAGACATGACATGACGCTCAAGGCAAGCATGAGCTCAAGTTC 161  
 DB 1374 ProIleAlaAspMetAlaGluHisThrGluArgLeuYsAlaAsnAspSerLeuLysLeu 1393  
 QY 162 TCCGAGAGATGTAGTCCATGACCGCTGAGCAGAGAGTTCACGTGGAGGAATTCAAACCTG 221  
 DB 1394 SerGlnIleuYrGlnSerIleAspProGlyGlnGlnPheThrTrpGlnHisSerAsnLeu 1413  
 QY 222 GAGGTGAACAACGCCAGAACCGCTATGCGAATGTCATCGCTGACGACCAATCGAGTGC 281  
 DB 1414 GluValAsnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAspHisPheArgVal 1433  
 QY 282 ATCCTTACCTTATGATGAGGCGCTCCCGGAGTACTACATGACATGACATGATGAT 341  
 DB 1414 GluValAsnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAspHisPheArgVal 1433

Db 1434 lIeLeuGlnProIleGlLylIleMetGlySerAspTyrIleAsnAlaSerTyrValAsp 1453  
 QY 342 GGCTACCGCAGAGATGCTCATCGCCACGACGAGGCCCTCGCCGAGCATGAGC 401  
 Db 1454 GYTTYArGArGlnAsnAlaTyrIleAlaThrGlnGlyProIleuProGlnThrPheGly 1473  
 QY 402 GATTTCGAGAAATGGTGTGGGAACAGCCGACGCGCACTGTGGTCATGATGACAGGCTG 461  
 Db 1474 AspPheTrpArgMetValTrpGlnArgSerAlaThrIleValMetMetTrpArgLeu 1493  
 QY 462 GAGGAGAGCGCCGGGTAATGATGATGACTGAGCCGCGCCGCGCCGAGCGCTGT 521  
 Db 1494 GlnGlnLysSerArgIleLysCysAspGlnTyrTrpProAsnArgGlnThrGlnTyr 1513  
 QY 522 GGCTATTTCAGGTGACCGCTGTGGACAGAGTGGAGCTGGCCACATACCTGTGGCACC 581  
 Db 1514 GlyPheIleGlnValIleThrIleuAspTrpIleGlnLeuAlaThrPheCysValArgThr 1533  
 QY 582 TTCGACCTCCACAGAGTGGCTCCAGTGAAGCGTGAAGCTGGCTCAGTTTCAGTTTCAG 641  
 Db 1534 PheSerLeuHisLysAsnGlySerSerGlnLysArgGlnValArgGlnPheGlnPheThr 1553  
 QY 642 GCCTGGCCAGACATGAGATGCTCTGAGTACCCACACTCCACTCGCTTCACAGACGG 701  
 Db 1554 AlaTrpProAspHisGlnValProGlnTyrProThrProPheLeuAlaPheLeuArgArg 1573  
 QY 702 GTCAAGCGCTGCNAACCCCTAGACGAGGCGCCATGGTGGTGCACAGCGGCGGTG 761  
 Db 1574 ValLysThrCysAsnProProAspAlaGlyProIleValAlaHisCysSerAlaGlyVal 1593  
 QY 762 GGCGGACCGCGGTGCTTCATCGTGAATGATGCCATGTTGGAGCGGATGAACAGAGAG 821  
 Db 1594 GlyArgThrGlnCysPheIleValIleAspAlaMetLeuGlnArgIleLysProGlnLys 1613  
 QY 822 AGCGTGGACATCATGATGGCCACGTCGATCGATCGCATACAGAGAACTAATCATAGTGCAC 881  
 Db 1614 ThrValAspAlaTyrIleLysValIleThrLeuMetArgSerGlnArgAsnTyrMetValGln 1633  
 QY 882 AGCGAGACCACTAGTCTGTTTCATCATGAGGCGCTCGAGGCTGCGACGTCGCGCCAC 941  
 Db 1634 ThrGlnAspGlnTyrSerPheIleHisGlnAlaLeuLeuGlnValAlaGlnCysGlnAsn 1653  
 QY 942 ACAGAGGTGCTGCGCCGCAACCTGTATGCCCATCCAGAAAGCTGGGCCACGCTGCCA 1001  
 Db 1654 ThrGlnValProAlaArgSerLeuTyrAlaTyrIleGlnLysLeuAlaGlnValGlnPro 1673  
 QY 1002 GGGAGAGGTGTGACCGCCCTGAGCTCGAGTTCAAGTGGTGGCCAGTCCAGGCGCCAC 1061  
 Db 1674 GlyGlnHisValIleThrGlnMetGlnLeuGlnPheLysArgLeuAlaAsnSerLysAlaHis 1693  
 QY 1062 AGCTCCCGCTTCATCAGCGCCAACTGCCCTGCACAAAGTTCAAGAACCGGCTGTGAAC 1121  
 Db 1694 ThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLysAsnArgLeuValAsn 1713  
 QY 1122 ATCATGCGCTAGCAATGACCGCTGTGTGTCTGTGACCCCATCGGTGTGTGGAGGCTCT 1181  
 Db 1714 IleMetProTyrGlnSerThrArgValCysLeuGlnProIleArgIleValGlnGlySer 1733  
 QY 1182 GACTACATCAAGCGCCAGTCTCGATGGTGTATAGACAGAGAAAGCTAATAGCTACA 1241  
 Db 1734 AspTyrIleAsnAlaSerPheIleAspGlnTyrArgGlnGlnLysAlaTyrIleAlaThr 1753  
 QY 1242 CAGGGGCTCTGTGACAGAGACCGAGGACTTGTGGCGCATGCTATGAGGACCAATTC 1301  
 Db 1754 GlnGlyProLeuAlaGlnThrThrGlnAspPheTrpArgMetLeuTrpGlnAsnAsnSer 1773  
 QY 1302 ACCATCATGCTCATGCTGACCAAGCTTCGGAGATGGGACGAGAGAAATGCCACCACTAC 1361  
 Db 1774, ThrIleValIleValMetLeuThrLysLeuArgGlnMetGlnArgGlnLysCysHisGlnTyr 1793  
 QY 1362 TGGCCGAGAGAGCGCTCTGCTGCTACGACTCTTGTGTTGATACCGGATGGCTGAGTAC 1421  
 Db 1794 TrpProAlaGlnArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGlnTyr 1813

QY 1422 AACATGCCCCAGTATATCCCTGCTGAGTTCAAGTCAAGGATGCCGGATGGGCACTCA 1481  
 Db 1814 AsnMetProGlnTyrIleLeuArgGlnPheLysValIleThrAspAlaArgAspGlnSer 1833  
 QY 1482 AGCAACAATCCGGCAGTATCCAGTTTCACAGACTGCCACAGACGCGGTGCCAAGACAGC 1541  
 Db 1834 ArgThrValArgGlnPheGlnPheThrAspTrpProGlnGlnValAlaProLysSerGly 1853  
 QY 1542 GAGGAGATCATGACTTTCATCGGCGAGGTGCATTAAGCCAAAGAGCAAGTTTGGACGGAT 1601  
 Db 1854 GlnGlyPheIleAspPheIleGlnValAlaHisLysThrLysGlnGlnPheGlnAsp 1873  
 QY 1602 GGCCCTATCAGCGTGCACAGTGCAGTGTGGCGTGGCGCCACGCGGCTGTTCACACTGT 1661  
 Db 1874 GlyProIleSerValHisCysSerAlaGlyValGlyArgThrGlyAlaPheIleThrLeu 1893  
 QY 1662 AGCATGCTCTGGAGCGCATGCCCTATGAGGCGGTGGTGCACATGTTTCAGACCGTGAAG 1721  
 Db 1894 SerIleValLeuGlnArgMetArgTyrGlnGlyValAlaAspIlePheGlnThrValLys 1913  
 QY 1722 ACCCTGGTACAGAGGCTCTGCTGCGATGTCGACAGAGGACGAGTATCAGCTGTGCTAC 1781  
 Db 1914 MetLeuArgThrGlnArgProAlaMetValGlnThrGlnAspGlnTyrGlnPheCysTyr 1933  
 QY 1782 CGTGGCGCCCTGGAGTACTCGGCGACCTTTCAGACACTATGCAAGC 1826  
 Db 1934 GlnAlaAlaLeuGlnTyrIleuGlnLysSerPheAspHisTyrAlaThr 1948  
 RESULT 14  
 Q90M00  
 ID Q90M00 PRELIMINARY; PRT; 1501 AA.  
 AC Q90M00;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE Receptor protein tyrosine phosphatase-sigma, Rptp-sigma.  
 OS Rattus sp.  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NC NCBL\_TaxID-10118;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-94043351; PubMed-8227050;  
 RA Yan H., Grossman A., Wang H., D'Eustachio P., Mossie K.,  
 RA Musacchio J.M., Silvennoinen O., Schlesinger J.;  
 RT "A novel receptor tyrosine phosphatase-sigma that is highly expressed  
 RT in the nervous system".  
 RL J. Biol. Chem. 268:24880-24886(1993).  
 DR HSSP; P18052; 1YFO.  
 DR InterPro; IPRO03962; Enfil\_repeat.  
 DR InterPro; IPRO03961; FN\_III.  
 DR InterPro; IPRO03598; IG\_C2.  
 DR InterPro; IPRO03006; Ig\_MHC.  
 DR InterPro; IPRO00387; Tyr\_MHC.  
 DR InterPro; IPRO00242; Tyr\_PP.  
 DR Pfam; PF00041; fn3; 4.  
 DR Pfam; PF00047; ig; 3.  
 DR Pfam; PF00102; Y-phosphatase; 2.  
 DR PRINTS; PRO0014; ENTPEPITI.  
 DR PRINTS; PRO0700; PRTYPHPTASE.  
 DR SMART; SM00060; FN3; 4.  
 DR SMART; SM00408; IGC2; 3.  
 DR SMART; SM00194; PTPC; 2.  
 DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Hydrolase; Immunoglobulin domain; Repeat.  
 SQ SEQUENCE 1501 AA; 168336 MW; C3E0889B4BEF430D CRC64;

Alignment Scores: 1.03e-215 Length: 1501  
 Pred. No.: 2850.00 Matches: 523

Percent Similarity:	93.99%	Conservative:	40
Best Local Similarity:	87.31%	Mismatches:	36
Query Match:	44.23%	Indels:	0
DB:	11	Gaps:	0

US-09-743-492-1 (1-3467) x Q9QW00 (1-1501)

OY	30	CACCCTCTGACCGCTGGAGATGGCGAGGCTCCACTACCAACACCCACAGTTCGGACAC	89
Db	903	HisProlysaapProValaGluMetalaArgaValaLeasnPhelInthProdiLmetLeuser	922
OY	90	CACCCACCCATCCCCATCCACCGACTGGCGGACAAACATGAGAGCGCTCAACACCAACAT	149
Db	923	HisProProlleProIlethraPmetalaGluHisMeGluuArgLeuLysalaasnsp	942
OY	150	GGCCTCAAGTTCCTCCAGAGATAGATGCATATGACCCCTGGACAGACAGTTCACTGGGAG	209
Db	943	SerLeuLysLeuSerGlnGluTyrGluSerLLeaspProGlyGlnIlePhethrTrpGlu	962
OY	210	AATTCACAACTGGAGGTGAGCAACGCCCAACACCGCTATGCGAATGCTATGCCCTACGAC	269
Db	963	HisSerasnLeuGlualaasnLysProLysasnArgTyrAlaasnValIleleatIatyrsp	982
OY	270	CACCTCTGAGTCACTCTTACCTCTATGCATGCGCTGCCCGGAGTACTACTACATGCC	329
Db	983	HisSerArgValaIleLeuGlnProLeuGlnGlyIleMeGlySeraspTyrLLeasnIa	1002
OY	330	AACACATCATGGCTGCTCCGACGACGAATGCTCATATGCCACGAGGCGCCCTGGCC	389
Db	1003	AsnTyrValaaspGlyTyrAlaArgGlnasnAlaTyrIleleatPhGlnIlyProLeuPro	1022
OY	390	GAGACATGGCGCATTTCTGAGAAATGCTGGGAACAGCGACGCGCACTGGTGCATG	449
Db	1023	GluThrPhethrGlyaspPhetrArgMetValaTyrGlnArgSerAlaThrValaIleMet	1042
OY	450	ATGACACGGCTGGAGGAGAGTCCCGGCTAAATGTGATCATCTACTGGCCACCGCTGGC	509
Db	1043	MetThrArgLeuGlnGluLysSerArgValaLysCysaspGlnTyrTrpProasnArgGly	1063
OY	510	ACCGAGACCTGTGGCCCTTATTCAGAGTGACCTTGTGACACAGTGGAGCTGGCCACATAC	569
Db	1063	ThrGluThrTyrGlyPheIleGlnValThrLeuLeuaspPhrMetGluLeuValaIthrPhe	1083
OY	570	ACTGTGGCACCTTGCCACTCCACAAGAAGTGGCTCCAGTGGAGAACGGCTGCGGTACG	629
Db	1083	CysValaArgThrPheSerLeuHisLysaspGlySerSerGluLysArgValaIArgHis	1102
OY	630	TTTTAGTTCAAGGCTGGCCGACGACATAGGAGTCTCGAGACCCAACTCCCTCTGGCC	689
Db	1103	PheGlnPheThrAlaIatTrpOaspPhisGlyValaIProGluTyrProThrProPheLeuIa	1122
OY	690	TTCCTACGACGGGTCAAGGCTCGCAACCCCTAGACGACGAGGCCCATGGTGGTGCATGC	749
Db	1123	PheLeuArgValaLysThrCysaspProProaspAlaGlyProValaValaHisCys	1142
OY	750	AGCGCGGCGTGGGCGCCACCGGCTGTTATCGATGATGAGGACATGGAGCGGATG	809
Db	1143	SerIleaglyValaGlyAlaGlnGlyCysPheIleValaIleaspIleMetLeuGluIatGlyIle	1162
OY	810	AACGACGACGAAGAGCGTGGACATCTATGGCCACAGTACCTGGATGCGATCACAGAGAAC	869
Db	1163	ArgThrGlnLysThrValaaspValaTyrGlyHisValaThrLeuMetArgSerGlnIatrgsn	1182
OY	870	TACATGGTCGACGAGGAGGACCAAGTACGTATTATCCATGAGAGCGCTGCTGGAGCTGCC	929
Db	1183	TyrMetValaGlnThrGlnaspGlnTyrSerPheIleHisGluIaLeuLeuGluIaVala	1202
OY	930	ACGTGCGCGCCACACAGAGAGTGGCTGGCCGACCTATGACCCACATCCAGAAAGCTGGGC	989
Db	1203	GlyLysGlyasnThrGluValaProIlaIatrgSerLeuTyrThrTyrIleGlnLysLeuIa	1222
OY	990	CAAGTGCCTCCAGGAGAGTGTACCGCCATGAGAGCTCGAGTTCCAAGTTGCTGGCCAGC	1049

Dd	1223	GlnValGlnProGlyGlnHisValThrGlyMetGlnLeuGlnPheLysArgLeuAlaSer	1242
Qy	1050	TCCAAGGCCACACAGCTCCGCTTCATCAGCGCCCAACCTCCCTGCACAGATTCAAGAAC	1109
Dd	1243	SerLysAlaHisThrSerArgPheIlePheAlaSerLeuProCysAlnLysPheLysAsn	1262
Qy	1110	CGGCTGTGAACATCATGCCCTACAGATTGACCCGTGTGTCTGCAGCCATCCGTGT	1169
Dd	1263	ArgLeuValAsnIleLeuProTyrGlnSerSerArgValCysLeuGlnProIleArgGly	1282
Qy	1170	GTGGAGGCGCTGCATTCATCATGGCAGCTTCCTGATGGTTATATACAGACAGAGCC	1229
Dd	1283	ValGlnGlySerAspTyrIleAsnAlaSerPheIleAspGlyTyrArgGlnGlnLysAla	1302
Qy	1230	TACATACCTACACAGGGGCGCTGTGCAGAGAGACCCGAGAGACTTGTGGCGATGCATAG	1289
Dd	1303	TyrIleAlaThrGlnGlnGlyProLeuAlaGlnThrThrGlnAspPheThrArgAlaLeuTyr	1322
Qy	1290	GAGCAACAATTCACACATCATCGTCATGTCAGCCAGCTTCGGGAGATGGGACGAGGAAA	1349
Dd	1333	GlnAsnAsnSerThrIleValIleValMetLeuThrLysLeuArgGlnMetGlnYArgGlnLys	1342
Qy	1350	TGGCCACAGATACAGCCGACAGAGAGCCCTGTGCTCGCTACCACTACTTTGTGTGACCCG	1409
Dd	1343	CysHisGlnTyrTrpProAlaGlnArgSerAlaArgTyrGlnTyrPheValValAspPro	1362
Qy	1410	ATGGCTCATGATCAACATGCCCCAGTATATCCGCGAGATTCACAGATCAAGGATCCCGG	1469
Dd	1363	MetAlaGlnTyrAsnMetProGlnTyrIleLeuAlaGlnPheLysValThrAspAlaArg	1382
Qy	1470	GATGGCGAGTCAGAGACAATCCGGCAGTCCAGTTCCAGACTGCGCCAGAGACAGGCGCTG	1529
Dd	1383	AspGlnSerIleArgThrValArgGlnPheGlnPheThrAspTyrProGlnGlnGlyAla	1402
Qy	1530	CCCAAGACAGGCGGAGGATTCATTACTTCATCGGGCAGGTGCATATACCAAGAGACAG	1589
Dd	1403	ProLysSerIleGlnGlnPheIleAspPheIleGlnValHisLysThrLysGlnGln	1422
Qy	1590	TTTGGACAGATGGGCGCTTATCAGCGGTCACATGTCAGTGCAGGCGGCGCACCGGGGTG	1649
Dd	1423	PheGlnGlnAspGlyProIleSerValHisCysSerAlaGlyValGlnYArgThrGlnYal	1442
Qy	1650	TTTCATCACTGTGAGCATCGTCTGGAGCGCATGCCGTATAGAGGCGGTGTCGACATGTT	1709
Dd	1443	PheIleThrLeuSerIleValLeuGlnArgMetArgTyrGlnGlyValValAspIlePhe	1462
Qy	1710	CAGACCGTGAAGACCCCTGCGTATACACAGCGTCTGCCATGCTGTGCACACAGAGACCATAT	1769
Dd	1463	GlnThrValLysValLeuArgThrGlnArgProAlaMetValGlnThrGlnAspLeuTyr	1482
Qy	1770	CAGGTGGCTACCGTGGCGGCGTGGAGTACCTGGCAGCTTGACACCATATAGCAAG	1826
Dd	1483	GlnPheCysPheGlnAlaIleAlaLeuGlnTyrLeuGlySerPheAspHisTyrAlaThr	1501
RESULT 15			
064605 PRELIMINARY: PRT: 1863 AA.			
ID	064605		
AC	064605: 064675: 007808: 064621:		
DT	01-NOV-1996 (TREMBlrel. 01, Created)		
DT	01-NOV-1996 (TREMBlrel. 01, Last sequence update)		
DT	01-MAR-2002 (TREMBlrel. 20, Last annotation update)		
DE	Leu3.0 cycle common antigen-related phosphatase PP2B precursor		
DE	(EC 3.1.3.48) (Protein-tyrosine phosphatase LAR-PP2B) (Phosphotyrosine		
DE	phosphatase LAR-PP2B) (P1phase LAR-PP2B) (P1P NE-3) (P1P-P1) (CPTP1)		
DE	(P1P-stigma).		
GN	LAR-PP2B.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RM	[1]		
RF	SEQUENCE FROM N.A. (ISOFORMS LAR-PTP2 AND LAR-PTP2B).		
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER, AND BRAIN.		



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Db 1325 HisSerAsnLeuGluAlaHisnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAsp 1344
QY 270 CACTCTCGAGTATCTCTTACCTCTATCGATGCGGCTCCCGGAGAGTACTTACATCAATGCC 329
Db 1345 HisSerArgValIleLeuLeuProLeuGluGlyIleMetGlySerAspTyrIleAsnAla 1364
QY 330 AACCTACATGATGGCTACCGCAAGCAGATGCTTACATCGCCACGAGGCCCCCTGGCC 389
Db 1365 AsnTyrValAspGlyTyrArgArgGlnAsnAlaTyrIleAlaThrGlnLysProLeuPro 1384
QY 390 GAGACCATGCGGATTTCTGAGAAATGTGTGGAAACACGCGACGCGCCACTGTGTCATG 449
Db 1385 GlnThrPheGlyAspPheTrpArgMetValTrpGlnGlnArgSerAlaThrValAlaMet 1404
QY 450 ATGACACGCGCTGGAGAGAGATCCCGGCTAAATGTGATCACTACTGCCACCGCTGGC 509
Db 1405 MetTrpArgLeuGluGlnLysSerArgValLysCysAspGlnTyrTrpProAsnArgGly 1424
QY 510 ACCGAGACCTGTGGCTTATTCAGGTGACCTGTGGACACAGTGGAGCTGGCCACATAC 569
Db 1425 ThrGlnThrTyrGlyPheIleGlnValIleThrLeuAspThrMetGlnLeuAlaThrPhe 1444
QY 570 ACTGTGCGACCTTGTGCACTCCACAAGATGGCTCCAGTGAAGAGCGTGAAGCTGCGTCA 629
Db 1445 CysValArgTyrPheSerLeuHisLysAsnGlySerSerGlnLysArgGlnValArgHis 1464
QY 630 TTTCACTTCATGCGCTGCGCCAGACCATGAGTTCCTGAGTACCCATCCATCCTGGCC 689
Db 1465 PheGlnPheThrAlaTrpProAspHisGlyValProGlnTyrProThrProPheLeuAla 1484
QY 690 TTCCTACGAGCGGTCAAGCGCTGCAACCCCTAGACCGCGGCGCCATGGTGGTGCATC 749
Db 1485 PheLeuAspArgValLysThrLysAsnProProAspAlaGlyProValValIleHisCys 1504
QY 750 AGCGCGGCGTGGCGCGCACCGGCTCTCATCGTATGATGATGATGATGATGATGATGATG 809
Db 1505 SerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeuGlnArgIle 1524
QY 810 AAGCAGAGAGAGCGGTGACATCTATGGCCACGTGACCTGCATCGATCCAGAGAGAAC 869
Db 1525 ArgThrGlnLysThrValAspValTyrGlyHisValThrLeuMetArgSerGlnArgAsn 1544
QY 870 TACATGGTGCAGAGGAGGACCATGATACCTGATCCATGAGGCGCTGCGAGGCTGCC 929
Db 1545 TyrMetValGlnThrGluAspGlnTyrSerPheIleHisGlnAlaLeuLeuGlnAlaVal 1564
QY 930 ACGTGGCGCCACAGAGAGTGGCTGCCCGCACCTGTATGCCACATCCAGAGCTGGCG 989
Db 1565 GlyCysGlyAsnThrGluValProAlaArgSerLeuTyrThrTyrIleGlnLysLeuAla 1584
QY 990 CAAGTGCTCCAGGGGAGAGTGAACCGCATGAGAGCTCGAGTTCAGTTCGCTGGCCAC 1049
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QY 1050 TCCAGAGCCCAAGCTCCCGCTTCATCCAGCGCCACCTGCTCCGACCAAGTTCAAGAAC 1109
Db 1605 SerLysAlaHisThrSerArgPheIleThrAlaSerLeuProCysAsnLysPheLysAsn 1624
QY 1110 CGGCTGGTGAACATATGCTTACCAATGACCTGATGCTGCTGATGCTGATGCTGATGCTG 1169
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QY 1170 GTGAGGCGCTGATACATCAATGCCAGCTTCCTGATGTTATAGACAGAGAGGCC 1229
Db 1645 ValGlnGlySerAspTyrIleAsnAlaSerPheIleAspGlyTyrArgGlnGlnLysAla 1664
QY 1230 TACATAGCTACACAGGCGCTGTGCGACAGAGACACCGAGAGACTTCTGGCGCATGCTAT 1289
Db 1665 TyrIleAlaThrGlnGlyProLeuAlaGlnLysThrGlnAspPheTrpArgAlaLeuTrp 1684
QY 1290 GAGCACATTCACCATCATCTCATGTCAGCAAGCTTCGGAGATGGCGAGGAGAAA 1349

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Db 1685 GluAsnAsnSerThrIleValAlaMetLeuThrLysLeuArgGlnMetGlyArgGlnLys 1704
QY 1350 TGCACCATGACTGGCGCACAGAGCCCTGCTGCTGCTACCACTTGTGTGACCCG 1409
Db 1705 CysHisGlnTyrTrpProAlaGlnArgSerAlaArgTyrGlnTyrPheValAlaAspPro 1724
QY 1410 ATGGCTGATACAAACATGGCCCGCATATCCCTGCGAGTTCAGAGTTCAGAGTCCGAGTCC 1469
Db 1725 MetAlaGlnTyrAsnMetProGlnTyrIleLeuArgGlnPheLysValIleHisAlaArg 1744
QY 1470 GATGGCAGTCAAGACAAATCCGGCAGTTCCAGTTCCAGACTGCGCAGAGCAGGCGCTG 1529
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QY 1530 CCCAGACAGCGGAGGATTCATGACTTCATCGCGCAGCTGATAGACCAAGAGCAG 1589
Db 1765 ProLysSerGlyGlnGlyPheIleAspPheIleGlyGlnValHisLysThrLysGlnGln 1784
QY 1590 TTTGGACAGATGGGCTTATTCACGCGTCACTGCAAGTGGCGGTGGCGCACCCGGGGTG 1649
Db 1785 PheGlyGlnAspGlyProIleSerValHisCysSerAlaGlyValGlyArgThrGlyVal 1804
QY 1650 TTCATCACTCTGAGCATCGCTGCTGGAGCCATGCGCTATGAGGCGCTGGTGCATGTT 1709
Db 1805 PheIleThrLeuSerIleValLeuGlnArgMetArgTyrGlnGlyValAlaAspIlePhe 1824
QY 1710 CAGACCGTGAAGACCTCGCTACACAGCGTCTGCGCATGCTGCAGACAGAGACCATAT 1769
Db 1825 GlnThrValLysValLeuArgThrGlnArgProAlaMetValGlnThrGlnAspGlnTyr 1844
QY 1770 CAGCTGTGCTACCGCGGCGCTGAGAGTACCTGCGAGCTTGGACCATGCAAG 1826
Db 1845 GlnPheCysPheGlnAlaIleLeuGlnTyrLeuGlySerPheAspHisTyrAlaThr 1863

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Search completed: January 17, 2003, 10:12:15  
Job time : 288.5 secs

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SUMMARIES						
Result No.	Score	Query Match	Length	DB	ID	Description
1	3236	50.2	607	21	AAV81783	Human protein tyrosine
2	3236	50.2	607	21	AAV56098	LAR tyrosine phosph
3	3236	50.2	647	22	AAW23746	Human EST encoded
4	3236	50.2	647	22	AAU14379	Human novel protei
5	3236	50.2	1897	21	AAH19712	Human protein tyros
6	3236	50.2	1897	21	AAH18785	Human protein tyros
7	3236	50.2	1897	21	AAV56100	LAR tyrosine phosph
8	3236	50.2	1907	22	AAU14143	Human novel protei
9	2880	44.7	1911	16	AAH71726	Human PTP-OB. Hom
10	2880	44.7	1911	18	AAW27225	Human protein tyros
11	2880	44.7	1911	20	AAW94027	Human protein tyros
12	2880	44.7	1911	22	AAU01459	Human protein tyros
13	2874.5	44.6	1291	16	AAH72501	Tyrosine phosphata
14	2850	44.2	1501	16	AAH72858	LAR receptor type
15	2823.5	43.8	1904	23	AAH57100	Mouse ischaemic co
16	2753.5	42.7	1495	23	AAH57380	Rat mucocardial ce
17	2503	38.8	2037	22	AAH71928	Human melanog
18	2347	36.4	442	21	AAH56372	Human prostate can
19	1552	24.1	793	13	AAH20743	Murine receptor ty
20	1552	24.1	793	17	AAW02282	Murine receptor ty
21	1552	24.1	793	20	AAV04695	Mouse receptor-tyr
22	1551	24.1	802	17	AAW02283	Human receptor ty
23	1551	24.1	802	20	AAV04694	Human receptor-tyr
24	1551	24.1	807	23	ABP42006	Human ovarian anti
25	1544	24.0	802	13	AAH20744	Human receptor-tyr
26	1429	22.2	700	22	AAW23827	Human EST encoded
27	1429	22.2	700	22	AAH38831	Human polypeptide
28	1429	22.2	717	22	AAW40617	Human polypeptide
29	1423	22.1	699	18	AAW27226	Mouse protein tyros
30	1423	22.1	699	20	AAU94420	Mouse protein tyros
31	1423	22.1	699	22	AAU01468	Mouse protein tyros
32	1421	22.1	699	23	AAH57081	Mouse ischaemic co
33	1398	21.7	870	22	AAU30244	Novel human secret
34	1335	20.7	306	22	AAH78268	Human DCA-D1. Hom
35	1327	20.6	250	22	AAH59370	Human protein tyros
36	1297	20.1	623	22	AAH25675	Human protein sequ
37	1297	20.1	1452	22	AAH79159	Human protein tyros
38	1297	20.1	1455	22	AAH80143	Human protein SEQ
39	1295	20.1	294	22	AAH59389	Human protein tyros
40	1288	20.0	245	22	AAH59389	Human BCA-D2. Hom
41	1255	19.5	1439	15	AAH36332	Human receptor-tyr
42	1255	19.5	1440	20	AAH29591	Human protein phosph
43	1244.5	19.3	1462	23	AAH97521	Novel human protei
44	1243	19.3	1457	23	AAH57308	Mouse ischaemic co
45	1240	19.2	1407	15	AAH63631	Murine receptor-ty
ALIGNMENTS						
RESULT 1						
AAV81783						
ID	AAV81783	standard; Protein; 607	AA.			
XX	AAV81783;					
AC	07-JUN-2000	(first entry)				
DT	Human protein tyrosine phosphatase specific antibody protein sequence.					
DE	Human protein tyrosine phosphatase; antibody; intracellular domain; LAR; CD45; PTP; diagnosis; insulin resistance related disease; syndrome X; non-insulin dependent diabetes mellitus; arteriosclerosis; therapy; heart disorder.					
KW	Human; protein tyrosine phosphatase; antibody; intracellular domain; LAR; CD45; PTP; diagnosis; insulin resistance related disease; syndrome X; non-insulin dependent diabetes mellitus; arteriosclerosis; therapy; heart disorder.					
XX	Homo sapiens.					
OS	Homo sapiens.					
XX	W0200002922-A1.					



DB 521 GlnValHisIsthrhrLysGlnInpHeGlyGlnAspGlyProIlethrValHisCysSer 540  
QY 1626 GCTGGCGTGGGGCCGACCGGGGTTCATCATCTGAGATCGTCTGGAGCCGATCGC 1685  
DB 541 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGlnArgMetArg 560  
QY 1686 TATGAGGGGGTGGTGCATGTTTCAGACCGTGAAGCCCTGGGTACACAGCGTCCGGC 1745  
DB 561 TyrGlnGlyValValAlaAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 580  
QY 1746 ATGGTCACAGACAGAGACCGATGATCATGCTGTACCGTGGCGCCCTGAGATCACTCGGC 1805  
DB 581 MetValGlnThrGlnAspGlnThrGlnLeuGlnCysTyrArgAlaIleLeuGlnTyrLeuGly 600  
QY 1806 AGCTTGACCACTATGCAACG 1826  
DB 601 SerPheAspHisTyrAlaThr 607  
RESULT 2  
ID AAY56098  
AC AAY56098; Protein; 607 AA.  
XX 17-APR-2000 (first entry)  
DE LAR tyrosine phosphatase intracellular domain.  
XX Intracellular domain; P-subunit; human; leucocyte antigen related; LAR;  
KW tyrosine phosphatase; antibody; thyroid cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO964591-A1.  
XX  
PD 16-DEC-1999.  
XX  
PF 07-JUN-1999; 99MO-JP03054.  
XX  
PR 08-JUN-1998; 98MO-JP02542.  
XX  
PA (FUSO ) FUSO PHARM IND LTD.  
XX  
PI Yamamoto H, Tsujikawa K, Uchino Y, Konishi N;  
XX  
DR WPI: 2000-097539/08.  
DR N-PSDB; AA259132.  
XX  
PT Antibody recognizing the intracellular domain of the human tyrosine  
PT phosphatase LAR -  
XX  
PS Claim 4; Page 73-78; 104pp; Japanese.  
XX  
CC This sequence represents the intracellular domain (P-subunit) of the  
CC human leucocyte antigen related (LAR) tyrosine phosphatase (complete  
CC sequence in AAY56098). The invention relates to the generation of an  
CC antibody recognizing the intracellular domain of the human LAR tyrosine  
CC phosphatase. The antibody is used for the diagnosis and treatment of  
CC thyroid cancer.  
XX  
SQ Sequence 607 AA:  
Alignment Scores:  
Pred. No.: 3,386-257 Length: 607  
Score: 3236.00 Matches: 607  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 50.22% Indels: 0  
DB: 21 Gaps: 0  
US-09-743-492-1 (1-3467) x AAY56098 (1-607)  
QY 6 GGACTAAGAGACTTCCTGGTGGCCCACTCTCTGACCCCTGTGGAGATGCGGAGGCTCAAC 65

DB 1 GlnLeuLysAspSerIleuLeuAlaHisSerSerAspProValGlnMetAlaArgLeuAsn 20  
QY 66 TACCAGACCCCAAGTATGAGAGACACACCCATCCCATCAACGACTGGGAGACAC 125  
DB 21 TyrGlnThrProGlnMetArgAspHisProProIleThrIleThrAspLeuAlaAspAsn 40  
QY 126 ATGAGCGCCCTCAAGCCAAAGCATGGCCCTCAAGTCTCCAGAGATATGATGCTATGAC 185  
DB 41 IleGlnArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGlnTyrGlnSerIleAsp 60  
QY 186 CTTGGACAGAGATTACAGTGGGAGATTCAACCTGGAGGTGAACAAGCCCAAGAACCGC 245  
DB 61 ProGlnGlnGlnPheThrTrpGlnAsnSerAsnLeuGlnValAsnLysProLysAsnArg 80  
QY 246 TATCCGAATGTCAATGCGCTAGACGACACTCTGAGTCAATCCATTCAATGATGAGCGTC 305  
DB 81 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 100  
QY 306 CCCGGAGTACTATCATCAATGCCAACTACATGATGATGATCCGCAAGCAAGATCCCTAC 365  
DB 101 ProGlnSerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgGlnAsnAlaTyr 120  
QY 366 ATGCGCCAGAGGGCCCCCTGGCCGAGACATGGCGCATTTTCGGAATGCTGGGAA 425  
DB 121 IleAlaThrGlnGlnProLeuProGlnThrMetLysPheThrArgMetValTrpGln 140  
QY 426 CACGCGACGGCCACTGTGTCATGATGACACGGCTGAGAGAGAAAGTCCCGGTAATGT 485  
DB 141 GlnArgThrLarThrValMetMetThrArgLeuGlnGlnLysSerArgValLysCys 160  
QY 486 GATCAGTACTGGCCAGCCCTGGACACGAGACCTGTGGCTTATTCAGGTGACCTGTG 545  
DB 161 AspGlnTyrTrpProAlaArgGlyThrGlnThrCysGlyLeuIleGlnValThrLeuLeu 180  
QY 546 GACACAGTGGAGCTGGCCACATACACTGCGCACTTCGCACTCCCAAGAGTGGCTC 605  
DB 181 AspThrValGlnLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 200  
QY 606 AGTGAGAACCGTGAAGCTGCTCAGTTTCAGTTCATGCGCTGGCCAGACATGAGTTCCT 665  
DB 201 SerGlnLysArgGlnLeuAlaGlnPheGlnPheMetLarTrpAlaAspHisGlyValPro 220  
QY 666 GAGTACCAACTCCCATCTGGCCCTTCTAGACAGGGGTCAAGGCTTCAACCCCTAGAC 725  
DB 221 GlnTyrProThrProIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAsp 240  
QY 726 GCAAGGCCCATGTGTGGTGCATGCTGACGGGGGGTGGCCGACCGGCTCTTCATGTG 785  
DB 241 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 260  
QY 786 ATTGATGCCATGTTGGAGCGGATGAAGCAGAGAAAGAGGTGAGATCTTGGCCACGTG 845  
DB 261 IleAspAlaMetLeuGlnArgMetLysGlnLysThrValAspIleTyrGlnHisVal 280  
QY 846 ACCTGCATCGATACAGAGAACTACATGCTGCACAGGAGACAGATACGTGTTATC 905  
DB 281 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGlnAspGlnTyrValPheIle 300  
QY 906 CATGAGGGCGTGGTGGAGGGTGCACAGTGGCGGACACAGAGGCTGGCCGCAACCTG 965  
DB 301 HisGlnAlaLeuLeuGlnAlaAlaThrCysGlyHisThrIleValProAlaArgAsnLeu 320  
QY 966 TATGCCCATATCCAGAGTGGGCAAGTCCCTCCAGAGAGATGAGCCGATGAG 1025  
DB 321 TyrAlaHisIleGlnLysLeuGlnValProProGlyLysSerValThrAlaMetGln 340  
QY 1026 CTCGAGTTCAAGTTGCTGGCCAGCTCCAAAGCCACAGCTCCGCTTCATCAACGCCAAC 1085  
DB 341 LeuGlnPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 360  
QY 1086 CTCGCCCTGCAACAAGTTCAAGAACCGGCTGTGAACATCATGCCCTTACGAATGACCCGT 1145

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Db 361 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 380
QY 1146 GTGTCTGTCACACCCATCGTGTGTGGAGGCTCTGACTACATCAATGCCAGCTTCCTG 1205
Db 381 ValCysLeuGlnProIleArgIleValGluGlySerAspTyrIleAsnIleSerPheLeu 400
QY 1206 GATGCTTATAGACACAGAGCCCTACATAGCTTACACAGAGGCTCTGGCAGAGACACC 1265
Db 401 AspGlyTyrArgGlnGlnIleValIleAlaThrGlnGlnIleProLeuIleGlnSerThr 420
QY 1266 GAGGACTTCTGGCGATGATGGGAGACACATTCACCATCATGCTGTCGTGACCAAG 1325
Db 421 GluAspPheThrPArgMetLeuThrPgluHisAsnSerThrIleValMetLeuThrLys 440
QY 1326 CTTCCGGAGATGGCAGGAGAAATGCCACCACTACTGGCCAGACAGCGCTCTGCTGCC 1385
Db 441 LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg 460
QY 1386 TACCACTACTTGTGTGTGACCCGATGGCTGAGTACACATGCCCGCATATCTGCGCT 1445
Db 461 TyrGlnTyrPheValIleValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 480
QY 1446 GAGTCAAGGTCACGAGATGCCGGGTGGGAGGAGTCAAGGACATCCGCGAGTTCAGTTC 1505
Db 481 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 500
QY 1506 ACAGACTGGCCAGACAGAGCGCTGCCCAAGACAGCGAGGATTCATTCATTCATCGCG 1565
Db 501 ThrAspTrpProGlnGlnIleValProLysThrGlyGlnGlyPheIleAspPheIleGly 520
QY 1566 CAGTGGCATTAAGACCAAGAGACAGATTGGACAGATGGGCTTATACGCTGCTGCACT 1625
Db 521 GlnValHisLysThrLysGlnGlnIlePheGlyGlnAspGlyProIleThrValHisCysSer 540
QY 1626 GCTGCGCGGGCGGCGGCGGGGTTCATCACTGAGATGCTGAGATGCTGAGGCGGCGG 1685
Db 541 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGlnArgMetArg 560
QY 1686 TATGAGGCGTGGTGCAGATGTTTCAGACCGTGAAGACCCCTGCTACACAGCGTCTGCC 1745
Db 561 TyrGlnGlyValIleValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 580
QY 1746 ATGGTGCAGACAGAGAGCAGTATGAGCTGTGCTACCGTGGCGGCTGGAGTACCTCGCG 1805
Db 581 MetValGlnThrGlnAspGlnTyrGlnLeuGlySerTyrArgAlaIleLeuGlnTyrLeuGly 600
QY 1806 AGCTTGAACCACTATGCAACG 1826
Db 601 SerPheAspHisTyrAlaThr 607

```

RESULT 3  
 ID AAM23746  
 ID AAM23746 standard; Protein: 647 AA.  
 AC AAM23746;

12-OCT-2001 (first entry)

Human EST encoded protein SEQ ID NO: 1271.

Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
 tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 diagnostics; forensic test; gene mapping; genetic disorder;  
 biodiversity; gene therapy; nutrition.

Homo sapiens.

MO200154477-A2.

02-AUG-2001.

25-JAN-2001; 2001WO-US02687.

XX

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PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
PA (HSE-) HSE INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI: 2001-476164/51.
DR N-PSDB: AAH98405.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
PS Claim 20; Page 916-917; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention.
XX
SQ Sequence 647 AA:

```

#### Alignment Scores:

Pred. No.:	3,496-257	Length:	647
Score:	3236.00	Matches:	607
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	50.22%	Indels:	0
Db:	22	Gaps:	0

US-09-743-492-1 (1-3467) x AAM23746 (1-647)

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QY 6 GGACTGAAGAGCATCCCTGCTGGCCCACTGCTGACCCCTGGAGAGTGGGAGGCTCAAC 65
Db 41 GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetArgIleuAsn 60
QY 66 TACAGACCCCGAGTATGGAGAGACCAACCCATCCCATCAGCAGCAGCTGGCGGACAC 125
Db 61 TyrGlnThrProGlyMetArgAspHisProIleProIleThrAspLeuAlaAspAsn 80
QY 126 ATCGAGCGCCTAAAGCCACAGATGGCTCAGATTCTCCAGAGATGATGTCATGCAC 185
Db 81 IleGluArgLeuLysAlaHisAspGlyLeuLysPheSerGlnGluTyrGlnSerIleAsp 100
QY 186 CCTGGACAGCATTCACCGGGGAGAAATCAACCTGGAGAGTCAACAGCCCAAGAACCCG 245
Db 101 ProGlyGlnGlnPheThrTrpIleuSerSerAsnLeuGluValAsnLysProLysAsnArg 120
QY 246 TATGCAATGTCATCGCTTACGACCACTCTCGAGTCATCTTACCTTATCGATGGCGTC 305
Db 121 TyrAlaAsnValIleAlaIleTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 140
QY 306 CCCGGAGTGTACTACATCAATGCCAACTACATGATGCTTACCGCAGACAGAAATGCTTAC 365
Db 141 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgGlnAsnAlaTyr 160
QY 366 ATCCGACAGCAGAGGCGCCCTGCGCCAGACCAATGCGGATTTCTGGAAGATGCTGGGAA 425
Db 161 IleAlaThrGlnGlyProLeuProGlnThrMetGlyAspPheThrPArgMetValTrpGlu 180
QY 426 CAGCCAGCGGCACATGTGTGTCATGATGACACGCTGGAGAGAGACCCGGGTAAATGT 485
Db 181 GlnArgThrAlaThrValValMetMetThrArgLeuGlnLysSerArgValLysCys 200
QY 486 GATCAGTACTGGCCAGCCCGTGGACCGAGACCTTGCGCTTATTCAGGTGACCTGTGG 545

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Db      201 AspGlnTyrTrpProAlaArgLysThrGluThrCysGlyLeuIleGlnValThrLeuLeu 220
QY      546 GACACAGTGGAGTGGCCACATACACTGTGGCAGCTTGGCACTCCACAGAGTGGCTCC 605
        |||
        |||
        |||
Db      221 AspThrValGluIleuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 240
QY      606 AGCGAGAACGCGAGTGGGTGAGTTCAGTTCATGGCTGGCCGACACAGTGAAGTTCCT 665
        |||
        |||
        |||
Db      241 SerGluLysArgGluIleuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 260
QY      666 GAGTACCACTCCATCCCTGGCTTCTACAGACGGGTCAAGGCTCAAGCCCTCAAGAC 725
        |||
        |||
        |||
Db      261 GluTyrProThrProIleuAlaPheLeuArgArgValLysAlaCysAsnProLeuAsp 280
QY      726 GCAGGGCCCATGGTGGTGCAGTGCAGCGGGCGGTGGCCGACCGGCTTCATCGTG 785
        |||
        |||
        |||
Db      281 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal 300
QY      786 ATTGATGGCATGTTGGAGGGGATGAAGCAGAGACGGTGGACATTCATGGCCACGTG 845
        |||
        |||
        |||
Db      301 IleAspAlaMetLeuGluIleuArgMetLysHisGluLysThrValAspIleTyrGlyHisVal 320
QY      846 ACCTGCATCGCATACACAGAGAACTACATGTTGCACAGCAGAGACCATACGTTCATC 905
        |||
        |||
        |||
Db      321 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 340
QY      906 CATGAGGCGCTGTGGAGGCTGCACGTGGCGGCACACAGAGGTGCTGGCCGCAACTG 965
        |||
        |||
        |||
Db      341 HisGluAlaIleuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu 360
QY      966 TATGCCCAATCCAGAAAGTGGGGCCCAAGTCCCTCCAGGGGAGAGTGCACCCGATGAG 1025
        |||
        |||
        |||
Db      361 TyrAlaHisIleIleLysLeuGlyGlnValProProGlyGlySerValThrAlaMetGlu 380
QY      1026 CTCGAGTTCAAGTTCGTGGCCACGCTCCAGGGCCACAGCTCCGCTTCATCAGCGCAC 1085
        |||
        |||
        |||
Db      381 LeuGlnPheLysIleuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 400
QY      1086 CTGCCCTGCACAAAGTTCAAGAACCGGCTGGTGAACATCATGCGCTACGAATTCACCCGT 1145
        |||
        |||
        |||
Db      401 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 420
QY      1146 GTGTGCTGCAGCCCATCCGTGGTGGAGGGCTGTGCATCACTCACTGCACCTTCCTG 1205
        |||
        |||
        |||
Db      421 ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu 440
QY      1206 GATGGTTATAGACAGCAGAGGCTCATAGCTACACAGAGGCGCTGGCAGAGCACC 1265
        |||
        |||
        |||
Db      441 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGlnSerThr 460
QY      1266 GAGGACTTCTGGCGCATGCTATGGAGACAAATTCACCATCATGCTCATGTCAGCACA 1325
        |||
        |||
        |||
Db      461 GluAspPheTrpArgMetLeuTrpGlnHisAsnSerThrIleLeuValMetLeuThrLys 480
QY      1326 CTTCCGGGAATGGGCGGAGGAGAAATCCACCACTACTGGCCAGCAGAGCGCTTGGCTCG 1385
        |||
        |||
        |||
Db      481 LeuArgGluMetIleYArgGlnLysCysHisGlnTyrTrpProAlaGlnArgSerAlaArg 500
QY      1386 TACCACTACTTGTGTTTACCCGATGGGTGAGTACACATGGCCAGATATATCCGCGG 1445
        |||
        |||
        |||
Db      501 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 520
QY      1446 GAGTTCAAGGTCAAGGATCCCGGATGGGAGTCAAGGACAAATCCGCGCATGTCAGTTT 1505
        |||
        |||
        |||
Db      521 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 540
QY      1506 ACAGACTGGCCAGAGCAGGCGCTGCCAAGACAGCGGAGGAGATTCAATTCATCGCGG 1565
        |||
        |||
        |||
Db      541 ThrAspTrpProGlnGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly 560
QY      1566 CAGGTGCATATAGACCAAGGAGGTTTGACAGAGATGGCGCTTCACGGTGCACCTGCAGT 1625
        |||
        |||
        |||
Db      561 GluValHisLysThrLysGlnPheGlyGlnAspGlyProIleThrValHisCysSer 580

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QY      1626 GCTGGCGTGGGCGGACCGGGGTTCATCATCTGAGACATGCTCTGGAGCCATGCGC 1685
        |||
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        |||
Db      581 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg 600
QY      1686 TATGAGGGGTGGTTCGACATGTTTCAGACCGGTGACGCCCTGGCTACACAGCTCCGCC 1745
        |||
        |||
        |||
Db      601 TyrGlnGlyValAlaLaspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla 620
QY      1746 ATGGTCAGACAGAGGACACCATATCAGCTGTGCTACCGTGGCGGCGCTGGAGTACCTGGC 1805
        |||
        |||
        |||
Db      621 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluIuTyrLeuGly 640
QY      1806 AGCTTGACCATCATGTCACAGC 1826
        |||
        |||
        |||
Db      641 SerPheAspHisTyrAlaThr 647

RESULT 4
AAU14379
ID      AAU14379 standard; Protein; 647 AA.
XX
AC      AAU14379;
XX
DT      24-OCT-2001 (first entry)
XX
DE      Human novel protein #250.
XX
KW      Human; novel protein; Anlanaemic; osteopathic; antiinflammatory;
KW      immunomodulatory; cytoskeletal; neuroprotective; vulnerrary; nocotropic;
KW      anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW      antibacterial; antiallergic; dermatological; haemostatic; antiasclmatic;
KW      thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW      Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW      tissue regeneration; immune disorder.
XX
OS      Homo sapiens.
XX
PN      WO200155437-A2.
XX
PD      02-AUG-2001.
XX
PF      25-JAN-2001; 2001WO-US02623.
XX
PR      25-JAN-2000; 2000US-0491404.
XX
PA      (HYSE-) HYSEQ INC.
XX
PI      Tang YT, Liu C, Drmanac RT;
XX
DR      WPI; 2001-451939/48.
XX
DR      N-PSDB; AAS22684.
XX
PT      Isolated polypeptides useful for treating anti-inflammatory diseases,
XX
PS      nervous system disorders, and for regenerating bone and cartilage -
XX
PS      Example 4; Page 792-793; 894pp; English.
XX
CC      The invention relates to polynucleotides encoding novel human
CC      proteins or their active domains. The polypeptides, polynucleotides and
CC      antibodies raised against the polypeptides are used in a method of
CC      treatment of a mammal and prevention of disorders caused by the aberrant
CC      protein expression or activity. The polypeptides can be used as
CC      molecular weight markers, food supplements, and in antibody production.
CC      The polypeptides are used to identify compounds which bind to the
CC      polypeptides. Polynucleotides of the invention are used as probes and
CC      primers, for sequencing, for chromosome or gene mapping, in the
CC      production of recombinant proteins, and in generating anti-sense DNA or
CC      RNA and in gene therapy. Polypeptides of the invention can be used to
CC      target drugs to a tumour, in assays to determine biological activity, to
CC      raise antibodies/elicit an immune response, to determine quantitative
CC      protein levels, as tissue markers, and to isolate receptors or ligands.
CC      Polypeptides of the invention may also be useful in treating platelet
CC      disorders, stem cell disorders, regenerating bone, cartilage, tendon,

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CC ligament and/or nerve tissue, wound healing, treating burns, promoting  
CC the proliferation, differentiation and survival of stem cells, as a  
CC contraceptive, treating osteoporosis and osteoarthritis, anemia,  
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral  
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or  
CC fungal infection or from autoimmunity, cancer, allergy, asthma,  
CC graft-versus-host disease, eczema, hemophilia, thrombosis,  
CC anti-inflammatory diseases, nervous system disorders, and infection.  
CC The present sequence represents a protein of the invention.

xx Sequence 647 AA;

Alignment Scores:

Pred. No.:	3,49e-257	Length:	647
Score:	3236.00	Matches:	607
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	50.22%	Indels:	0
DB:	22	Gaps:	0

US-09-743-492-1 (1-3467) x AAU14379 (1-647)

QY 6 GGAGTGAAGGAGCTCTTGGTGGCCACCTGCTGACCTGTGAGAGATGGGAGCTCAAC 65  
DB 41 GlyLeuLysAspSerLeuLeuAlaHisSerSerAspProValGluMetArgArgLeuAsn 60  
QY 66 TACGAGCCCGCAGGTATCGAGAGCCACCACCATCCCATCCAGCAGCTGGCGAGAAC 125  
DB 61 TyrGlnThrProGlyMetArgAspHisProProIleProIleThrAspLeuAlaAspAsn 80  
QY 126 ATCGAGCCCTCAAGCCAGACGATGGCTCAAGTTCTCCAGAGATAGATCCATCGAC 185  
DB 81 IleGluArgLeuLysAlaAsnAspLysLeuLysPheSerGlnGluTyrGluSerIleAsp 100  
QY 186 CCGGACAGCAGATTACGCGGAGATCAAAACCTGGAGGAGAACAGCCCAAGACCGC 245  
DB 101 ProGlyGlnGlnPheThrTTPeLunSerSerAsnLeuGluValAsnLysProLysAsnArg 120  
QY 246 TATGCGAATGTCATCGCTAGCAGCCACTCTCGAGTCATCTTACCTTATCGATGGCGTC 305  
DB 121 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal 140  
QY 306 CCCGGAGTGAATACATCAATGSCCACTACATCGATGGCTTACCGGAGACAGATCCCTAC 365  
DB 141 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyr 160  
QY 366 ATCGCAGCAGGGGGCCCTGGCCGAGACCAATGGCGGATTCCTGGAGATGGTGGGA 425  
DB 161 IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheTyrArgMetValITrGlu 180  
QY 426 CAGGCGACGGCCACTGTGTGTCATGATGACACGGCTGGAGAGAACTCCCGGTAAATGT 485  
DB 181 GlnArgThrAlaThrValIleMetMetThrArgLeuGluGluLysSerArgValLysCys 200  
QY 486 GATCAGTACTGGCCAGCCCGTGGCAGCAGACCTGTGGCTTATTCAGATGACCTGTGG 545  
DB 201 AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu 220  
QY 546 GACGACAGGAGGAGCTGGCCATACACCTGGGCACTTGGCACTCCACAAAGAGTGGCTCC 605  
DB 221 AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerIlySer 240  
QY 606 AGTGAAGAGCTGAGCTGCTCAGTTCAGTTTCATGATGAGCTGGCCGAGACATGAGATTCCT 665  
DB 241 SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaITrProAspHisGlyAlaPro 260  
QY 666 GAGTACCCCACTCCCATCTGGCTTCTTACGAGCGGTCAAGGCTGCAACCCCTAGAC 725  
DB 261 GlnTyrProThrProIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAsp 280  
QY 726 GCAGGGCCCGATGGTGCAGCTGACGCGGGCGGGGCGCCGACCGGCTGCTTACTCTG 785  
DB 281 AlaGlyProMetValValHisCysSerAlaGlyAlaGlyArgThrGlyCysPheIleVal 300

QY 786 ATTGATGCCATGTTGGAGCGGATGAAGCAGAGACGCTGAGACATCTATGCGCAGTG 845  
DB 301 IleAspAlaMetLeuGluLysArgMetLysHisGlyLysThrValAspIleTyrGlnHisVal 320  
QY 846 ACCGTGATGCCATGCACAGAGAACTACATGCTGCACAGCAGGACAGCAGTACTGTTCAATC 905  
DB 321 ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle 340  
QY 906 CATGAGGCGCTGCTGAGGCTGCCAGCTGGCCGACAGAGAGTGGCTCCCGCAACTG 965  
DB 341 HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu 360  
QY 966 TATGCCCATTCAGAAAGCTGGGCCAAGTCCCTCCAGGGGAGAGTGTACCCGCAATGAG 1025  
DB 361 TyrAlaHisIleGlnLysLeuGlnValProProGlyGlnSerValIThrIleMetGlu 380  
QY 1026 CTCGAGTTCAGTTGCTGGCCAGCTCCAAAGGCCACACAGCTCCCGCTTCAATCAGGCCAAC 1085  
DB 381 LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 400  
QY 1086 CTGCCCTGCACAGATTCAGAAACCGGCTGTGAACATCATGCTCCATGCAATTCGACCGCT 1145  
DB 401 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg 420  
QY 1146 GTGTGCTGACAGCCCATCCGTGCTGGAGGCTGTGACTATCATCAATGCGCAGTTCTCTG 1205  
DB 421 ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu 440  
QY 1206 GATGGTATACAGCAGAGAGCCCTACATAGCTACACAGGGGCTCTGGCAGAGACACC 1265  
DB 441 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr 460  
QY 1266 GAGGACTCTGGCGCATGCTATGGAGGACATTCACCATCATGCTCATGCTGACCAAG 1325  
DB 461 GluAspPheITrArgMetLeuITrPheLunHisAsnSerThrIleIleValMetLeuThrLys 480  
QY 1326 CTTGCGGAGATGGGAGGAGAAATGCCACACAGTACTGGCCGAGAGCGCTCTCTGCGC 1385  
DB 481 LeuArgGluMetGlyArgGluLysCysHisGlnTyrITrProAlaGluArgSerAlaArg 500  
QY 1386 TACCGACTATTGTTGTTGACCCGATGGCTGAGTTCACAACATGCCCCAGTATATCTGGCT 1445  
DB 501 TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg 520  
QY 1446 GAGTCAAGGTCAGGATGGCCGGGATGGGCGCTCAAGACAAATCCGCGAGTCCAGTTC 1505  
DB 521 GluPheLysValIThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 540  
QY 1506 ACAGACTGGCCAGACGAGCGGCTGCCCAAGACAGGCGAGGGAATTCATGACTTCAATCGGG 1565  
DB 541 ThrAspITrProGluGlnGlyAlaProLysThrGlyGlnGlyPheIleAspPheIleGly 560  
QY 1566 CAGGTGCATTAAGCAGAGAGAGCATTTGGACAGAGATGGGCTTATGACGCTGACCTGACT 1625  
DB 561 GlnValHisLysThrLysGlnGlnPheGlyGlnAspGlyProIleThrValHisCysSer 580  
QY 1626 GCTGGCGTGGGCGGACCGGGGTTCATCACTGAGCATGCTCCGAGGCGCATGGCGC 1685  
DB 581 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGlnArgMetArg 600  
QY 1686 TATGAGGCGCTGTGTCAGATGTTTCAGACCGGTGAAGACCTTGCCTTACAGAGCTCTGCC 1745  
DB 601 TyrGluGlyValValAspMetPheGlnThrValLysThrIleArgIThrGlnArgProAla 620  
QY 1746 ATGTGTCAGACAGAGACAGCATGATGAGCTGTGCTACCGCTGGCGGCTGAGTACTCGGC 1805  
DB 621 MetValGlnIThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGlnTyrGlnLeu 640  
QY 1806 AGCTTGAACCATATGCAAGC 1826  
DB 641 SerPheAspHisTyrAlaIThr 647

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RESULT 5
AAB19712
ID AAB19712 standard; Protein; 1897 AA.
XX
AC AAB19712;
XX
DT 19-FEB-2001 (first entry)
XX
DE Human protein tyrosine phosphatase PTP LAR.
XX
KW PTP LAR; protein tyrosine phosphatase; leukocyte antigen related;
KW human; epithelial cell; cell migration; cell proliferation; cancer;
KW antitumour; metastasis; antimetastatic; wound healing; vulneryary;
KW diagnosis; therapy.
XX
OS Homo sapiens.
XX
XX
Key Location/Qualifiers
FH 1..16
FT /label= Signal_peptide
FT 17..1897
FT /label= Mature_protein
FT 37..99
FT /label= Immunoglobulin_domain
FT 139..199
FT /label= Immunoglobulin_domain
FT 236..290
FT /label= Immunoglobulin_domain
FT 309..391
FT /label= Fibronectin-type-III_domain
FT 403..490
FT /label= Fibronectin-type-III_domain
FT 502..584
FT /label= Fibronectin-type-III_domain
FT 596..686
FT /label= Fibronectin-type-III_domain
FT 698..799
FT /label= Fibronectin-type-III_domain
FT 811..894
FT /label= Fibronectin-type-III_domain
FT 905..990
FT /label= Fibronectin-type-III_domain
FT 1365..1596
FT /label= Protein-tyrosine_phosphatase
XX
XX
W0200061180-A2.
XX
XX
19-OCT-2000.
XX
XX
06-APR-2000; 2000W0-US09274.
XX
XX
09-APR-1999; 9905-0128673.
XX
XX
(PLAC ) MAX PLANCK INST.
XX
XX
Ullrich A, Muller T;
XX
XX
WPI: 2000-647399/62.
XX
XX
N-PSDB: AAA88739.
XX
XX
Treating a disease or a disorder characterized by epithelial cell
PT migration comprises administering a pharmaceutically acceptable
PT composition comprising PTP LAR -
XX
XX
Disclosure; Fig 9; 107pp; English.
XX
XX
PS
XX
The present sequence is that of human protein tyrosine phosphatase
CC PTP LAR (leukocyte antigen related), a negative regulator of
CC epithelial cell migration and tumour formation, for which
CC beta-catenin is a substrate. A dysfunction of PTP LAR may lead to
CC tumour invasion and metastasis. The invention provides methods for
CC diagnosing, preventing, or treating a disease or disorder
CC characterized by epithelial cell migration, increased tyrosine

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CC phosphorylation of beta-catenin, and/or increased levels of
CC the pool of free beta-catenin, especially cancer, metastasis and
CC aberrant wound healing (claimed). The methods may also be used to
CC treat diseases and disorders with abnormal cell proliferative
CC conditions, including fibrotic and mesangial disorders, abnormal
CC angiogenesis and vasculogenesis, psoriasis, diabetes mellitus and
CC inflammation. Methods are provided for identifying compounds that
CC modulate PTP LAR activity for use in treatment.
XX
XX
SQ Sequence 1897 AA:
XX
Alignment Scores:
Pred. No.: 6 16e-257 Length: 1897
Score: 3236.00 Matches: 607
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.22% Indels: 0
DB: Gaps: 21
US-09-743-492-1 (1-3467) x AAB19712 (1-1897)
QY 6 GCACGTGAAGGACCTCTGCTGGCCACATCTCTGACCTGTGGAGATGCGGAGCTCAAC 65
DB 1291 G1yleuLysAspSerLeuLeuAlaHisSerAspProValGluMetArgArgLeuAsn 1310
QY 66 TACCAGACCCAGGTATGCGAGACCAACCCATCCCATCCAGCAGCTGGCGGACAC 125
DB 1311 TylrGlnThrProGlyMetArgAspHisProProlleProlleThrAspLeuAlaAspAsn 1330
QY 126 ATCGAGCGGCTCAAGCAACGATGGCCCTCAATTTCTCCAGAGATGATGTCATCGAC 185
DB 1331 l1eGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnl1uYrGluSerl1eAsp 1350
QY 186 CCTGGACACAGCTTCACAGTGGGAGAAATTCAAACCTGGAGGTGAACAAGCCCAAGACCGC 245
DB 1351 ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg 1370
QY 246 TATGCAATGTCTATGCGCTTACGACCACTCTCGAGTATCTTACCTTATCGATGGCGTC 305
DB 1371 TylrAlaAsnVal11leAlaTylrAspHisSerArgVal11leuThrSerl1eAspGlyVal 1390
QY 306 CCCGGAGTGACATACATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 365
DB 1391 ProGlySerAspTrpL1eAsnAlaAsnTrpL1eAspGlyTylrArgLysGlnAsnAlaTyr 1410
QY 366 ATCGCCACGACGAGGCCCCCTGGCCGAGACCATGGGCGATTTCTGAGAAATGGTGGGAA 425
DB 1411 l1eAlaThrGlnGlyProLeuProGluTrnMetGlyAspPheTrpArgMetVal1TrpGlu 1430
QY 426 CAGCGCAGCGCCACTGTGTCATGATGACAGGCTGGAGAGAGATGCCGGTAAATGT 485
DB 1431 GlnArgThrAlaThrValAlaMetMetThrArgLengluGluLysSerArgVal1Lys 1450
QY 486 GATCAGTACTGGCCACCGCTGGCCAGGAGCTGTGGCTTATTCAGTAAACCTGTG 545
DB 1451 AspGlnTrpTrpProAlaArgGlyTrnGluTrnGlyGlyLeuL1eGlnVal1TrnLeuLeu 1470
QY 546 GACACAGTGAGCTGGCCACATACACTGTGCGACCTTGCACTCCACAAGATGGCTCC 605
DB 1471 AspThrValGluLeuAlaThrTrpThrValArgThrPheAlaLeuHisLysSerGlySer 1490
QY 606 AGTGAGACGCTGAGCTGCTCAGTTTCAGTTTCAGTTTCAGTTTCAGTTTCAGTTTC 665
DB 1491 SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro 1510
QY 666 GAGTACCAGACCTCCCTGCTGCTCCATGACGAGGCTGAAGGCGTCAACCCCTAGAC 725
DB 1511 GluTyrProThrProLeuLeuAlaPheLeuAlaArgValAlaLysAsnProLeuAsp 1530
QY 726 GCAGGCGCCATGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 785
DB 1531 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGluLysPheL1eVal 1550

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QY	786	ATTGATGCGCATGTTGGAGCGGATTAACACAGAGAAAGCGGTGACATCTATGCGGACGTC	845
Db	1551	TTespralamectileu6glnuagmelyshis6ludsthyValaAspIleuTolynh3val	1570
QY	846	ACSTGCATGCGCATGACAGAGAGAACTAATGATGTCAGACAGCGAGAGACCAATGCTGTATATC	905
Db	1571	ThrcysmetatgserglnatgAsnTtymeValGlnthrcGlnuAspIlnTtlyValPheIle	1590
QY	906	CATGAGCGGCTGCTGGAGAGCTGCCACSTGGCGCCACAGAGAGTGGCTCTGCCGCAACCTGG	965
Db	1591	hnsGlnalaleuileuGlnlualalathrcCysGlnhsthrGlnlvalProalaIatgAsnIleu	1610
QY	966	TATGGCCCATCTCCAGAGAGCTGGCGCAAGTGCCTCCAGGGGAGAGTGTGACCGGCATGGAG	1025
Db	1611	TtYalalnshIleGlnLysleuGlnlvalProIogIyGlnuIserValThrralameGln	1630
QY	1026	CTCGAGTTCAAGTGTCTGGCCAGCTGCCAGAGGCCACAGCTGCCGCTTCAATGACGCCCAAC	1088
Db	1631	LeuGlnrPheLysleuIleuAlaIaserSerLysAlalnshsthrSerLthrPheIleSerAlasn	1650
QY	1086	CTGCCCTGCACAAAGATTCCAAAGAACGGGCTGGTAACATCATGCGCTTACGAATTGACCGCT	1145
Db	1651	LeuProCysAsnLysrPheLysAsnArgLeuValAsnIlemerProthylGlnuIleuThrarg	1670
QY	1146	GTGTGTCTGCAGAGCCCATCTCGGTGTGTGGAGGCTGTGCATATCAATGACAGCTTCTGG	1205
Db	1671	ValCysLeuGlnrProIleArgGlnlvalGlnlYserAsprryTlleAsnAlaserPheLys	1690
QY	1206	GATGGTTTATACAGACAGAAAGGCGCTTACATAGCTATACAGAGGCGCTGTGCACAGAGACAC	1265
Db	1691	AspGlnYtYtArgGlnlGlnlYsalatYtIleAlathrcGlnlYrProleuAlaGlnuIserThr	1710
QY	1266	GAGACATTTCTGGCGCATGCTATGGGAGCACAAATTCACCATCATGCTCATGCTGCACAG	1325
Db	1711	GlnAsprrhetrArgmetLeuItrPrglnhshAsnserThrIleIleValmetLeuThrLys	1730
QY	1326	CTTGCGGAGATGGGCGAGGAGAAATGGCCACACATGACCTGGCCACAGAGGCGTCTGTGCC	1385
Db	1731	LeuArgGlnmetGlnYtArgGlnLysCysshisGlnlYtTrrProAlaGlnrYserAlaIarg	1750
QY	1386	TACACAGTACTTGTGTGTGACCCCGATGGCTGAGTATACATGCGCCACAGTATTCCTGCGCT	1445
Db	1751	TtYrGlnTtYrPheValIvalAsprrIometAlaGlnTtYrAsnmerProslnTtYrIleleuArg	1770
QY	1446	GAGTTCAAGGTCCACGGATCCCGGGATGGGAGTCAAGGACAAATCCGGACGTTCCAGTTTC	1505
Db	1771	GlnrPheLysValThrrAspAlaIargAspGlnYGlnIserArgThrIleargGlnrPheGlnrPhe	1790
QY	1506	ACAAGACTGGCCAGAGACAGGCGCTGCCAAACAACAGCGGAGGATTCATTATCTTCATCGGG	1566
Db	1791	ThrrAsprrProIoglnlGlnlYvalProLysrThrcGlnlYrPheIleAsprrheIleGlnl	1810
QY	1566	CAGGCGCATTAAGACCAAGAGAGGAGTTGGACAGATGAGGCGCTATCCAGGTGCAGTCGAGT	1625
Db	1811	GlnValhshLysrTtYrLysGlnlGlnrPheGlnYGlnAspIyProIleThrValhshCysSer	1830
QY	1626	GCTGGCGTGGGCGCCAGCGGGGTGTTCATCACTCATAGATCGCTCTGCAGCGCATGCGGC	1685
Db	1831	AlaGlnYalGlnYtGlnrGlnlYvalPheIleThrLeuSerIleValLeuGlnrYrmetLarg	1850
QY	1686	TATGAGGCGGTGTGCACATGTTTACAGACCGTGAAGACCCCTGGGTACACAGCGTCTGTGC	1745
Db	1851	TtYrGlnlYvalIvalAsprrPheGlnIthrValLysrThrcLeuArgThrGlnItrProAla	1870
QY	1746	ATGGGCGAGAGAGAGACCGATACAGTTCACGCTGTGTACCGTGGCGCCCTGGAGTACCTGGC	1805
Db	1871	MetValGlnrTtYrGlnAsprrGlnlTtYrGlnLysCysTtYrArgAlaIaleuGlnlYtYrleuGlnl	1890
QY	1806	AGCTTTGACACACTATGCACAG 1826	
Db	1891	SerPheAsprrhstYtYrAlaIthr 1897	
RESULT - 6			

AY81785	standard; Protein: 1897 AA.		
AY81785			
AY81785			
07-JUN-2000	(first entry)		
Human protein tyrosine phosphatase, LAR, protein sequence.			
Human; protein tyrosine phosphatase; antibody; intracellular domain; LAR			
CD45; PTP; diagnosis; insulin resistance related disease; syndrome X;			
non-insulin dependent diabetes mellitus; arteriosclerosis; therapy;			
heart disorder.			
Homo sapiens.			
WO200002922-A1.			
20-JAN-2000.			
06-JUL-1999; 99WO-JP03656.			
10-JUL-1998; 98WO-JP03120.			
(FUSO ) FUSO PHARM IND LTD.			
Yamamoto H, Tsujikawa K, Uchino Y;			
WPI: 2000-182215/16.			
N-PSDB; AA291908.			
Antibody for diagnosis and treatment of insulin resistance disorders			
and syndrome X recognises the intracellular domains of tyrosine			
phosphatase -			
Example 1; Page 61-77; 83pp; Japanese.			
This sequence is the protein tyrosine phosphatase LAR. The invention			
relates to an antibody specifically recognising the intracellular domain			
of two or more protein tyrosine phosphatases (PTPs). The antibody is			
useful for the detection and assay of PTP including novel phosphatases			
generated by cloning; and diagnosis, treatment and prevention of insulin			
resistance related diseases and non-insulin dependent diabetes mellitus,			
syndrome X and arteriosclerosis and heart disorders.			
Sequence 1897 AA:			
Alignment Scores:			
Pred. NO.:	6,16e-257	Length:	1897
Score:	3236.00	Matches:	607
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	50.22%	Indels:	0
DB:	21	Gaps:	0
US-09-743-492-1 (1-3467) x AY81785 (1-1897)			
6	GGATGGAAGGACCTCTGGGCGCCAACTCTGACCCCTTGAGAGATGGGAGGCTCAAC	65	
1291	GIILeuLYsAsPSeRleuLeuAlaAlaHisSeSeRAsPProValGIuMetArgArgLeuAsn	1310	
66	TACAGACCCAGGTATGAGAGACACACCCATCCCATCAGACGACCTGGCGAGCAAC	125	
1311	TyrGIInThrProGIuMetArgAsPHisProProlIeProlIeThrAsPLeuAlaAspSn	1330	
126	ATCGAGCCGCTCAAGCCAAAGCATGAGGCGCTCAAGTCTCCAGAGCATGATGCATGAC	185	
1331	ILleGIuArgLeuLYsAlaAsnAsPGLyeuLYsPheSeRcInGIuTYGIuSeRleAsp	1350	
186	CGTGAGACGAGCTTCAGTGGGAGAAATTCAAACCTGAGAGTGAGCAACGCCAAGAAGCG	245	
1331	ProGIuInGIuInPheThrITTPGIuAsnSeRAsnLeuGIuValAsnLYsProLYsAsnArg	1370	



QY 246 TATGCAATGTCATCGGCTAGACACATCTGAGTCATCTTACCTGATGATGCGCTC 305  
 |||||  
 Db 1371 TyAlaAsnValIleAlaIleTyAspHisSerArgValIleLeuThrSerIleAspGlyVal 1330  
 QY 306 CCGGGAGTACTACATCAATGCCAACTACATGCGTACCGCAAGCAAGATGCTTAC 365  
 |||||  
 Db 1391 ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgGlyGlnAsnAlaTyr 1410  
 QY 366 ATGGCCAGGAGGGCCCCCGCCGAGACACATGGGGCATTTCTGGAAATGGTGGGAA 425  
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 Db 1411 IleAlaThrGlnGlyProLeuProGlyIleThrMetGlyAspPheTyrPargMetValTyrGly 1430  
 QY 426 CACGCGACGGCCACTGTGTGTCATGATGACACGGCTGGAGGAAGTCCCGGGTAAATGT 485  
 |||||  
 Db 1431 GlnArgThrIleThrValIleValMetLeuThrArgLeuGlnGlySerArgValIleGlyCys 1450  
 QY 486 GATCAGTACTGGCCACGCCGTGGACCCGAGACCTGTGGCTTATTCAGTGAACCTGTG 545  
 |||||  
 Db 1451 AspGlnTyrTyrProAlaIleArgGlyThrGlnThrCysGlyLeuIleGlnValIleThrLeu 1470  
 QY 546 GACACAGTGGAGCTGGCCACATACACTGTGGCACCTTGGCACTCCACAAAGATGGCTCC 605  
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 Db 1471 AspThrValGlyLeuAlaIleThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer 1490  
 QY 606 AGTGAAGAGCGTAGCTGCGTCACTTCACTTCACTGCGCCAGACCATGGAGTTCCT 665  
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 Db 1491 SerGlnLysArgGlnLeuAlaGlnGlnPheGlnPheMetAlaIleProAspHisGlyValPro 1510  
 QY 666 GAGTACCCAACTCCACTCTGGCCCTTCTAGACAGGGGTCAAGGCTGCAACCCCTAGAC 725  
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 Db 1511 GlnTyrProThrProIleLeuAlaPheLeuArgArgValIleLysAlaCysAsnProLeuAsp 1530  
 QY 726 GCAGGGCCCATGGTGGTGCATCGACAGCGGGCGGTGGCCGCGCATGCTGTCATGTG 785  
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 Db 1531 AlaGlyProMetValIleHisCysSerAlaGlyValGlyIleArgThrGlyCysPheIleVal 1550  
 QY 786 ATTGATGCGCATGTTGGAGCGGATGAAGCAGAGAGAGAGCGGTGACATCTATGGCCAGCTG 845  
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 Db 1551 IleAspAlaMetLeuGlnIleGlnMetLysHisGlnLysThrValAspIleTyrGlnHisVal 1570  
 QY 846 ACCTGCATGCGCATCAGAGAGAACTACATGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 905  
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 Db 1571 ThrCysMetArgSerGlnArgAsnTyrMetValGlnIleThrGlnAspGlnTyrValPheIle 1590  
 QY 906 CATGAGGCGGTGCTGGAGGCTGCCACGTGGCGGCACACAAAGTGGCTGGCCCGCAACCTG 965  
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 Db 1591 HisGlnAlaLeuLeuGlnAlaIleAlaThrCysGlyHisThrGlnValProAlaIleArgAsnLeu 1610  
 QY 966 TATGCCCATCTCCAGAAAGTGGGCGCAAGTCCCTCCAGAGGAGAGTGGAGCGGCATGGAG 1025  
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 Db 1611 TyrAlaHisIleGlnLysLeuGlnValIleProProGlyIleSerValIleThrAlaMetGln 1630  
 QY 1026 CTGCAAGTTCAGTGTGGCCAGCTCCAGAGGCCACACAGTCCCGCTTCATCAGCGGCCAAC 1085  
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 Db 1631 LeuGlnPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn 1650  
 QY 1086 CTGCGCTGCACAAAGTTCAGAGAACCGGTGTAACATCATGCCCTTACGAATGACCCCT 1145  
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 Db 1651 LeuProCysAsnLysPheLysAsnArgLeuValAlaHisIleMetProTyrGlnLeuThrArg 1670  
 QY 1146 GTGTGCTGTGAGCCCATCCCTGTGTGGAGGGCTGTGATACATCAATGCGCAGCTTCCTG 1205  
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 Db 1671 ValCysLeuGlnProIleArgGlyValGlnGlySerAspTyrIleAsnAlaSerPheLeu 1690  
 QY 1206 GATGCTTATAGACAGAGAAAGCTTACATGATGATACACAGGGGCTGTGGCAGAGAGACC 1265  
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 Db 1691 AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnIleProLeuAlaGlnSerThr 1710  
 QY 1266 GAGGACTTCTGGGGCATGCTATGAGGAGACAAATTCACACATCATGCTGATGCTGACCAAG 1325  
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 Db 1711 GlnAspPheThrPargMetLeuTyrGlnHisAsnSerThrIleIleValMetLeuThrLys 1730  
 QY 1326 CTTCGGGAGATGGGCGAGGAGAAATGCCACCATGACTGGCCAGAGAGCCCTGTGCTCGC 1385

Db 1731 LeuArgGlnMetGlyArgGlnLysCysHisGlnIleTyrTyrProAlaGlnArgSerAlaArg 1750  
 QY 1386 TACCAGTACTTGTGTGTGACCCGATGGCTGAGTACAAATGCCAGTATATCCTCGT 1445  
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 Db 1751 TyrGlnTyrPheValIleAspProMetAlaGlnIleTyrAsnMetProGlnTyrIleLeuArg 1770  
 QY 1446 GAGTTCAAAGTCCACGGATGCCCGGATGGGCAGTCAAGAGACATCCGGCAGTTCCAGTTC 1505  
 |||||  
 Db 1771 GlnPheLysValIleThrAspAlaIleArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1790  
 QY 1506 ACAGACTGGCCAGAGCAGGGGGTCCCAAGACAGCGGAGGATTCATGATTCATGCGG 1565  
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 Db 1791 ThrAspTyrProGlnGlnGlnValIleProLysThrGlyGlnGlyPheIleAspPheIleGly 1810  
 QY 1566 CAGGTGCATTAAGACCAAGAGACAGTTCGACAGAGATGGGCTTACAGGTGACATGCACT 1625  
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 Db 1811 GlnValHisLysThrLysGlnGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1830  
 QY 1626 GCTGGCGTGGCCCGCACCGGGGTTCATCACTGTGACATCGTCTGGAGCGCATGCGC 1685  
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 Db 1831 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValIleGlnArgMetArg 1850  
 QY 1686 TATGAGCGCGTGGTGCATGTTTCAGACCGGTGAAGACCCGTGACACAGCGCTGCGC 1745  
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 Db 1851 TyrGlnGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnAlaProAla 1870  
 QY 1746 ATGGTCAGACAGAGAGACAGATACAGTGTGCTGACCGGTGCGGCGCTGAGATACCTGCGC 1805  
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 Db 1871 MetValGlnThrGlnAspGlnTyrGlnLeuCysTyrArgAlaIleLeuGlnTyrLeuGly 1890  
 QY 1806 AGCTTGACCATGTCGACAGC 1826  
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 Db 1891 SerPheAspHisTyrAlaThr 1897.  
 RESULT 7  
 ID AAY56100 standard; Protein; 1897 AA.  
 AC AAY56100;  
 DT 17-APR-2000 (first entry)  
 XX  
 DE LAR tyrosine phosphatase.  
 XX  
 KW Intracellular domain; P-subunit; human; leucocyte antigen related; LAR;  
 KW tyrosine phosphatase; antibody; thyroid cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0964591-A1.  
 XX  
 PD 16-DEC-1999.  
 XX  
 PF 07-JUN-1999; 99WO-JP03054.  
 XX  
 PR 08-JUN-1998; 98WO-JP02542.  
 XX  
 PA (FUSO ) FUSO PHARM IND LTD.  
 XX  
 PI Yamamoto H, Tsujikawa K, Uchino Y, Konishi N;  
 XX  
 DR WPI; 2000-097539/08.  
 DR N-PSDB; AA591133.  
 XX  
 PT Antibody recognizing the intracellular domain of the human tyrosine  
 PT phosphatase LAR -  
 XX  
 PS Disclosure; Page 81-97; 104pp; Japanese.  
 XX  
 CC This sequence represents the complete human leucocyte antigen related  
 CC (LAR) tyrosine phosphatase. The invention relates to the generation of  
 CC an antibody recognizing the intracellular domain of the human LAR

CC tyrosine phosphatase (AAV56098). The antibody is used for the diagnosis  
 CC and treatment of thyroid cancer.

XX Sequence 1897 AA;

Alignment Scores:

Pred. No.:	6,16e-257	Length:	1897
Score:	3236.00	Matches:	607
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	50.22%	Indels:	0
DB:	21	Gaps:	0

US-09-743-492-1 (1-3467) x AAV56100 (1-1897)

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QY 6 GGAAGTGAAGAGCTCTTGGTGGCCCACTGCTGACCTGTGGAGATGGAGGCTCAAC 65
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Db 1291 GYleuLysAspSerleuLeuAlaHisSerSerAspProValGluMetArgIleuAsn 1310
QY 66 TACCAAGCCCAAGTATGCGAAGACCAACCCATCCCATCCAGCAGCTGGCGAACA 125
    |||
Db 1311 TYrGlnThrProGlyMetArgAspHisProIleProIleThrAspLeuAlaAspAsn 1330
QY 126 ATCGAGCGGCTCAAAAGCCAAAGCATGGCTTCAGTTCTCCAGAGATATAGTCCATGAC 185
    |||
Db 1331 IlegIuArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGlnIuSerIleAsp 1350
QY 186 CCTGGACAGCAGTTCACGTGGGAGAAATTCAAACCTGAGAGTGAACAGCCCAAGAACCG 245
    |||
Db 1351 ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg 1370
QY 246 TATGGGAATGTCATGCGCTACGACCACTCTCGATCCCTTACCTATTCATGAGTGGCTC 305
    |||
Db 1371 TYrAlaAsnValIleIleIleArgAspHisSerArgValIleIleuThrSerIleAspGlyVal 1390
QY 306 CCCGGAGTGACTACATCATATGCAACTACATGATGCGTACCGCAAGAGAATGCTTAC 365
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Db 1391 ProGlySerAspTYrIleAsnAlaAsnTYrIleAspGlyTYrArgLysGlnAsnAlaTYr 1410
QY 366 ATCGCAGCAGGAGGCCCCCTGGCCCCGAGACCATGAGGAGTTCGTGGAGAAATGGTGGAA 425
    |||
Db 1411 IleAlaThrGlnGlyProIleuProGlnIuThrMetGlyAspPheTrpArgMetValITrpglu 1430
QY 426 CAGCCGACGCGCACATGTGTGATGATGACACAGCGCTGGAGAGAAAGTCCCGGTAATAATG 485
    |||
Db 1431 GlnArgThrAlaThrValValIleMetMetThrArgLeuGlnGluLysSerArgValLysCys 1450
QY 486 GATCAGTACTGGCGCAGCCCGCGGACCGAGACCTGTGGCTTATTCAGTGAACCTGTGG 545
    |||
Db 1451 AspGlnTYrTrpProAlaIleArgGlnTYrThrGlnIuThrCysGlyLeuIleGlnValIThrLeuLeu 1470
QY 546 GACACAGTGGAGCTGGCCACATACACTGTGGCAGCACTTGCCACTGCACAAAGATGGCTCC 605
    |||
Db 1471 AspThrValGluLeuAlaThrIleTYrThrValArgThrPheAlaLeuHisLysSerGlySer 1490
QY 606 AGTGAAGACGCTGAGCTGGCTGAGTTTCAGTTTCATGAGCTTGCCGACCAACCATGGAGTTCT 665
    |||
Db 1491 SerGlnLysArgGluIleuArgGlnPheGlnPheMetAlaITrProAspHisGlyValPro 1510
QY 666 GAGTACCCCACTCCCATCTGGCTTCCTTCACGAGGGGTCAAGGCTTCGAACCCCTAGAC 725
    |||
Db 1511 GlnTYrProThrProIleuAlaIlePheLeuArgValIleLysAlaCysAsnProLeuAsp 1530
QY 726 GAGAGGCCCATGTTGATGCTGACGAGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 785
    |||
Db 1531 AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlnLysPheIleVal 1550
QY 786 ATTGATGCCATGTTGAGCGGATGAAGACAGAGAACCGGTGACATTCATGAGCCACGTG 845
    |||
Db 1551 IleAspAlaMetLeuGlnArgMetLysHisGlnLysThrValAspIleTYrGlnHisVal 1570
QY 846 ACCTGATGCGCATCACAGAGAACTACATGTTGACGAGCGAGAGACCATGATGCTTTCATC 905
    |||

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Db 1571 ThrCysMetArgSerGlnArgAsnTYrMetValGlnThrGlnAspGlnTYrValPheIle 1590
QY 906 CATGAGAGCGCTGCTGGAGCGCTGCCACCTGGCGGCACACAGAGTGGCTGGCCCAACTG 965
    |||
Db 1591 HisGlnAlaLeuLeuGlnAlaIleThrIleCysGlyHisIleThrGlnValProAlaIleAsnLeu 1610
QY 966 TATGCCCACTCCAGAAAGCTGGGCGCAAGTGGCTTCACAGGGGAGAGTGTGACCGCATGAG 1025
    |||
Db 1611 TYrAlaHisIleGlnLysLeuGlnValProProGlyGluSerValIThrAlaMetGlu 1630
QY 1026 CTCGAGTTCAGATTGGCTGGCGACCTCCAAAGGGCCCAACCTCCCGCTTCATCAGCGGCAAC 1085
    |||
Db 1631 LeuGlnPheLysLeuLeuAlaSerSerLysAlaHisIleThrArgThrIleSerAlaAsn 1650
QY 1086 CTGCCCCGCAACAAGTTTCAAGAACCGGCTGGTAACATCATCGCTTACAGAAATGACCCGT 1145
    |||
Db 1651 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTYrGlnLeuThrArg 1670
QY 1146 GTGTGTCTGACGCCATCCGTGGTGTGAGAGGCTGTGACTACATGCATGCCACCTTCCTG 1205
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Db 1671 ValCysLeuGlnProIleArgGlyValGlnGlySerAspTYrIleAsnAlaSerPheLeu 1690
QY 1206 GATGCTTATAGACAGAGAAAGGCTTACATAGCTTACACAGAGGCGCTTCGACAGAGACACC 1265
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Db 1691 AspGlyTYrArgGlnGlnLysAlaTYrIleAlaIThrGlnIleProLeuAlaGlnSerThr 1710
QY 1266 GAGCACTTCGCGCATGCTATGAGAGACAAATTCACCACTCATCGTCATGTCAGACAA 1325
    |||
Db 1711 GluAspPheTrpArgMetLeuTrpGlnHisAsnSerThrIleIleValIleMetLeuTrpLys 1730
QY 1326 CTTCGGGAGATGGCGGAGGAGAAATGCCAACACAGTACTGGCCACAGAGCGCTGCTGCG 1385
    |||
Db 1731 LeuArgGluMetGlyArgGlnLysCysHisGlnTYrTrpProAlaGlnArgSerAlaArg 1750
QY 1386 TACCACTACTTTGTTGTTGACCCGATGCGTGAATACAACTGCCCCAGTATATCTGCGT 1445
    |||
Db 1751 TYrGlnTYrPheValValAspProMetAlaGlnTYrAsnMetProGlnTYrIleuArg 1770
QY 1446 GAGTTCAGAGTCCAGATGCGCGGATGGGCGACTCAAGGACATCCGGCGAGTTCAGATTG 1505
    |||
Db 1771 GluPheLysValIThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1790
QY 1506 ACAGACTGGCCACAGAGGCGCTGCCCAAGACAGCGGAGGAGATTCATGACTTCATCGGG 1565
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Db 1791 ThrAspTrpProGlnGlnGlyValProLysThrGlyGlnGlyPheIleAspPheIleGly 1810
QY 1566 CAGGTGCATAAAGCAAGAGACAGCTTGGACACAGAGATGGGCTTACAGGTGACATGCA 1625
    |||
Db 1811 GlnValHisLysThrLysGlnGlnPheGlnPheGlyGlnAspGlyProIleThrValHisCysSer 1830
QY 1626 GCTGGCGTGGCGCCAGCGGGGTTCATACACTGTGAGCATGCTGCGGAGCGCATGGCG 1685
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Db 1831 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValIleuGlnArgMetArg 1850
QY 1686 TATGAGCGCGTGGTGCACATGTTTCAGACCGTGAAGACCTGGCTGACACAGCGTCTGCG 1745
    |||
Db 1851 TYrGlnGlyValValAlaAspMetPheGlnIThrValLysIThrLeuArgThrGlnArgProAla 1870
QY 1746 ATGCTGCAACAGAGACAGCATGATCAGCTGTGTACCCTGGCGGCTCGAGTACTCTGGG 1805
    |||
Db 1871 MetValGlnIThrGlnAspGlnTYrGlnLeuCysTYrArgAlaIleuGlnIuTYrLeuGly 1890
QY 1806 AGCTTGACACATATGCAACG 1826
    |||
Db 1891 SerPheAspHisIleTYrAlaThr 1897

```

RESULT 8

AAU14143

ID AAU14143 standard; Protein; 1907 AA.

XX

AC AAU14143;

XX

24-OCT-2001 (first entry)

XX Human novel protein #14.  
 DE  
 XX  
 XX Human: novel protein; Antianaemic; osteopathic; antiinflammatory;  
 KW Immunomodulatory; cytostatic; neuroprotective; vulnery; nootropic;  
 KW anticonvulsant; antirheitic; cerebroprotective; antifungal; antiviral;  
 KW antibacterial; antiallergic; dermatological; haemostatic; antishematic;  
 KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;  
 KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;  
 KW tissue regeneration; immune disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 XX MO200155437-A2.  
 PN  
 XX 02-AUG-2001.  
 PD  
 XX 25-JAN-2001; 2001WO-US02623.  
 PF  
 XX 25-JAN-2000; 2000US-0491404.  
 PR  
 XX (HYSE-) HYSEQ INC.  
 PA  
 PI Tang YT, Liu C, Drmanac RT;  
 XX  
 XX WPI: 2001-451939/48.  
 DR N-PSDB; AAS22448.  
 XX  
 PT Isolated polypeptides useful for treating anti-inflammatory diseases,  
 PT nervous system disorders, and for regenerating bone and cartilage -  
 XX  
 PS Example 4; Page 533-537; 894pp; English.  
 XX  
 CC The invention relates to polynucleotides encoding novel human  
 CC proteins or their active domains. The polypeptides, polynucleotides and  
 CC antibodies raised against the polypeptides are used in a method of  
 CC treatment of a mammal and prevention of disorders caused by the aberrant  
 CC protein expression or activity. The polypeptides can be used as  
 CC molecular weight markers, food supplements, and in antibody production.  
 CC The polypeptides are used to identify compounds which bind to the  
 CC polypeptides. Polynucleotides of the invention are used as probes and  
 CC primers, for sequencing, for chromosome or gene mapping, in the  
 CC production of recombinant proteins, and in generating anti-sense DNA or  
 CC RNA and in gene therapy. Polypeptides of the invention can be used to  
 CC target drugs to a tumor, in assays to determine biological activity, to  
 CC raise antibodies/elicit an immune response, to determine quantitative  
 CC protein levels, as tissue markers, and to isolate receptors or ligands.  
 CC Polypeptides of the invention may also be useful in treating platelet  
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,  
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting  
 CC the proliferation, differentiation and survival of stem cells, as a  
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,  
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral  
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or  
 CC fungal infection or from autoimmunity, cancer, allergy, asthma,  
 CC graft-versus-host disease, eczema, haemophilia, thrombosis,  
 CC anti-inflammatory diseases, nervous system disorders, and infection.  
 CC The present sequence represents a protein of the invention.  
 XX  
 SQ Sequence 1907 AA;  
 Alignment Scores:  
 Pred. No.: 6,18e-257 Length: 1907  
 Score: 3236.00 Matches: 607  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 50.22% Indels: 0  
 DB: 22 Gaps: 0  
 US-09-743-492-1 (1-3467) x AAU14143 (1-1907)  
 OY 6 GGAGTGAAGACATCTGTGGCCCACTCTGACCCCTGGAGATGCGAGGCTCAAC 65  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1301 G1LeuLysAspSerLeuLeuAlaHisSerSerAspProValG1uMetArgArgLeuAsn 1320  
 OY 66 TACCAGACCCCAAGGTATGCGAGACACCCACCATTCCCATACCGACCTGGCGGACAC 125  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1321 TycGlnThrProG1uMetArgAspHisProProLeuThrThrAspLeuAlaAspAsn 1340  
 OY 126 ATGAGCGGCTCAAGGCAAGCAAGCAAGGCTCAAGCTCCAGGAGTGTAGTGCATTCGAC 165  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1341 IleG1uArgLeuLysAlaAsnAspG1uLeuLysPheSerGlnG1uTyrG1uSerIleAsp 1360  
 OY 186 CCTGACAGCAGTTCACAGTGGGAGAAATTCAAACCTGGAGGTGAACAAGCCCAAGACCCG 245  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1361 ProG1uSlnGlnPheThrTrpG1uAsnSerAsnLeuGluValAsnLysProLysAsnArg 1380  
 OY 246 TATGCCAATGTCAATGCCCTACGACACACTCTGAGTCAATCCTTACCTTATGATGGCGTC 305  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1381 TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspG1uVal 1400  
 OY 306 CCGGGAGTGACTACATCAATGCCAATACATGATGGCTACCGGCAAGCAAGTACGCTAC 365  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1401 ProG1uSerAspTyrIleAsnAlaAsnTyrIleAspG1uTyrArgLysGlnAsnAlaTyr 1420  
 OY 366 ATGCGCACAGGAGCCCTGCGCCGAGACCATGGGCGATTTCGAGAAATGTCTGGGAA 425  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1421 IleAlaThrGlnG1uProLeuProG1uThrMetC1yAspPheTrpArgMetValITrpg1u 1440  
 OY 426 CACGCGACGGGCACTGTGTCATGATGACACGGCTGGAGGAGAGATCCCGGTAATAATGT 485  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1441 GlnArgThrAlaThrValValMetMetThrArgLeuGluG1uLysSerArgValLysCys 1460  
 OY 486 GATCAGTACAGCGGCGCGCGTGGCAGCAGACCTGTGGCTTATGAGTGGACCCGTG 545  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1461 AspGlnTyrTrpProAlaArgG1uThrG1uThrCysG1uLeuIleGlnValIThrLeuLeu 1480  
 OY 546 GACACAGTGAAGTGGGCGCACATACATGCTGCGGACCTTCACATCCAAAGATGGCTCC 605  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1481 AspThrValGluLeuAlaThrTrpTyrThrValArgThrPheAlaLeuHisLysSerG1uSer 1500  
 OY 606 AGTGAGAAGCGTGAAGTGGCTCACTTCACTTCACTGAGCTGGCCAGACCTGAGATTGCT 665  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1501 SerG1uLysArgG1uLeuArgGlnPheGlnPheMetAlaTrpProAspHisG1uValPro 1520  
 OY 666 GAGTACCCCACTCCATCCGAGGCTTCTACGACGGGTCAAGGCGTGCACACCCCTAGAC 725  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1521 GlnTyrTrpThrProIleLeuAlaPheLeuArgValLysAlaCysAsnProLeuAsp 1540  
 OY 726 GCAAGGCGCATGTGTGTGCACTGACGCGGCGGTGGCGCCGACCGGCTCTCATCTG 785  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1541 AlaG1uProMetValValHisCysSerAlaG1uValG1uArgThrG1uCysPheIleVal 1560  
 OY 786 ATGATGCCATGTGGAGCGGATGAAACACGAGAAAGCGTGCATGTATGGCCACGTG 845  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1561 IleAspAlaMetLeuGluArgMetLysHisG1uLysThrValAspTrpG1uHisVal 1580  
 OY 846 ACGTCATGCGATCAGACAGAGAACTACATGTCAGAGCGGAGGACAGTACGTTTCATC 905  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1581 ThrCysMetArgSerGlnArgAsnTyrMetValG1uThrLysPrgL1uTyrValPheIle 1600  
 OY 906 CATGAGCGCTGTGAGGCTGCGACGTGCGGCGCCACACAGAGGTGCTGCCCAACTG 965  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1601 HisGluAlaLeuLeuGluAlaIleAlaThrCysG1uHisThrGluValProAlaIleArgAsnLeu 1620  
 OY 966 TATGCCCAATCCAGAAAGCTGGGCGCAAGTGCCTCCAGGGAGAGTGTGACCGCATGAG 1025  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1621 TyrAlaHisIleGlnLysLeuG1uGlnValProProG1uLysSerValIThrAlaMetG1u 1640  
 OY 1026 CTCGAGTCAAGTGTGGCGGCGACGTCGCAAGGCCCAACGTCGCTCAACAGCGCAAC 1085  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1641 LeuGluPheLysLeuLeuAlaSerLysAlaHisThrSerArgPheIleSerAlaAsn 1660  
 OY 1086 CTCGCCCTGCACAAGTTCAGAAGACCGGCTGGTGAACATCAATGCTTACGAATTCACCCGT 1145  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1661 LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrG1uLeuThrArg 1680

```

QY 1146 GTCGTCTGACAGCCATCCGCTGTGAGGGCTCTGACTACATCATGCCAGCTTCCTG 1205
DB 1681 ValCysLeuGlnProIleArgIValGlnGlySerAspTyrIleAsnIleAsnIleSerPheLeu 1700
QY 1206 GATGGTTATAGACAGCAAGAGCCCTACATAGCTACACAGGGCCTTGGCAGAGACACC 1265
DB 1701 AspGlyTyrArgGlnGlnGlnIleAlaTyrIleAlaThrGlnGlyProLeuAlaGlnSerThr 1720
QY 1266 GAGGACTTCGGCGCATGCTATGGGAGCAATTCACCATCATCGTCATGGCTGACCAAG 1325
DB 1721 GluAspPheThrParGmetLeuThrPgluHisSerThrIleIleValIleLeuThrLys 1740
QY 1326 CTTCCGGAGATGGCGAGGAGAAATGCCACCATGACTGGCCAGCAGAGCGCTCTGCTCC 1385
DB 1741 LeuArgGlnMetGlyValArgGlnLysCysHisGlnTyrTrpProAlaGlnArgSerAlaArg 1760
QY 1386 TACCACTACTTTGTTGTTTACCCGATGCTGAGTACACATGCCAGTATATCTGCGCT 1445
DB 1761 TyrGlnTyrPheValIValAspPheMetAlaGlnTyrAsnMetProGlnTyrIleLeuArg 1780
QY 1446 GAGTTCACAGTCACGGATCCCGGATGGGAGTCACAGCAATCCGAGTTCACGTC 1505
DB 1781 GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe 1800
QY 1506 ACAGACTGGCCAGAGAGCGCTGCCCAAGACAGCGGAGGATTCATTGACTTCATCGGG 1565
DB 1801 ThrAspTrpProGlnGlnGlnIValProLysThrGlnGlyPheIleAspPheIleGly 1820
QY 1566 CAGGTCGATTAACACCAAGAGCAAGTTCGACAGAGATGGCCCTATCATCGCTGACCT 1625
DB 1821 GlnValIHisLysThrLysGlnGlnPheGlyGlnAspGlyProIleThrValIHisCysSer 1840
QY 1626 GCTGGGAGTGGCGGACCGGGGTTGCATCATCTGAGCATGCTCGGAGGACATCGGC 1685
DB 1841 AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValIleuGlnArgMetArg 1860
QY 1686 TATGAGGGCGTGTGCACATGTTTCAGACCGTGAAGACCCCTGATACAGAGCGTCTGCC 1745
DB 1861 TyrGlnGlyValIValAspPheThrGlnThrValLysThrLeuArgThrGlnArgProAla 1880
QY 1746 ATGGTCGACAGACAGAGCAATGATGCTGTGCTACCGTGGCGCCCTGGAGTACCTCGGC 1805
DB 1881 MetValIHisThrGlnAspGlnTyrGlnLeuGlyTyrArgAlaIleuGlnTyrLeuGly 1900
QY 1806 ACCTTGACCACTATGCACAG 1826
DB 1901 SerPheAspHisTyrAlaThr 1907

RESULT 9
AAR71726
ID AAR71726 standard; Protein; 1911 AA.
XX
AC AAR71726;
XX
DT 17-OCT-1995 (first entry)
XX
DE Human PTP-OB.
XX
KW PTP-OB; protein tyrosine phosphatase; osteoblast; differentiation;
KW osteoclast; osteoporosis; bone; cancer; osteosarcoma.
XX
OS Homo sapiens.
XX
FH Key
FH Peptide 1..29 Location/Qualifiers
FT /label= Sig_peptide
FT Modified-site 250
FT /label= N-glycosylation_site
FT Modified-site 721
FT /label= N-glycosylation_site
FT Modified-site 919
FT /label= N-glycosylation_site

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FT Domain 1253..1277
FT /label= Extracellular_domain
PN WO9507935-A.
XX
PD 23-MAR-1995.
XX
PF 09-SEP-1994; 94WO-US10166.
XX
PR 14-SEP-1993; 93US-0122032.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Rodan GA, Rutledge SJ, Schmidt A;
XX
DR WPI: 1995-131318/17.
DR N-PSDB: AA086478.
XX
XX
XX Protein tyrosine phosphate protein ptp-ob specifically expressed
XX in bone cells - modulators of which are used to treat, e.g.
XX osteoporosis, and prevent and treat bone loss and cancer.
PS Claim 1: Page 44-45; 63pp; English.
XX
XX PCR amplification of cDNA derived from human osteosarcoma
XX CC Saos-2/B10 using primers based on conserved regions of protein
XX CC tyrosine phosphatases and subsequent screening of a human
XX CC brain cDNA library yielded a cDNA-clone (sequence given in
XX CC AA086473) that encoded a novel human protein, PTP-OB (AAR71726).
XX CC Recombinant PTP-OB was expressed in E. coli, yeast, insect
XX CC and mammalian cells.
XX
SQ Sequence 1911 AA;

Alignment Scores:
Pred. No.: 1.2e-227 Length: 1911
Score: 2880.00 Matches: 530
Percent Similarity: 94.32% Conservative: 35
Best Local Similarity: 88.48% Mismatches: 34
Query Match: 44.69% Indels: 0
Gaps: 0

US-09-743-492-1 (1-3467) x AAR71726 (1-1911)
QY 30 CACTCCTGTGACCCCTGTGAGATGGGAGGCTCACTACCAAGCCAGTATGGAGAC 89
DB 1313 HisProLysAspProValGlnMetAlaArgIleAsnPheGlnThrProGlyMetLeuSer 1332
QY 90 CACCCACCCATCCCATCACAGCCTGGCGGACAAACATGACGCGCTCAACCCACGAT 149
DB 1333 HisProIleProIleProIleAlaAspMetAlaGlnHisThrGlnArgLeuLysAlaAsnAsp 1352
QY 150 GGCCTCAAGTCTCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 209
DB 1353 SerLeuLysLeuSerGlnIleTyrGlnSerIleAspProGlyGlnGlnPheThrTrpGlu 1372
QY 210 AATTCAAACTGGAGGTGAACAAGCCCAAGAACCCGTATGCCAATGTCTGCTACAGAC 269
DB 1373 HisSerAsnLeuGlnValAlaAsnLysProLysAsnAlaGlyTyrAlaAsnValIleAlaTyrAsp 1392
QY 270 CACTCGAGTCATCCTTACTCTATCGATGGCGTCCCGGAGGTGACTACATCATGCC 329
DB 1393 HisSerArgValIleLeuGlnProIleGlnGlyIleMetGlySerAspTyrIleAsnAla 1412
QY 330 AACTACATGATGCTACCCGCAAGCAAGATGCTTACATGCGCAGCAGGCGCCCTGCC 389
DB 1413 AsnTyrValAspGlyTyrArgArgGlnAsnAlaTyrIleAlaThrGlnGlyProLeuPro 1432
QY 390 GAGACATGGCGGATTTCTCGAGAAATGGTGGGAAACAGCGACGCGCATGTGGTCAATG 449
DB 1433 GluThrPheGlyAspPheThrParGmetValTrpGlnGlnArgSerAlaThrIleValMet 1452
QY 450 ATGACACGGCTGAGAGAGACATCCCGGGTAAATGTGATCACTAGTGGCAGCCGCTGGC 509

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Db 1453 MetThrArgLeuclululysSerArgIleLysCysAspGlnTrpProAsnArgGly 1472
QY 510 ACCGAGACCTGTGGCTTATTACAGTGAGCCCTTTGGACACAGTGGAGCGGCACATAC 569
Db 1473 ThrGlnThrTyrTyrPheIleGlnValThrLeuLeuAspThrIleGluLeuAlaTrpPhe 1492
QY 570 ACTGTGCGACCTTTCAGCTCCACAGAGGCTCCAGAGAGAGGCTGAGCGGTGAC 629
Db 1493 CysValArgThrPheSerLeuHisLysAsnGlySerSerGlnLysArgGlnValArgGln 1512
QY 630 TTTCAGTTTCATGCGCTGGCCAGACACATGAGTTCCTGAGTACCCAACTCCATCTGGCC 689
Db 1513 PheGlnPheThrAlaTrpProAspHisGlyValProGlnLysProThrProPheLeuAla 1532
QY 690 TTTCCTACGACGGGTCAAGCGCTTCGAACCCCTTAGACGACGAGGCCCATGGTGTGCACTGC 749
Db 1533 PheLeuAlaArgValLysThrCysAsnProProAspAlaGlyProIleValAlaHisCys 1552
QY 750 AGCGGGGGGTGGGGCCGACCGGCTGCTCATGCTGATGATGATGATGATGATGATGATGATG 809
Db 1553 SerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeuGlnValArgIle 1572
QY 810 AAGCAGAGAGAGACGGGTGACATCTATGGCCACGTGACCTGACCTGACATCAGAGAGAAC 869
Db 1573 LysProGlnLysThrValAspValTyrGlnHisValThrLeuMetLysArgGlnArgAsn 1592
QY 870 TTACATGTGTCAAGCAGAGAGACCATGATGTTTCATCATGAGGCGCTGTGTGAGCGTCC 929
Db 1593 TyrMetValGlnThrGlnAspGlnTyrSerPheIleHisGlnValLeuLeuGlnAlaVal 1612
QY 930 AGGTGGGGCCACAGAGGTGCTGCGCCGACCTGATGCGCCACATCCAGAACTGGGGC 989
Db 1613 GlyCysGlyAsnThrGlnValProAlaArgSerLeuTyrAlaLysIleGlnLysLeuAla 1632
QY 990 CAAGTGCCTTCAGGGGAGAGTGTGACCGGACCTGAGCTGAGTTCAGTTCGTCGCCACG 1049
Db 1633 GlnValGlnProGlnLysLysValThrGlnMetGlnLeuGlnPheLysArgLeuAlaAsn 1652
QY 1050 TCCAGAGGCCACACGTCGCCGTTTCATCAGCGCCACCTCCCTGCAACAAGTTCAAGAAC 1109
Db 1653 SerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysLysLysPheLysAsn 1672
QY 1110 CGGCTGTGATCATGATGCGCTTACGAAATGACCGGCTGTGCTGTGACGCCATCCCTGGT 1169
Db 1673 ArgLeuValAlaAsnIleMetProTyrGlnSerThrArgValCysLeuGlnProIleArgGly 1692
QY 1170 GTGAGAGGCTGTGACTATCATGATGCGCAGCTTCCTGATGTTATGAGACAGGAGAGGCC 1229
Db 1693 ValGlnGlySerAspTyrIleAsnAlaSerPheIleAspGlyTyrArgGlnGlnLysAla 1712
QY 1230 TACATAGCTTACACAGGGGCTTGGCAGAGACCGGAGACTTTCGGCCATGCTATGG 1289
Db 1713 TyrIleAlaThrGlnGlyProLeuAlaGlnLysThrGlnAspPheThrArgMetLeuTrp 1732
QY 1290 GAGCAACAATTCACATCATCTGTCATGCTGACCAAGCTTCGGGAGATGGCGAGGAGAA 1349
Db 1733 GluAsnAsnSerThrIleValIleValMetLeuThrLysLeuAlaGlnMetLysArgGlnLys 1752
QY 1350 TCCGACACAGTACTGGCAGACAGGCGCTGTGCTGCTACAGTACTTCTTGTGTCACCG 1409
Db 1753 CysHisGlnTyrTrpProAlaGlnLysSerAlaArgTyrGlnTyrPheValValAspPro 1772
QY 1410 ATGCGTAGTACACATGCGCCAGATATATCTGCGTAGTTCAGGTCACGAGTCCCGG 1469
Db 1773 MetAlaGlnTyrAsnMetProGlnTyrIleLeuArgGlnPheLysValThrAspAlaArg 1792
QY 1470 GATGGGACATGACAGCATCCGGAGTCCAGTTCACAGACATGGCCACAGAGCGCGG 1529
Db 1793 AspGlyGlnSerArgThrValArgGlnPheGlnPheThrAspTrpProGlnGlnVal 1812
QY 1530 CCCAAGACAGGCGAGGATTCATTGACTTCATCGGCGAGGTGCATTAAGACCAAGAGCAG 1589

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Db 1813 ProLysSerGlyGlnGlyPheIleAspPheIleGlyGlnValHisLysThrLysGlnGln 1832
QY 1590 TTTCGACAGATGGGCTTATCACGGTGCACCTGCAGTGTGCGGTGGCCGACCGGGGTG 1649
Db 1833 PheGlyGlnAspGlyProIleSerValHisCysSerAlaGlyValGlyArgThrGlyVal 1852
QY 1650 TTTCATGCTGTGAGCATCGCTCGGAGCGCATGCGCTATGAGGAGCGGTGCGCATGTT 1709
Db 1853 PheIleThrLeuSerIleValIleGlnLysArgMetArgTyrGlnValValAspIlePhe 1872
QY 1710 CACAGCCGTGAAGACCTCGGTATACACAGCGTCTGCTGATGGTGCAGACAGACAGTAT 1769
Db 1873 GlnThrValLysMetLeuArgThrGlnArgProAlaMetValGlnThrGlnAspGlyTyr 1892
QY 1770 CAGCTGTGCTACCGCTCGCGGCTGTGAGTACCTCGGACAGCTTTGACCATATGCAACG 1826
Db 1893 GlnPheCysTyrGlnAlaIleAlaLeuGlnTyrLeuGlySerPheAspHisTyrAlaThr 1911

RESULT 10
AAM27225
ID AAM27225 standard; Protein; 1911 AA.
XX
AC AAM27225;
XX
DE 19-DEC-1997 (first entry)
XX
DE Human protein tyrosine phosphatase PTP-OB.
XX
KW Protein tyrosine phosphatase' PTP-OB; PTPepsillon; osteoblast;
KW recombinant protein; growth; differentiation; brain; human.
XX
OS Homo sapiens.
XX
PN US5658756-A.
XX
PD 19-AUG-1997.
XX
PF 14-SEP-1993; 93US-0122032.
XX
PR 01-DEC-1994; 94US-0348006.
XX
PR 14-SEP-1993; 93US-0122032.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Rodan GA, Rutledge SJ, Schmidt A;
XX
DR WPI: 1997-424232/39.
XX
DR N-PSDB; AAT85389.
XX
PT DNA encoding protein tyrosine phosphatase PTP-OB - isolated from
XX human osteoblasts and useful for production of recombinant PTP-OB
XX
PS Claim 1; Column 23-34; 34pp: English.
XX
CC The present sequence represents human protein tyrosine phosphatase
CC (PTP-OB) protein. The DNA encoding this protein is useful for the
CC production of the recombinant protein, which is a protein tyrosine
CC phosphatase which may be involved in the growth and differentiation
CC of osteoblasts and brain cells and is useful for identifying compounds
CC that modulate PTP-OB activity and as a therapeutic agent for treating
CC PTP-OB-related diseases.
XX
SQ Sequence 1911 AA;

Alignment Scores:
Pred. No.: 1,2e-227 Length: 1911
Score: 2880,00 Matches: 530
Percent Similarity: 94,32% Conservative: 35
Best Local Similarity: 88,48% Mismatches: 34
Query Match: 44,69% Indels: 0
DB: 18 Gaps: 0

US-09-743-492-1 (1-3467) x AAM27225 (1-1911)

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[illegible]

QY	1110	CGCGTGGTGAACATCATGACCCCTACGAATTGACCCGCTGTGCTGCAGCCCATCCGTGTG	1169
Db	1673	ArgLeuValAsnIleMetProTyrGlnSerThrArgValCysLeuGlnProIleArgGly	1692
QY	1170	GTGGAGGCGCTGTGACTACATCATGATGCCAGCTTCCTGGATGCTTATAGACAGCAGAACCC	1239
Db	1693	ValGlnGlySerAspTyrIleAsnAlaSerPheIleAspGlyTyrArgGlnGlnIlyAsnIle	1712
QY	1230	TACATAGCTACACAGGGGCGCTCTGGCAGAGAGACCCGAGACTTCTGGCGCATGCTATGG	1289
Db	1713	TyrIleAlaThrGlnGlnGlyProLeuAlaGlnThrThrGlnAspPheThrPArgMetLeuP	1732
QY	1290	GAGCACAATTTCACACATCATGCTCATGCTGACCACAAGCTTCGGGAGATGGCGAGGAGAA	1349
Db	1733	GlnAsnAsnSerThrIleValIValMetLeuThrLysLeuArgGlnMetClyArgGlyLys	1732
QY	1330	TGCCACACAGTACTGCGCCAGCAGACAGCCGTCTGCTGCTACCACTACTTGTGTTGACCCG	1409
Db	1753	CysHisGlnTyrTrpProAlaGlnArgSerAlaArgTyrGlnTyrPheValIValAspPro	1772
QY	1410	ATGGCTAGTCAACATGACCCCGAGTATATCCGTCGCGAGTTCACAGTCAAGTCAAGATCCCGG	1469
Db	1773	MetAlaGlnTyrAsnMetProGlnTyrIleLeuArgGlnPheLysValThrAspAlaArg	1792
QY	1470	GATGGCGAGTCAAGACAAATCCGCGAGATTCCAGTTCCAGTTCACAGACTGGCCAGCAGCGCGTG	1529
Db	1793	AspGlyGlnSerArgThrValArgGlnPheGlnPheThrAspTrpProGlnGlnIlyal	1812
QY	1530	CCCAAGACAGCGCGAGGATTCATTGACTTCATGTGGCGAGGTGCTATAGACCAAGAGCAG	1589
Db	1813	ProLysSerThrGlyGlnGlyPheIleAspPheIleGlyGlnValHisLysThrLysGlnIln	1832
QY	1590	TTTGAGACAGATGGGCGCTATCACAGGTGACATCGATGATGCTGCGCGCGCACCGGSGTG	1649
Db	1833	PheGlyGlnAspGlyProIleSerValHisCysSerAlaGlyValGlyArgThrIlyal	1852
QY	1650	TTTCATCACTCTGAGCATGCTCTGGAGACCGATGCGCTATAGAGCGGTGGTGCATGTGTT	1709
Db	1853	PheIleThrLeuSerIleValIleuGlnArgMetArgTyrGlnGlyValIValAspIlePhe	1872
QY	1710	CAGACCGTGAAGACCCCTGCTTACACAGCGCTCCGATGGTCAGACAGAGACACAGAT	1769
Db	1873	GlnThrValLysMetLeuArgThrGlnArgProAlaMetValGlnThrGlnAspGlyLyr	1892
QY	1770	CAGCTGTGCTAACCGTGGCGCCCTGGAGTACCTGGCAGCGCTTGTACCATATGCAACG	1826
Db	1893	GlnPheCysTyrGlnAlaIleAlaLeuGlnTyrLeuGlySerPheAspHisTyrAlaThr	1911
RESULT 11			
AAW94027			
ID	AAW94027 standard; Protein; 1911 AA.		
XX			
AC	AAW94027:		
XX			
DT	01-APR-1999 (first entry)		
XX			
DE	Human protein tyrosine phosphatase (PTP-OB).		
XX			
KW	Protein tyrosine phosphatase; PTP; PTP-OB; bone; brain; cancer;		
KW	osteoporosis.		
XX			
OS	Homo sapiens.		
XX			
PN	US5866397-A.		
XX			
PD	02-FEB-1999.		
XX			
PF	14-FEB-1997; 97US-080825.		
XX			
PR	01-DEC-1994; 94US-0348006.		
PR	14-SEP-1993; 93US-0122032.		
PR	14-FEB-1997; 97US-080825.		









Db 1673 ArgLeuValAlaSnIleMetProTyrGluSerThrArgValCysLeuGlnProIleArgGly 1692  
QY 1170 GTGGAGGCGCTGCTACATCATCGCAGGTCTCTGGATGGTATTATGACAGCGAAGGCC 1229  
Db 1693 ValGIuGlySerAspTyrIleAsnAlaSerPheIleAspLysTyrArgGlnGlnVal 1712  
QY 1230 TACATGACTACACAGGGCGCTGGGACAGAGACCGAGACCTTCGGCCATGCTATGG 1289  
Db 1713 TyrIleAlaThrGlnGlnIleProLeuAlaGluThrThrGluAspPheThrPargMetLeuTTP 1732  
QY 1290 GAGCACAATTCACCATCATCGTCATCGTACACCAAGCTTCGGGAGATGGGACGAGAAA 1349  
Db 1733 GluAsnAsnSerThrIleValIleMetLeuThrLysLeuArgGluMetGlyArgGluLys 1752  
QY 1350 TGGCACCAGTACTGGCCGACGAGAGCGCTGCTGCTGCTACCAAGTACTTTGTTGGACCG 1409  
Db 1753 CysHisGlnTyrTyrProAlaGluArgSerAlaArgTyrGlnTyrPheValAlaAspPro 1772  
QY 1410 ATGGCTGAGTACACATGCCCCAGTATATCTGCTGAGTTCAGAGTTCAGAGTGGCCCG 1469  
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QY 1470 GATGGCAGTCAAGACAATCCGAGATCCGACATTCACAGACTGGCCAGAGCGCGTG 1529  
Db 1793 AspGlyGlnSerArgThrValArgGlnPheGlnPheThrAspTyrProGluGlnGlyVal 1812  
QY 1530 CCCAAGACAGCGGAGGATTCATTGACTTCATCGGCGAGGTGCATTAAGACCAAGAGCAG 1589  
Db 1813 ProLysSerGlnTyrPheIleAspPheIleGlyGlnValHisLysThrLysGlnGln 1832  
QY 1590 TTTGGCAGATGGGCGCTTCACAGGTGCAGTGCAGTGGCGGTGGCGCCGACGGGGTG 1649  
Db 1833 PheGlyGlnAspLysProIleSerValHisCysSerAlaGlyAlaLysArgGlnGlyVal 1852  
QY 1650 TTCATCACTCTGAGATCTCTCTGAGCGCATGCGCTATGAGGCGGTGTGACATGTTT 1709  
Db 1853 PheIleThrLeuSerIleValLeuGluArgMetArgTyrGluGlyValValAspIlePhe 1872  
QY 1710 CAGACCGTGAAGACCTCGGTACAGACGCTCTGCGCATGGTGCAGACAGAGCAAGTAT 1769  
Db 1873 GlnThrValLysMetLeuArgThrGlnArgProAlaMetValGlnThrGlnAspGluTyr 1892  
QY 1770 CAGCTGTGCTACCGTGGCCCTGGAGTACCTGCGAGCTTTGACCACTATGCAAGG 1826  
Db 1893 GlnPheCysTyrGlnAlaIleAlaLeuGluTyrLeuGlySerPheAspHisTyrAlaThr 1911  
RESULT 13  
AAR75201  
ID AAR75201 standard: Protein: 1291 AA.  
XX  
AC AAR75201:  
XX  
DT 10-MAY-1996 (first entry)  
XX  
DE Tyrosine phosphatase MPTP-delta.  
XX  
KM Tyrosine phosphatase MPTP-delta; murine; brain tissue;  
KM glutathione-S-transferase; fusion protein; E. coli; differentiation;  
KM activation; information transmission; nervous system; immune system;  
KM carcinogenesis.  
XX  
OS Mus musculus domesticus.  
XX  
PN JP07236487-A.  
PD 12-SEP-1995.  
XX  
PF 28-FEB-1994; 94JP-0054726.  
XX  
PR 28-FEB-1994; 94JP-0054726.  
PA (TOKS-) TOKYO SHINKAI KAGAKU SOGO KENKYUSHO ZH.  
XX

DR WPI: 1995-347455/45.  
DR N-PSDB; AAO94311.  
XX  
PT DNA encoding tyrosine phosphatase MPTP delta - useful for  
PT elucidation of signal transmission mechanisms.  
XX  
PS Claim 1; Page 5-11; 14pp; Japanese.  
XX  
CC This sequence represents murine tyrosine phosphatase MPTP-delta. The  
CC cDNA sequence encoding this protein was isolated from murine brain  
CC tissue and was cloned, for expression, into the downstream region of a  
CC glutathione-S-transferase sequence and expressed as a fusion protein  
CC in E. coli. MPTP-delta proteins regulate differentiation and  
CC activation of cells. This sequence can be used in the elucidation of  
CC the molecular mechanism for information transmission in cells,  
CC regulation mechanisms in the nervous system or immune system, or in  
CC the mechanism of carcinogenesis.  
XX  
SQ Sequence 1291 AA:  
Alignment Scores:  
Pred. No.: 2, 77e-227 Length: 1291  
Score: 2874.50 Matches: 534  
Percent Similarity: 95.16% Conservative: 36  
Best Local Similarity: 89.15% Mismatches: 26  
Query Match: 44,618 Indels: 3  
DB: 16 Gaps: 3  
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QY 90 CACCACCCATCCCATCACCAGCTGGCGGACCAATCCAGCGCCCTCAAGCCAAACGAT 149  
Db 716 HisProIleProIleProIleLeuGluLeuAlaAspHisIleGluArgLeuLysAlaAsnAsp 735  
QY 150 GGCCTCAAGTTTCCACAGAGATGATGATCCATGACCCCTGAGACAGCATTCACGTGGAG 209  
Db 736 AsnLeuLysPheSerGlnGluTyrGluSerIleAspProGlyGlnGlnPheThrProGlu 755  
QY 210 AATTCAACCTGGAGGAGGAAACAGCCCAAGACCGCTATCGATGCTACAGCTGACGAC 269  
Db 756 HisSerAsnLeuGluValAlaLysProLysAsnArgTyrAlaAsnValIleAlaTyrAsp 775  
QY 270 CACTCTGAGTCACTCTTACCTCTATCGATGGCGGTCCCGAGTGAAGTCAATCAATGCC 329  
Db 776 HisSerArgValLeuLeuSerAlaIleGluGlyIleProGlySerAspTyrValAlaSer 795  
QY 330 AACTCATCGATGGCTACCGCAGACAGAAATGCTACATCGCCAGCGAGGGCCCTGCC 389  
Db 796 AsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGlySerLeuPro 815  
QY 390 GAGACCATGGCGATTTCTGAGAAATGCTGGGACAGCGCAAGCCCACTGTGCATG 449  
Db 816 GluThrPheGlyAspPheThrPargMetIleTyrGlnGlnIleValAlaThrValMet 834  
QY 450 ATGACAGCGCTGAGAGGAGATCCCGGATTAATGTGATGATGATGATGATGATGATGATG 509  
Db 835 MetThrLysLeuGluGluArgSerArgValLysCysAspGlnTyrTyrProSerArgGly 854  
QY 510 ACCGAGACCTGTGGCTTATTCAGGTGACCTGTGGACACAGTGAAGTGGCCACATAC 569  
Db 855 ThrGluThrHisGlyLeuValGlnValThrLeuLeuAspThrValGluLeuValThrTyr 873  
QY 570 ACTGTGGCAGCTTCGCAATCCACAGAGTGGCTCCAGTGAAGAAGTGAAGTGAAGTGAAG 629  
Db 874 CysValArgThrPheAlaLeuTyrAsnAsnGlySerSerGlnLysArgLysValArgGln 893  
QY 630 TTTCACTTCAATGCGCTGGCGACGACCAATGAGTTCGTGATGATGATGATGATGATGATG 689  
Db 894 PheGlnPheThrAlaThrProAspHisGlyValProGlnHisProThrProPheLeuAla 913

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OY 690 TTCTACGACGGGTCAGAGCCCTGCAACCCCTAGACGCGAGGCCCATGGTGTGCACTGC 749
Db 914 PheleuAArgValIlySerThrCysAsnProAspAlaGlyProMetValValHisCys 933
OY 750 AGCGGGGGCGTGGGCGCCGCGCTTCATCGTGATGATGATGATGATGATGATGATGATG 809
Db 934 SerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeuIleuArgIle 953
OY 810 AAGCAGAGAACGAGCGGTGACATCTATGAGCAGGTGACCTGATGATGATGATGATGATG 869
Db 954 LysHisGlyIleValThrValAspIleTyrGlyHisValThrLeuMetArgAlaGlnArgAsn 973
OY 870 TACATGTGTCAGACGAGGAGCAGATGATGATGATGATGATGATGATGATGATGATGATG 929
Db 974 TyrMetValGlnThrGlyAspGlnTyrIlePheIleHisAspAlaLeuIleuGlnAlaVal 993
OY 930 AGTCCGGGCGCACAGAGAGTGCCTGCCGCAACCTGTATGCCACATCCAGAACCTGGGC 989
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OY 990 CAAGTGCCTCCAGGGAGAGTGTGACCCGCTGAGAGCTGAGTGTGATGATGATGATGATG 1049
Db 1014 GlnIleGlyThrGlyGlyIleAsnValThrGlyMetGlyLeuGlnPheLysArgLeuAlaSer 1033
OY 1050 TCCAAAGGCCACACAGCTCCCGCTTCATCAGCGCCCAACCTGCGCCGCAACAGTTCAAGAAC 1109
Db 1034 SerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLysAsn 1053
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Db 1054 ArgLeuValAsnIleMetProTyrGlyIleSerGlyArgValCysLeuGlnProIleArgGly 1073
OY 1170 GTGAGAGCTGTGATACATCATGATGATGATGATGATGATGATGATGATGATGATGATG 1229
Db 1074 ValGlnGlySerAspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGlnGlnIleVal 1093
OY 1230 TACATAGCTACACAGAGGCGCTGTGACAGAGACACCGAGAGCTTGTGCGCATGTATGG 1289
Db 1094 TyrIleAlaThrGlnGlyProLeuAlaGlnThrGlnIleAspPheTyrArgMetLeuTyr 1113
OY 1290 GAGCAGCATTCACCATCATGCTCATGCTGACCAAGCTTGGGAGATGGGAGGAGAA 1349
Db 1114 GlnHisAsnSerThrIleValIleMetLeuThrLysLeuArgGlnMetIleValArgGlyLys 1133
OY 1350 TGCCACGATGATGAGCGCAGACAGAGGCGCTGCTGCTACAGTACTTGTGTCAGCCG 1409
Db 1134 CysHisGlnTyrTyrProAlaGlnArgSerAlaAlaGlyGlnTyrPheValValAspPro 1153
OY 1410 ATGGCTGATACACACATGCCCATATATCTGCGTGAAGTTCAAGATGACGCGCCG 1469
Db 1154 MetAlaGlnTyrAsnMetProGlnTyrIleLeuArgGlnPheLysValThrAspAlaArg 1173
OY 1470 GATGGGCGATCAGACACATCCGCGAGTCCAGTTCACAGACTGGCCAGACAGGCGGTG 1529
Db 1174 Asp---GlnSerArgTyrValArgGlnPheGlnPheThrAspTyrProGlnGlnGlyVal 1192
OY 1530 CCCAAGACAGGCGAGGATTCATGATGATGATGATGATGATGATGATGATGATGATGATG 1589
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OY 1590 TTTGGACAGAGTGGCGTATCATGAGGTGCACTGACGTGCGGTGGGCGGCGACCGGGGTG 1649
Db 1213 PheGlyGlnAspGlyProIleSerValHisCysSerAlaGlyValGlyArgThrGlyVal 1232
OY 1650 TTTCATCATCTGAGCATGCTCTGAGAGCGCATGCGCTATGAGGCGGTGTCACATGTT 1709
Db 1233 PheIleThrLeuSerIleValAlaLeuGlnArgMetArgTyrGlnGlyValValAspIlePhe 1252
OY 1710 CAGACCGTAGAGACCTGTGTCACAGGCTGCTGCGCATGTCAGACAGAGACAGAT 1769
Db 1253 GlnThrValLysMetLeuArgThrGlnArgProAlaMetValGlnThrGlnAspGlnTyr 1272

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OY 1770 CAGCTGTGCTACCGTGGCGCCCTGGAGTACCTGGGCACTTTGACCCTATGCAACG 1826
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RESULT 14
AAR72858
ID AAR72858 standard; Protein: 1501 AA.
AC AAR72858;
XX
XX 21-NOV-1995 (first entry)
DE Rat receptor type-protein tyrosine phosphatase sigma.
XX
XX Receptor type tyrosine phosphatase sigma; cell; differentiation;
XX metabolism; cell cycle; behaviour; motility; contact inhibition;
XX virus; inflammation; cellular transformation; cancer;
XX neuroblastomas; antibody; detection; quantification.
XX
XX Rattus rattus.
XX
XX WO9509656-A.
XX
XX 13-APR-1995.
XX
XX 30-SEP-1994; 94WO-US11163.
XX
XX 01-OCT-1993; 93US-0130570.
XX
XX (UNIV ) UNIV NEW YORK STATE.
XX
XX Schlessinger J, Yan H;
XX
XX WPI: 1995-155068/20.
XX
XX N-PSDB: AAO86902.
XX
XX Novel, isolated receptor-type protein tyrosine phosphatase-sigma
XX - and encoding DNA, useful e.g. for detecting neuro-blastomas
XX
XX Claim 2: Figure 2: 105pp; English.
XX
XX
XX Ligands binding to the receptor-type protein tyrosine phosphatase
XX sigma (RTP sigma) protein may be used as drugs to modulate cellular
XX processes, such as differentiation, metabolism and cell cycle
XX control, and cellular behaviour such as motility and contact
XX inhibitions. In addition they may affect abnormal or potentially
XX deleterious processes such as virus-receptor interactions,
XX inflammation and cellular transformation to a cancerous state. They
XX may also be used to treat RTP sigma related neuronal disorders such
XX as neuroblastomas. The DNA encoding the RTP sigma is useful for
XX the diagnosis of diseases resulting from its aberrant expression.
XX Antibodies directed against RTP sigma may be used in detection and
XX quantitative analysis.
XX
XX
XX Sequence 1501 AA:
SQ
Alignment Scores:
Pred. No.: 3,11e-225 Length: 1501
Score: 2850.00 Matches: 523
Percent Similarity: 93.99% Conservative: 40
Best Local Similarity: 87.31% Mismatches: 36
Query Match: 44.23% Indels: 0
DB: 16 Gaps: 0
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Db 903 HisProLysAspProValGlnMetArgArgIleAsnPheGlnThrProGlyMetLeuSer 922
OY 90 CACCACCATTCCTCCATACCGACTGGGCGGACACATGAGAGCGCTCAACAGCAGAT 149
Db 923 HisProIleProIleThrAspMetAlaGlnHisMetGlnArgLeuValAsnAsp 942

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QY 150 GGCTCAAGTTCTCCAGAGTATGATTCATGCAGCCCTGGAGACGAGTTCACGTGGAG 209  
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 QY 210 AATTCAAACCTGGAGGTGAACAAGCCCAAGACCCGCTATGCGAATGCTCATCGCCTACGAC 269  
 DB 963 HisSerAsnLeuGlnLalaSnlyspProlysAsnArgTyrAlaSnValIlealAtyaaP 982  
 QY 270 CACTCTCGAGTCACTTTCATCTATCATGATGGCGTCCCGGGAGTACATCAATGCC 329  
 DB 983 HisSerArgValIleLeuGlnProLeuGlnGlyIleMetGlySeraspTyrIleAsnAla 1002  
 QY 330 AACTACATGATGGCTACCGCAAGAAATGCTTACATGCCCGACGAGGGCCCCCGTCCC 389  
 DB 1003 AsnTyrValAspLysPylTyrArgArgGlnAsnAlaTyrIleAlaThrIngluProlLeuP 1022  
 QY 390 GAGACCATGGCGATTTCTGAGAAATGCTGGGAGACAGCGACGCGCATGCTGTATG 449  
 DB 1023 GluThrPheGlyAspPheThrPargMetValTrpGluGlnArgSerAlaThrValIleMet 1042  
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 QY 510 ACCGAGACCTGTGGCCTTATTCAGTGCAGTGCCTGTGGACAGTGGAGCTGGCCATAC 569  
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 DB 1123 PheLeuAlaArgValLysThrCysAsnProProAspAlaGlyProValValAlaHisCys 1142  
 QY 750 ACCGCGGGCGTGGCGCCACCGGCTGCTTCATCGTGAATTCATGATGAGCCCATGTTGGAGCGATG 809  
 DB 1143 SerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeuGlnArgIle 1162  
 QY 810 AAGCAGCAGAGAAGCGTGGACATCTATGGCCACGTCGACCTGCATGGCATCACAGAGAAC 869  
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 DB 1243 SerLysAlaHisThrSerArgPheIleThrAlaSerLeuProCysAsnLysPheLysAsn 1262  
 QY 1110 CGGTGTGTGAACATCATGCTTACGAATTCGACCCGTGTGTCTGTGACGCCCATCCCTGAT 1169  
 DB 1263 ArgLeuValAsnIleLeuProTyrGlnLysSerArgValCysLeuGlnProIleArgGly 1282  
 QY 1170 GTGAGAGGCTGTGACTATCATTCATGCGCAGCTTCCTGGATGTTATAGACAGAGAGGCC 1229  
 DB 1283 ValGlnGlySeraspTyrIleAsnAlaSerPheIleaspGlyTyrArgGlnGlnLysAla 1302

QY 1230 TACATGACTACACAGGGGCGCTGTGGACAGAGCAGCCAGAGACTTGTGGCATGCTATGG 1289  
 DB 1303 TyrIleAlaThrIngluProlLeuAlaGluThrThrGlnAspPheThrPargAlaLeuTTP 1322  
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 QY 1410 ATGCTGAGTACAAATGCCCCAGTATATCCCTGCGAGTTCAGAGGTCAGCGATGCCCG 1469  
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 AC ABB57100;  
 DT 07-MAR-2002 (first entry)  
 DE Mouse ischemic condition related protein sequence SEQ ID NO:224.  
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 KW Mouse; ischemia; compressive ischemia; occlusive ischemia;  
 KW vasospastic ischemia; ischemic condition; ischemic disease.  
 OS Mus musculus.  
 PN M0200188188-A2.  
 PD 22-NOV-2001.  
 PF 18-MAY-2001; 2001WO-JP04192.  
 PR 18-MAY-2000; 2000JP-0145977.  
 XX  
 PA (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
 XX  
 PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;  
 DR WPI: 2002-034733/04.  
 DR N-PSDB: ABI9344.  
 XX  
 PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring  
 PT expression levels of particular genes defined in the specification or  
 PT by determining the expression profile of a gene group comprising these



QY 1770 CAGCTGCTACCGTGGCGCTGAGTACCTGGCAGCTTTGACCACTATGCACG 1826  
||| |||:|||||  
Db 1886 GlnPheCysPheGlnAlaAlaLeuGlnTyrLeuGlySerPheAspHisTyrAlaThr 1904

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Job time : 237 secs

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GenCore version 5.1.3  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 17, 2003, 10:12:20 ; Search time 25 Seconds

(without alignments)  
5513.505 Million cell updates/sec

Title: US-09-743-492-1

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Fgapop 10.0 , Fgapext 0.5	
Delop 6.0 , Delext 7.0	

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 241982

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2880	44.7	1502	9	US-09-808-602-54
2	2856	44.3	1948	3	US-09-808-602-55
3	2347	36.4	442	10	US-09-925-300-950
4	1335	20.7	306	10	US-09-788-626-8

5	1295	20.1	294	10	US-09-788-626-27	Sequence 27, Appl
6	1145.5	17.8	1430	9	US-10-087-993-34	Sequence 34, Appl
7	1120	17.4	2308	12	US-10-000-954-2	Sequence 2, Appl1
8	752.5	11.7	305	10	US-09-788-626-9	Sequence 9, Appl1
9	725	11.3	310	10	US-09-788-626-10	Sequence 10, Appl
10	703.5	10.9	319	10	US-09-788-626-6	Sequence 6, Appl1
11	700.5	10.9	313	10	US-09-788-626-7	Sequence 7, Appl1
12	699.5	10.9	309	10	US-09-788-626-11	Sequence 11, Appl1
13	690	10.7	316	10	US-09-788-626-5	Sequence 5, Appl1
14	690	10.7	316	10	US-09-788-626-26	Sequence 26, Appl
15	679.5	10.5	317	10	US-09-788-626-4	Sequence 4, Appl1
16	677.5	10.5	281	10	US-09-788-626-28	Sequence 28, Appl
17	630	9.8	288	10	US-09-788-626-25	Sequence 25, Appl
18	624.5	9.7	309	10	US-09-788-626-12	Sequence 12, Appl
19	611.5	9.5	248	10	US-09-848-294-10	Sequence 10, Appl
20	561.5	8.7	313	10	US-09-788-626-19	Sequence 19, Appl
21	555.5	8.6	313	10	US-09-788-626-17	Sequence 17, Appl
22	553.5	8.6	309	10	US-09-788-626-15	Sequence 15, Appl
23	540	8.4	310	10	US-09-788-626-15	Sequence 15, Appl
24	526	8.2	593	10	US-09-920-021A-3	Sequence 3, Appl1
25	524	8.1	307	10	US-09-788-626-20	Sequence 20, Appl
26	502	7.8	595	10	US-09-920-021A-1	Sequence 1, Appl1
27	493	7.7	360	12	US-10-028-748-2	Sequence 2, Appl1
28	492.5	7.6	322	10	US-09-788-626-14	Sequence 14, Appl
29	486.5	7.5	435	10	US-09-986-240-1	Sequence 1, Appl1
30	485	7.5	2485	10	US-09-802-669-46	Sequence 46, Appl
31	477.5	7.4	246	10	US-09-848-294-9	Sequence 9, Appl1
32	476.5	7.4	376	10	US-09-876-527-7	Sequence 7, Appl1
33	476.5	7.4	818	10	US-09-876-527-22	Sequence 22, Appl
34	476	7.4	341	10	US-09-788-626-23	Sequence 23, Appl
35	475	7.4	325	10	US-09-788-626-13	Sequence 13, Appl
36	473.5	7.3	641	10	US-09-876-527-2	Sequence 2, Appl1
37	473.5	7.3	1012	10	US-09-876-527-16	Sequence 16, Appl
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39	468.5	7.3	250	10	US-09-848-294-8	Sequence 8, Appl1
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42	455.5	7.1	234	10	US-09-788-626-2	Sequence 2, Appl1
43	448	7.0	448	9	US-10-087-993-32	Sequence 32, Appl
44	445	6.9	913	10	US-09-848-294-2	Sequence 2, Appl1
45	442	6.9	291	10	US-09-788-626-22	Sequence 22, Appl

#### ALIGNMENTS

RESULT 1  
US-09-808-602-54  
Sequence 54, Application US/09808602  
Patent No. US20020155115A1  
GENERAL INFORMATION:  
APPLICANT: Vermet, Corine A  
APPLICANT: Fernandes, Elma  
APPLICANT: Shinkets, Richard A  
APPLICANT: Herrman, John L  
APPLICANT: Majumder, Rumud  
APPLICANT: Mishra, Vishnu  
APPLICANT: Mezes, Peter S  
TITLE OF INVENTION: No. US20020155115A1el Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 15966-697 CIP  
CURRENT APPLICATION NUMBER: US/09/808, 602  
CURRENT FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 09/800, 198  
PRIOR FILING DATE: 2001-03-05  
PRIOR APPLICATION NUMBER: 60/186, 596  
PRIOR FILING DATE: 2000-03-03  
NUMBER OF SEQ ID NOS: 114  
SOFTWARE: Patentlin Ver. 2.1  
SEQ ID NO 54  
LENGTH: 1502  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-808-602-54

## Alignment Scores:

Pred. No.:	2,496-186	Length:	1502
Score:	2880.00	Matches:	530
Percent Similarity:	94.32%	Conservative:	35
Best Local Similarity:	88.48%	Mismatches:	34
Query Match:	44.69%	Indels:	0
DB:	9	Gaps:	0

US-09-743-492-1 (1-3467) x US-09-808-602-54 (1-1502)

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OY 150 GGCCTCAAGTTCTCCAGAGATGATGATCCATGACCCCTGGACAGCAGTTCACTGGAG 209
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DB 944 SerleuylsleuSerGlnGlnIutryGlnSerIleasProlGlnInpHehtrPrGln 963
OY 210 AATCAACCTGGAGTGAACAAGCCCAAGACCGCTATGCGAATGCTATGCGCTACGAC 269
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DB 964 HlsserAsnleuGlnValaslnsProlysasnaArgylAlasnaVallelaIaryasP 983
OY 270 CACTCTGAGTCATCCTTACTCTATCGATGCGTCCCGGAGTACATCAATGCG 329
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OY 330 AACTCATGATGCTTACCCGACAGAAATGCTTACATGCGCAGCAGGCCCCCTGCC 389
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OY 450 ATGACAGCGCTGGAGAGAAAGTCCCGGTAATGTGATCACTAGTGGCCAGCCCTGGCG 509
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DB 1044 MetHrArgleuGlnGlnIulysSerArgIleuysCysAspGlnTYrTrProlasnaArgly 1063
OY 510 ACCGAGACTGTGGCTTATTAGAGTGAACCTGTGGACAGCAGTGGAGCTGGCCACATAC 569
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DB 1064 ThrGlntrTYrGlyPheIleGlnValThrleuLeuAspThrIleGlnleuIatHrPhe 1083
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DB 1084 CysValArgIleuPheSerleuHlslusasnGlySerSerGlnulysArgGlnValArgln 1103
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DB 1124 PheleuArgArgValIlyThrCysasnProlasProlasIaGlyProlIleValIasHlscys 1143
OY 750 AGCGGGCGGCTGGCGGCGGCTTCATCGATGATTGATGACCATGTTGGAGGGGAGT 809
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DB 1144 SerIaIaGlyValArgIleuPheIleGlyCysPheIleValIleasPalaIleleuIatHrGlie 1163
OY 810 AAGCAGAGAGAGCGGTGACATCTATGAGCCACGTGACCTGATCGATACAGAGAGAAC 869
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OY 870 TACATGTGTCAGAGCGAGACCATGATGCTTTCATCATGAGCGCGCTGCTGGAGGCTGCC 929
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OY 930 ACGTGGCGGCACACAGAGAGTGGCTGGCCGCAACCTGTATGCCCAATCCAGAGCTGGGC 989
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DB 1264 ArgleuValaslnIleMetProlTYrGlnSerThrArgValCysleuGlnProlleatArgly 1283
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DB 1284 ValGlnGlySerAspIrylleasnaIasSerPheIleasPglTYTyrArglnGlnIulysAla 1303
OY 1230 TACATPAGCTACACAGGCGCTGTGGCAGAGACACCCAGAGACTTGTGGCGCATGCTAGG 1289
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DB 1444 PheIleHrleuSerIleValIleuGlnIulysMetArgTYrGlnIulysValIalaspIlePhe 1463
OY 1710 CAGACCGTGAAGACCCCTGGCTACAGAGCTCTCGCATGATGTCACAGAGAGACCATAT 1769
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DB 1464 GlntrHrValIylsMetleuArgHrGlnArgProlaIatMetValGlnThrGlnIulaspIulYr 1483
OY 1770 CAGCTGTGCTACCGTGGCGGCTGGAGTACCTGCGAGCTTTGACCACTATGCAACG 1826
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DB 1484 GlnPheCysTYrGlnAlaIalaleuGlnIulysIulysSerPheAsphlsthIulThr 1502

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RESULT 2  
 US-09-808-602-55  
 ; Sequence 55, Application US/09808602  
 ; Patent No. US2002015115A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Vernet, Corine A  
 ; APPLICANT: Fernandes, Elma  
 ; APPLICANT: Shinkets, Richard A  
 ; APPLICANT: Herrman, John L  
 ; APPLICANT: Majumder, Kumud  
 ; APPLICANT: Mishra, Vishnu  
 ; APPLICANT: Mezes, Peter S  
 ; APPLICANT: MacDougall, John  
 ; TITLE OF INVENTION: NO. US2002015115A1el Proteins and Nucleic Acids Encoding Same  
 ; FILE REFERENCE: 15966-697 CIP



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; CURRENT APPLICATION NUMBER: US-09/808,602
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 55
; LENGTH: 1948
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-808-602-55

Alignment Scores:
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Score: 2856.00 Matches: 529
Percent Similarity: 91.71% Conservative: 35
Best Local Similarity: 86.02% Mismatches: 35
Query Match: 44.32% Indels: 16
DB: 9 Gaps: 1

US-09-743-492-1 (1-3467) x US-09-808-602-55 (1-1948)

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QY 78 -----GATATGCGAGACCAACCCACCATT 101
DB 1354 ArgSerProLeuArgLupProGlyPheHISpHeGLuSerMetLeuSerHISpProIle 1373
QY 102 CCCATACCGACCTGGCGGCAACATCGAGCCCTCAAGGACAGCATGGCTTCAAGTTT 161
DB 1374 ProlLeuAlaSPMetAlaLunHISThrGLuArgLeuLysAlaSNASPSerLeuLysLeu 1393
QY 162 TCCAGAGATATGATGCATCGACCTGAGCAGCAGTCACTGCGGAGATTCAAACCTG 221
DB 1394 SerGLuInLuprGLuSerLLeaSPProGLuInGLuPheThrLuprLunHISerASNLeu 1413
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DB 1414 GLuValASNlySPRlysSNArGLyAlaASNValLLeaLarGLyASpHISpHeArGLyVal 1433
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QY 342 GGTACCGCAGAGCAAGTCTCATGCGCAGCAGGCGCCCTGCGCGAGACCATGGG 401
DB 1454 GLyTyArgArgGLuASNAlaLyrLLeaLarGLuInGLuProlLeuProlLuprPheGLy 1473
QY 402 GATTTCTGAGAAATGATGTGGGAAAGCGACGCGACCTGTGTCATGATGACAGCGCTG 461
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QY 462 GAGGAAATCCCGGGTAATATGTATCATGACTGCGCAGCCGCTGGCAGCAGACCTGT 521
DB 1494 GLuGLuLysSerArgLLeuScyASpGLuTyTrpProASNArgLylThrGLuLuprTy 1513
QY 522 GGCCTATTACAGTGACCTGTGGACAGACAGTGGAGCTGCCACATACACTGGCCAC 581
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QY 582 TTCGACCTCCACAGAGTGGCTTCAGTGAAGACGTGAGCTGGCTCAGTTTCAGTTTCAG 641
DB 1534 PheSerLLeuHISLysASNGLySerSerGLuLysArgGLuValArgLInPheGLu 1553
QY 642 GCTGCGCAGACCATGGAATGCTCTAGTACATCCAACTCCCTGCTTCTAGACGG 701
DB 1554 AlATrPProASNpHISGLyValProGLuTyTrpThrProPheLeuAlaPheLeuArGLy 1573
QY 702 GTCAAGGCTGACCCCTAGACGAGGGCCCATGTGTGTGACACAGCGGGCGTG 761
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DB 1574 ValLysThrCysASNProProASNpHISGLyProlLeuValHISLysSerAlaGLyVal 1593
QY 762 GCGCGCAGCCGGCTTCATCGTATGATGATCCATGTTGGAGCGGATGAGACGAGAG 821
DB 1594 GLyArgThrGLySPheLLeuValLLeaSPAlaMetLeuGLuArgLLeuLysProGLuLys 1613
QY 822 ACGGTGACATCTATGGCCACGTCGACCTGCATCGCATCACAGAGAACTACATGTGCGAG 861
DB 1614 ThrValASPValTyrgLylHISValLThrLeuMetArgSerGLuArgSNtyrMetValGLu 1633
QY 882 ACGGAGACCAATACGTTTCATCCATGAGGCGCTCTGGAGGCTCCACAGTCCGCGCCAC 941
DB 1634 ThrGLuASPInLuprSerPheLLeuHISGLuAlaLeuLeuGLuValAlaGLyCysLys 1653
QY 942 ACAGAGTGCCTCCCGCAACCTGTATGCCCATCGACATCCAGAACGTCGGGCAAGTCCGCA 1001
DB 1654 ThrGLuValProAlaArgSerLeuTyrgLylLLeuGLuLysLeuAlaGLuValPro 1673
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DB 1674 GLyGLuHISValThrGLuMetGLuLeuGLuPheLysArgLeuAlaSNSerLysAlaHIS 1693
QY 1062 ACGTCCCGCTTCATCAGCGGCAACCTGCCCTGCAACAAGTTCAGAAACGGGCTGGTGAAC 1121
DB 1694 ThrSerArgPheLLeuSerAlaASNLeuProCysASNpHISpHeLysSNArGLyValASN 1713
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DB 1754 GLuInGLyProlLeuAlaGLuThrGLuASNpHeTrpArgMetLeuLuprGLuASNASpSer 1773
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DB 1774 ThrLLeuValLarGLuMetLeuThrLysLeuArgGLuMetGLyArgGLuLysCysHISGLuTy 1793
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DB 1794 TrpProAlaGLuArgSerAlaArgTyrgLylTyPheValValaSPrometAlaGLuTy 1813
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DB 1874 GLyProlLeuSerValHISLysSerAlaGLyValAlaTyrgLylValPheLLeuThrLeu 1893
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Db 1934 GlnAlaAlaLeuGluTyrLeuGlySerPheAspHisTyrAlaThr 1948

RESULT 3  
US-09-925-300-950 : Sequence 950, Application US/09925300  
: Patent No. US20020151681A1  
: GENERAL INFORMATION:  
: APPLICANT: Craig Rosen,  
: APPLICANT: Steve Ruben  
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
: FILE REFERENCE: PA101  
: CURRENT APPLICATION NUMBER: US/09/925,300  
: CURRENT FILING DATE: 2001-08-10  
: PRIOR APPLICATION NUMBER: PCT/US00/05998  
: PRIOR FILING DATE: 2000-03-08  
: PRIOR APPLICATION NUMBER: 60/124,270  
: PRIOR FILING DATE: 1999-03-12  
: NUMBER OF SEQ ID NOS: 1890  
: SOFTWARE: PatentIn Ver. 2.0  
: SEQ ID NO 950  
: LENGTH: 442  
: TYPE: PRT  
: ORGANISM: Homo sapiens  
US-09-925-300-950

Alignment Scores:  
Pred. No.: 1,37e-150 Length: 442  
Score: 2347.00 Matches: 442  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 36.42% Indels: 0  
Gaps: 0

US-09-743-492-1 (1-3467) x US-09-925-300-950 (1-442)

QY 501 GCCCGTGGCAGGAGACCTGTGGCTTATTCAGGTGACCCCTTTGGACACATGGAGCTG 560  
Db 1 AAlaA9GgLyThGluThrCysGlyLeuIleGlnValThrLeuAlaSprThrValGluLeu 20  
QY 561 GCCACATACACTGTGCGACACTTCCGACATCCACAGAGAGTGCCTCCAGTGAAGCGTGA 620  
Db 21 AlaThrTyrThValAlaThrPheAlaLeuHisTyrSerGlySerCduLysArgGlu 40  
QY 621 CTGGCTCAGTTTCAGTTCATGGCTGCGCCGACAGCATGGAGTTCGAGTACCAACTGCC 680  
Db 41 LeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValProGluTyrProThrPro 60  
QY 681 ATCCGGGCTTCCTAGACGGGTCAAGGCTGCAACCCCTAGAGCGAGGCGCCATGGTG 740  
Db 61 IleLeuAlaPheLeuAlaArgValLysAlaCysAsnProLeuAspAlaGlyPrometVal 80  
QY 741 GTGCACTGACGGCGGGGTGGGCGGCGCACCGGCTTCATGCTGATGGATGGCATGGT 800  
Db 81 ValHisCysSerAlaGlyAlaGlyAlaArgThrGlyCysPheIleValIleAspAlaMetLeu 100  
QY 801 GAGCGGATGAACACGAGAAAGCGGTGAACATATATGGCCACGTGACCTGCATGGCATGA 860  
Db 101 GlnArgMetLysHisGlyLysThrValAspIleTyrGlnHisValThrCysMetArgSer 120  
QY 861 CAGAGAGATCATGTGTGTCAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 920  
Db 121 GlnArgAsnTyrMetValGlnThrGlnAspGlnTyrValPheIleHisGlnAlaLeuLeu 140  
QY 921 GAGGCTGCAGGCGGGCGGCGACACAGAGGTGCTGCCCAACCTGTATGCCACATGCCAG 980  
Db 141 GlnAlaAlaThrCysGlyHisThrGlnValProAlaAlaArgAsnLeuTyrAlaHisIleGln 160  
QY 981 AAGCTGGGCAAGTGCCTCCAGGAGGAGAGTGTGACCGGCATGAGACTGAGTTCAAGTTG 1040  
Db 161 LysLeuGlyGlnValProProGluLysSerValThrAlaMetGlnLeuGlnPheLysLeu 180  
QY 1041 CTGGCAGACTCAGAGGCCACACAGCTCCGCTTCATCAGGCGCAACCTGCTGCACAAG 1100  
|||||

Db 181 LeuAlaSerSerLysAlaHisThrSerAlaPheIleSerAlaAsnLeuProCysAsnLys 200  
QY 1101 TTCAGAAACCGCGTGGTGAACATCATGCCCTACGATTCGAGATTCGCGTGTGTCGAGCCC 1160  
Db 201 PheLysAsnArgLeuValAlaAsnIleMetProTyrGlnLeuThrAlaValCysLeuGlnPro 220  
QY 1161 ATCCGTGTGTGGAGGCTCTGATCATCATCAATGCCAGCTTCGTGATGGTTATGACAG 1220  
Db 221 IleArgGlyValGlnGlySerAspTyrIleAsnAlaSerPheLeuAspLysTyrArgGln 240  
QY 1221 CAGAAAGCTACATAGCTACACAGAGGCGCTGCGCAGAGACGACGAGACTTTCGGCC 1280  
Db 241 GlnLysAlaTyrIleAlaThrGlnGlnProLeuAlaGlnSerThrGlnAspPheTrpArg 260  
QY 1281 ATGCTATGGAGCACAAATTCACCAATCATCATGCTGACCTGACCAAGCTTCGGAGATGGCC 1340  
Db 261 MetLeuTrpGlnHisAsnSerThrIleIleValMetLeuThrLysLeuArgGlnMetGly 280  
QY 1341 AGGGAATAATGCCACAGTACGTGGCCAGACAGAGCGCTGTGCTACAGTACTTTGTT 1400  
Db 281 ArgGlnLysCysHisGlnTyrTrpProAlaGlnArgSerAlaArgTyrGlnThrPheVal 300  
QY 1401 GTTGACCGGATGGCTGAGTACACATGCCCGCATATTCCTGCTGAGTTCAAGTCAAG 1460  
Db 301 ValAspProMetAlaGlnTyrAsnMetProGlnTyrIleLeuAlaArgGlnPheLysValThr 320  
QY 1461 CATGCCCGGATGGGCGACGTCAAGGACAAATCCGCGAGTTCAGTTCACAGACTGGCCAGAG 1520  
Db 321 AspAlaAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPheThrAspTrpProGln 340  
QY 1521 CAGGCGGTGCCCAAGACAGCGGAGGATTCATGTGACTTCATCGGCGAGGTGCATTAAGCC 1580  
Db 341 GlnGlyValProLysThrGlyGlnGlyPheIleAspPheIleGlyGlnValHisLysThr 360  
QY 1581 AAGGACGAGTTTGGACAGAGATGGGCTATCAGAGTGCACGTGACAGTGCAGTGGCGCCG 1640  
Db 361 LysGlnGlnPheGlyGlnAspGlyProIleThrValHisCysSerAlaGlyAlaGlyArg 380  
QY 1641 ACCGGGCTTCATCACTCTGAGCATCGTCGTCGAGCGCATCGCTATGAGGCGCTGCTG 1700  
Db 381 ThrGlyValPheIleThrLeuSerIleValIleLeuGlnArgMetAlaArgTyrGlnValAla 400  
QY 1701 GACATGTTTCAGACCGGTGAAGACCTGCGTACACAGCGTCTGCCATGGTGCAGACAG 1760  
Db 401 AspMetPheGlnThrValLysThrLeuArgThrGlnArgProAlaMetValGlnThrGln 420  
QY 1761 GACGATGATCAGCTGTGTCACCGGTGCGGCGCGGTGAGTACCTGCGGAGCTTGACCACTAT 1820  
Db 421 AspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGlnTyrLeuGlySerPheAspHisTyr 440  
QY 1821 GCAACG 1826  
Db 441 AlaThr 442

RESULT 4  
US-09-788-626-8 : Sequence 8, Application US/09788626  
: Patent No. US20020009762A1  
: GENERAL INFORMATION:  
: APPLICANT: Flint, Andrew J.  
: APPLICANT: Cool, Deborah E.  
: TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE  
: FILE REFERENCE: 200125.401  
: CURRENT FILING DATE: 2001-02-13  
: NUMBER OF SEQ ID NOS: 40  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 8  
: LENGTH: 306  
: TYPE: PRT  
: ORGANISM: Homo sapiens  
US-09-788-626-8

## Alignment Scores:

Pred. No.: 1.73e-82 Length: 306  
Score: 1335.00 Matches: 232  
Percent Similarity: 93.41% Conservative: 3  
Best Local Similarity: 92.31% Mismatches: 4  
Query Match: 20.72% Indels: 14  
DB: 10 Gaps: 2

US-09-743-492-1 (1-3467) x US-09-788-626-8 (1-306)

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QY 195 CAGTTCACGTGGGAGAAATTCAAACCTGAGGTGAGAACAGCCCAAGACCGCTATGCCAAT 254
    |||||||
Db 1 GlnPheThrTrrPclunsnserlnleuGluValAlsnlyProlysnrgrlyAlaasn 20

QY 255 GTTCATGCCCTAGACCACTCTGTGAGTCAATCCTTATCGATGAGCGCTCCCGGAGAT 314
    |||||||
Db 21 ValIleAlaTyrAspHisserArgValIleleuThrSerIleasplValProglySer 40

QY 315 GACTACATCAATGCCAATCAATCGATGGCTACCCGCAACAGAAATGCCCTACATCGGCACG 374
    |||||||
Db 41 AspTyrIleAsnAlaasnTyrIleasprGlyTyrArgLysGlnAsnAlaTyrIleAlaThr 60

QY 375 CAGGGCCCCCTGCGGAGACCAATGGCGAATTCCTGAGAAATGGTGGGAGACGCGCAG 434
    |||||||
Db 61 GlnGlyProleuProgluThrMetGlyAspPheThrArgMetValTrrpGlnArgThr 80

QY 435 GCCACTGTGTCATGATGACACGCGCTGAGAGAAATGCCGGTAAATGTGATCAGTAC 494
    |||||||
Db 81 AlaThrValValMetMetThrArgLeuGlnGlyLysSerArgValLysCysAspGlnTyr 100

QY 495 TGGCCAGCCCTGGGACCCAGACCTGTGCTTATTCAGTACCTGTGGACACAGTg 554
    |||||||
Db 101 TrrProIaArgGlyThrIuThrCysGlyLeuIleGlnValThrleuAspThrVal 120

QY 555 GAGCTGGCCACATACACTGTGCGCACTTCGCACTCCACAGAGTGGTCCAGTGAAGA 614
    |||||||
Db 121 GlnleuAlaThrTyrThrVal -----PheAlaLeuHisLysSerGlySerGlnLys 138

QY 615 CGTGAAGCTCGTCAGTTCATGATGCTGCGGACCAAGCAATGAGTTCCTGAGTACCA 674
    |||||||
Db 139 ArgGlnleuAlaArgGlnPheGlnPheMetAlaTrrProAspHisGlyValProgluTyrPro 158

QY 675 ACTCCCATCGCTGCTTCTTACGACGGGTCAAGGCTGCAACCCCTTAACGAGAGGCC 734
    |||||||
Db 159 ThrProIleleuAlaPheleuArgValLysAlaCysAsnProleuAspAlaGlyPro 178

QY 735 ATGTGTGTCACATGACGCGCGGCGGTGGGCGGACCGGCTTCATCGATGATGAC 794
    |||||||
Db 179 MetValValHisCysSerIleAlaGlyValGlyArgThrGlyCysPheIleValIleAspAla 198

QY 795 AAGTTGGAGCGGATGAAGCAGAGAACGAGTGGACATGTATGCGCAGCTGACCTGATG 854
    |||||||
Db 199 MetLeuGlnArgMetLysHisGlnLysThrValAspIleTyrGlyHisValThrCysMet 218

QY 855 CGATCACAAGGAACATCACTGTGTGCGAGAGGAGGAGGACATAGCTGTTCATCCATGAGGG 914
    |||||||
Db 219 ArgSerGlnArgAsnTyrMetValGlnThrGlnAspGlnTyrValPheIleHisGlnAla 238

QY 915 CTGTGTCGAGGTCGACGTCGCGGCGGACACAGAGAGTG----- 950
    |||||||
Db 239 LeuLeuGlnAlaAlaThrCysGlnHisThrGlnValValIleAspAlaMetLeuGlnArg 258

QY 951 -----CCTGCGCGCAACCTGTATGCCACATC 977
    |||||||
Db 259 MetLysHisGlnLysThrValAspIleTyrGlnHisVal 271
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## RESULT 5

US-09-788-626-27  
; Sequence 27, Application US/09788626  
; Patent No. US20020009762A1  
; GENERAL INFORMATION:  
; APPLICANT: Flint, Andrew J.

; APPLICANT: Cool, Deborah E.  
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE  
; FILE REFERENCE: PHOSPHATES  
; CURRENT APPLICATION NUMBER: US/09/788,626  
; CURRENT FILING DATE: 2001-02-13  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 27  
LENGTH: 294  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-788-626-27

## Alignment Scores:

Pred. No.: 8.44e-80 Length: 294  
Score: 1295.00 Matches: 245  
Percent Similarity: 99.19% Conservative: 0  
Best Local Similarity: 99.19% Mismatches: 0  
Query Match: 20.10% Indels: 2  
DB: 10 Gaps: 1

US-09-743-492-1 (1-3467) x US-09-788-626-27 (1-294)

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QY 1062 ACCTCCCGCTTCTATCAGCCCAACCTGCGCTGCAACAATTCAAAGAACCGGCTGTGAA 1121
    |||||||
Db 1 ThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLysAsnArgLeuValaasn 20

QY 1122 ATCATCCCTTACGAATTCACCCGCTGTGTCTTCACAGCCCATCCGCTGTGAGGCTCT 1181
    |||||||
Db 21 IleMetProtyrGlnleuThrArgValCysLeuGlnProIleArgGlyValGlnGlySer 40

QY 1182 GACTACATCAATGCCAGCTTCTGATGGTTATAGACACAGAGGCTACATAGTACTACA 1241
    |||||||
Db 41 AspTyrIleAsnAlaSerPheleuAspGlyTyrArgGlnGlnLysAlaTyrIleAlaThr 60

QY 1242 CAGGGCGCTGGCAGAGACACCGAGACTTCGCGCATGCTATGGAGGACCAATTCG 1301
    |||||||
Db 61 GlnGlyProleuAlaGlnSerThrGlnAspPheThrArgMetLeuThrPclunHisAsnSer 80

QY 1302 ACCATCATCGTCATGCTGACCAAGCTTCGAGAGTGGCAGAGGAAATGCCACCACTAC 1361
    |||||||
Db 81 ThrIleIleValMetleuThrLysleuArgGlnMetGlyArgGlnLysCysHisGlnTyr 100

QY 1362 TGGCAGCAGAGCGCTCTCTGCTACCAAGTACTTTGTTGTGACCCGATGGCTGATAC 1421
    |||||||
Db 101 TrrProIaGlnArgSerAlaArgTyrGlnTyrPheValValAspPrometAlaGlnTyr 120

QY 1422 AACATCCCCCAGATATCTGCTGCTGATGTCMAAGTACAGGATGCCGGATGGGACGTCA 1481
    |||||||
Db 121 AsnMetProGlnTyrIleleu -----PheLysValThrAspAlaArgAspGlnSer 138

QY 1482 AGGACAATCCGCGAGTTCAGTTCACAGACTGCGGACAGAGGCGCTGCCAAAGACAGCG 1541
    |||||||
Db 139 ArgThrIleArgGlnPheGlnPheThrAspTrrProGlnGlnLysAlaProlysnThrGly 158

QY 1542 GAGGATTCATGACTTTCATCGGCGAGGTGCATTAAGACCAAGGACGATTTGGACAGAT 1601
    |||||||
Db 159 GlnGlyPheIleasprPheIleGlnValHisLysThrLysGlnGlnPheGlnGlnAsp 178

QY 1602 GGGCCTATACAGTGTGACATGCAATGCTGCGCGGCGGACCGGCTGTTCATCACTGTG 1661
    |||||||
Db 179 GlyProIleThrValHisCysSerIleAlaGlyValGlyArgThrGlyValPheIleThrLeu 198

QY 1662 AACATGCTCTGGAGGCGCATGCGCTATGAGAGGCGGTGTCAGACTGTTTCAGACCGGAG 1721
    |||||||
Db 199 SerIleValLeuGlnArgMetArgTyrGlnGlyValValValAspMetPheGlnThrValLys 218

QY 1722 ACCCTGCTGACACAGCGCTCTGCAATGTGACACAGAGACCAAGTATGATGCTGTCTAC 1781
    |||||||
Db 219 ThrLeuArgThrGlnArgProAlaMetValGlnThrGlnAspGlnTyrGlnLeuCysTyr 238

QY 1782 CGTGGCGCCCTGGAGTACCTC 1802
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DB      239 ArgAlaIaIaLeuGluTyrLeu 245
|||||
RESULT 6
US-10-087-993-34
: Sequence 34, Application US/10087993
: Patent No. US20020169303A1
: GENERAL INFORMATION:
: APPLICANT: Ullrich, Axel
: AOKI, Naohito
: Kim, Yeong Woong
: Wang, Hong Yang
: Chen, Zhengjun
: Naylor, Oliver
: Kharitonkov, Alexei Igorevich
TITLE OF INVENTION: NOVEL P1720, PCF-2, BDP1, CLK,
AND SIRP POLYPEPTIDES AND RELATED
PRODUCTS AND METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/087,993
FILING DATE: 05-Mar-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/877,150
FILING DATE: June 17, 1997
APPLICATION NUMBER: U.S. 60/019,629
FILING DATE: June 17, 1996
APPLICATION NUMBER: U.S. 60/023,485
FILING DATE: August 9, 1996
APPLICATION NUMBER: U.S. 60/030,860
FILING DATE: NO. US20020169303A1member 13, 1996
APPLICATION NUMBER: U.S. 60/034,286
FILING DATE: December 19, 1996
APPLICATION NUMBER: U.S. 60/030,964
FILING DATE: NO. US20020169303A1member 15, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 225/298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 1430 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-10-087-993-34
Alignment Scores:
Pred. No.: 1.54e-69 Length: 1430
Score: 1145.50 Matches: 246
Percent Similarity: 58.44% Conservative: 107
Best Local Similarity: 40.73% Mismatches: 231

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[illegible]

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QY 1037 GTTGTGCGCCAGC-----TCAAGGCCACACAGCTCCCTTCATGACGGCCACCTGCC 1090
   :      |||      |
Db 1165 nThrLeuAnSerValThrProProLeuAspValGluGluCysSerIleAlaLeuLeuP 1185
QY 1091 CTGCACAAGATTCAGAACCCGGCTGTGAACATCATGCCCCCTACGAATTGACCCGCTGTG 1150
   :      |||      |
Db 1185 oArgAnaArgAspLysAsnArgSerMetAspValLeuProProAspArg-----Cy 1202
QY 1151 TCTGCAGCCCATCCGCGGTGGTGGAGG-----TCTGACTACATCAATGACGCTTCC 1204
   :      |||      |
Db 1202 sLeuProPheLeuIleSerThAspLysSerAsnAsnTyrIleAsnAlaLeuTh 1222
QY 1205 GGATGCTTATAGACACAGCAGAGCCCTACATAGCTACACAGAGGCTCTGTGACAGACAC 1264
   :      |||      |
Db 1222 rAspSerTyrThrArgArgSerAlaPheMetValThrLeuHisProLeuGlnSerThr 1242
QY 1265 CAGAGCACTTGTGGCCATCTCTATGGAGCAATTCACCAATCATGCTGATGCTGACCA 1324
   :      |||      |
Db 1242 rProAspPheTyrArgLeuValTyrAspTyrGlyCysThrSerIleValMetLeuAsnG 1262
QY 1325 GCTTGCGGAGATGGGAGGAG-----AAATGCCACAGTACTGCCCCAGACAGCGCTCTGC 1381
   :      |||      |
Db 1262 nLeuAsnGlnSerAsnSerAlaTrrProCysLeuGlnTyrTrrProGluProGlyArgG 1282
QY 1382 TCGCTACACAGTACTTGTGTGACCCGCTGAGTACAACATGCCCAAGATATTCCT 1441
   :      |||      |
Db 1282 nGlnTyrGlyLeuMetGluValGluPheMetSerGlyThrAlaAspGluAspLeuValAl 1302
QY 1442 GCGTGAATTCAGAGTCACGAGATCCCGGAGTGGGAG-----TCAAGACAAATCCGACA 1495
   :      |||      |
Db 1302 aArgValPheArgValGlnAsnIleSerArgLeuGlnGluGlyAspLeuLeuValArg 1322
QY 1496 GTTCAGTCCACAGACTGGCCAGAG-----CAGGCGCTGCCACAGACAGGAGGAGATTCA 1552
   :      |||      |
Db 1322 sPheGlnPheLeuArgTrrPserAlaTyrArgAspThrProAspSerLysLysAlaPhe 1342
QY 1553 TGAATTCATCGGCGAGGCTCATAGACAGAGAGAGAGTTCGACAGAGAGCGCTTCAC 1612
   :      |||      |
Db 1342 uHisLeuLeuAlaGluValAspLysTrrPoliAlaGlnSerGly---AspGlyArgThr 1361
QY 1613 GGTGACATGCACTGCTGCTGGCGGCGGCGGAGGCTTCATCACTGATGATGCTGCT 1672
   :      |||      |
Db 1361 eValHisCysLeuAsnGlyGlyArgSerGlyThrPheCysAlaCysAlaThrVal 1381
QY 1673 GGAGGCGATCGGCTATGAGGGGCTGTGACATGTTTGACACCGTGAACACCTGGGTAC 1732
   :      |||      |
Db 1381 uGlnMetIleArgCysHisAsnLeuValAspValPhePheAlaAlaGlnThrLeuArgAs 1401
QY 1733 ACAGCGCTCGCATGTCAGACAGAGAGGACAGATACAGTGTGCTACCGTGGCGCCT 1792
   :      |||      |
Db 1401 nTyrLysProAsnMetValGluThrMetAspGlnTyrHisPheCysTyrAspValAla 1421
QY 1793 GGAGTACCTC 1802
   :      |||      |
Db 1421 uGlnTyrLeu 1424

```

## RESULT 7

US-10-000-954-2

Sequence 2, Application US/10000954

Patent No. US2002012726A1

GENERAL INFORMATION:

APPLICANT: Schlessler, Joseph

Barnea, Giliad

Grunet, Martin H.

Margolis, Richard U.

TITLE OF INVENTION: A NEW CLASS OF RPTPases: THEIR

STRUCTURAL DOMAINS AND LIGANDS

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSSEE: PENNIE &amp; EDMONDS

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

```

? COUNTRY: U.S.A.
? ZIP: 10036
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/10/000,954
? FILING DATE: 04-Dec-2001
? CLASSIFICATION: <unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/644,293
? FILING DATE: 23-Aug-2000
? APPLICATION NUMBER: 08/081,929
? FILING DATE: <unknown>
? ATTORNEY/AGENT INFORMATION:
? NAME: Coruzzi, Laura A.
? REGISTRATION NUMBER: 30742
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 212 790-9090
? TELEFAX: 212 869-8864/9741
? TELEX: 66141 PENNIE
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2308 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: unknown
? MOLECULE TYPE: protein
? SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-000-954-2

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Alignment Scores:
Pred. No.: 9,22e-68 Length: 2308
Score: 1120.00 Matches: 245
Percent Similarity: 57.00% Conservative: 105
Best Local Similarity: 39.90% Mismatches: 216
Query Match: 17.38% Indels: 48
DB: 12 Gaps: 15

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US-09-743-492-1 (1-3467) x US-10-000-954-2 (1-2308)

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QY 72 ACCCCAGATATCGAGACACCACCCATCCCATACCGACCTGGCGGAC----- 122
   :      |||      |
Db 1678 SerProArgValIleSerThrProThrProIlePheProIleSerAspValGly 1697
QY 123 -----AACATCGAGCGGCTCAAGGCCAACGATGGCCTC 155
   :      |||      |
Db 1698 AlaIleProIleLysHisPheProLysHisValAlaAspLeuHisAlaSerGly--- 1716
QY 156 AAGTCTCCACAGAGATGAG-----TCCATGACCCCTGGACAGCAGTTC 200
   :      |||      |
Db 1717 ---PheThrGluGluPheGlnGluValGlnSerCysThrValAspLeuGly----- 1733
QY 201 ACCTGGAGAAATTCAAACCTGAGGTGAACAAACCCAGACAGCCGCTATGCGATGTCATC 260
   :      |||      |
Db 1734 ThrAlaAspSerSerAsnHisProAspAsnLysHisLysAsnArgTyrIleAsnIleVal 1753
QY 261 GCCTAGCAGCACTTCGAGTGCATCTTACCTGTATCGATGGCGTCCCGCG-----AGT 314
   :      |||      |
Db 1754 AlaTyrAspHisSerArgValLysLeuAlaGlnLeuAlaGluLysAspLysLeuThr 1773
QY 315 GACTACATCAATGCCAATACATGATGCTACCGCCAGACAGAAATGCTACATCGCCACG 374
   :      |||      |
Db 1774 AspTyrIleAsnAlaAsnTyrValAspGlyTyrAsnArgProLysAlaTyrIleAlaAla 1793
QY 375 CAGGCCCCCTGCGCGAGACCATGGCGCATTTCTGAGAGANTGTGGAGACAGCGCAGC 434
   :      |||      |
Db 1794 GlnGlyProLeuLysSerThrAlaGluAspPheTrrArgMetIleTrrPoliHisAsnVal 1813
QY 435 GCCACTGTGCTATGATGACACAGCGCTGGAGGAGAGTCCCGGTAATAATGTGATCAGTAC 494

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Db 1814 GUVallIleValMetIleTherAsnLeuValGluLysGluArgArgLysCysAspIleThr 1833
Oy 495 TGGCAGGCCCGTGGACGAGACCTGTGGCCCTTATTGAGTGGACCCGTGTGGACACAGTG 554
Db 1834 TTProAlaAspGlySerGluGluIleLysAsnIleLeuValThrGlnLysSerValGln 1853
Oy 555 GAGTGGCCACATACACTGTGGCCACTTGCACACTCCAC-----AAGAGTGGC 602
Db 1854 ValLeuAlaIleLysThrValArgAsnIleThrLeuArgAsnThrLysIleLysGly 1873
Oy 603 TCCAGTGAAGCGTGAG-----CTGCCTCAGTTTCAGTTTCAATGAGCCCTGGCCA 650
Db 1874 SerGlnLysGluArgProSerGlyArgValAlaThrGlnIleLysIleThrGlnIlePro 1893
Oy 651 GACCATGAGTTCCTGATGATCCCAATCCCTGGCCCTTCTGACGAGCGGTGAAGGCC 710
Db 1894 AspMetGlyValProGlnIleLysSerLeuProValIleThrPheValArgLysAlaIleArg 1913
Oy 711 TGCAACCCCTAGACGAGGCCCATGTGGTGTGACACTGACAGCGCGGTGGCCGAC 770
Db 1914 AlaLysArgHisAlaValGlyProValValAlaHisCysSerIleAlaGlyValGlyArgThr 1933
Oy 771 GGTCTCTTCATCGTGTATGATGCCATGTTGGAGCGGATGAAACGACAGACAGCGTGAC 830
Db 1934 GlyThrIleValIleLeuAspSerMetLeuGlnGlnIleGlnHisGluGlyThrValAsn 1953
Oy 831 ATGTAGGCCCAAGTACATGCGATGATCAGACAGACTCATGATGCTGACAGCGGAGAG 890
Db 1954 IlePheGlyPheLeuLysHisIleLysSerGlnArgAsnIleValGlnIleThrIleGlu 1973
Oy 891 CAGTACGTGTTTCATTCATAGAGCGCTGTGAGCGCTGACCGTCCACGCTGGCCACAGAGGTG 950
Db 1974 GlnIleValPheIleHisAspThrLeuValGlnAlaIleLeuSerLysGluThrGlnVal 1993
Oy 951 CCTGCCCAACCTGTATGCCACATCCAGAAAGCTGGGCCCAAGTCCCTCCAGGGGAGAGT 1010
Db 1994 LeuAspSerHisIleHisAlaIleValAlaAsnAlaLeu---LeuIleProGlyProAlaGly 2012
Oy 1011 GTGACCGGCATGAGCGTGTGATGAGTGTGCGCCAGCTCCAAAGGCCACACAGCGCCGC 1070
Db 2013 LysThrLysLeuGlnLysGlnPheGlnLeuLeuSerGlnSerAsnIleGlnIleSerAsp 2032
Oy 1071 TTTCATCAGGCCCAACCTGCTCGCAACAAGTTCAAGAACCGCGTGTGACATGATGCC 1130
Db 2033 TyrSerAlaIleAlaLeuLysGlnCysAsnArgLysAsnArgThrSerIleIlePro 2052
Oy 1131 TACGATTCAGCCCGTGTGTGTGTGACGCCCATCCGTGTGTGAGAGGCTGTGACTATC 1190
Db 2053 ValGluArgSerArgValGlyIleSerSerLeuSerGly---GluGlyThrAspTyrIle 2071
Oy 1191 AATGCGACCTCTGATGATGTTATAGACGACGAAAGCGCTCATATGATACAGCGGCT 1250
Db 2072 AsnAlaSerIleLysMetGlyTyrGlnIleSerAsnGluPheIleIleThrGlnIlePro 2091
Oy 1251 CTGCGACGAGACCGACGAGACTTGTGGCATGCTATGAGGACACAAATTCACACATCATC 1310
Db 2092 LeuLeuHisThrIleLysAspPheIleArgMetIleIleTrpAsnHisAlaGlnLeuVal 2111
Oy 1311 GTCAATGTCAGCAACCTTGGGAGATGGGACGAGGAATAATCCASCACTACTGGCCA--- 1367
Db 2112 ValMetIleProAspGlyGlnAsnMetAlaGlnAspGlu---PheValIleTyrProAsn 2130
Oy 1368 GCACAGCGCTGTGCTGTGCTACGACTTGTGTGTGACCGCGATGCGGAG----- 1418
Db 2131 LysAspGluProIleAsnCysGluSerPheLysValIleThrLeuMetAlaGlnIleLys 2150
Oy 1419 -----TACAACATGCCCATATATCTGCTGCTGATGATCAAGTCAAGGATGCCGAGAT 1472
Db 2151 CysLeuSerAsnGlnGluLysLeuIleIleGlnAspPheIleLeuGlnAlaIleThrGlnAsp 2170
Oy 1473 GGGCAGTCAAGGACAAATCCGCGACTTCAGTTTCACAGACTGGCCAGAGCGGCGTGGCC 1532
```

```
Db 2171 AspTyrValIleGluValArgHisPheGlnCysProLysTyrProAsnProAspSerPro 2190
Oy 1533 -----AAGACAGCGGAGGATTCATTCATTCGCGGACGATGACATTAAGACAGAG 1586
Db 2191 IleSerLysThrPheGlu---LeuIleSerValIle-----LysGluGlu 2204
Oy 1587 CAGTTTGGACGAGATGAGCGCTATACAGGCTGCACGCTGCATGCTGGCGTGGCCCGCCGG 1646
Db 2205 AlaAlaAsnArgAspGlyProMetIleValHisAspGlnHisGlyValIleThrAlaGly 2224
Oy 1647 GTGTTCATCACTGTGAGATGCTCTGAGAGCGCAATCCGCTATGAGAGCGGTGTGCACATG 1706
Db 2225 ThrPheCysAlaLeuIleThrThrLeuMetHisGlnLeuGluLysGluAsnSerValAsp 2244
Oy 1707 TTTCAGACCGTGAAGACCGTGGCTGACACAGCGCTCCGCAATGCTGACAGACAGAGACAG 1766
Db 2245 TyrGlnValAlaLysMetIleAsnLeuMetArgProGlyValPheAlaAspIleGluGln 2264
Oy 1767 TATCAGCTGTGCTACCGTGGCGGCCCTGGAGTACCTGCGCAGC 1808
Db 2265 TyrGlnPheLeuTyrLysValIleLeuSerLeuValSerThr 2278

RESULT 8
US-09-788-626-9
; Sequence 9, Application US/09788626
; Patent No. US2002009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-9

Alignment Scores:
Pred. No.: 2.9e-43 Length: 305
Score: 752.50 Matches: 144
Percent Similarity: 72.69% Conservative: 37
Best Local Similarity: 57.83% Mismatches: 65
Query Match: 11.68% Indels: 3
DB: Gaps: 2

US-09-743-492-1 (1-3467) x US-09-788-626-9 (1-305)

Oy 204 TGGGGAATTCAAACTGTGAGGTGAACAACCCCAAGAACCCGCTATGCGATGTATGCC 263
Db 4 TTPspSerAlaLysLysAspGlnAsnArgMetLysAsnArgTyrGlyAsnIleIleAla 23
Oy 264 TACGACCACTGCTCGAGTATCTTACCTGATTCATGATGCGTGTGCGGAGAGTACATC 323
Db 24 TyrAspHisSerArgValArgLeuGlnIleThrIleGluGlnAspThrAsnSerAspTyrIle 43
Oy 324 AATGCAACTACATGATGCTGTACGCGACGACGAGATGCTCATGCTACATGCGCCACGAGGCC 383
Db 44 AsnGluAsnTyrIleAspGlyTyrHisArgProAsnHisTyrIleAlaIleThrGlnIlePro 63
Oy 384 CTGCGCGACGACATGCGGCGATTTGTGAGAAATGGTGTGGAAACAGCGACGCGCACTGTG 443
Db 64 MetGlnGlnIleThrIleTyrAspPheIleArgMetValIleTrpHisGluAsnThrAlaSerIle 83
Oy 444 GTCAATGATGACAGCGCTGAGAGAGAGAGTCCGCGTAAATATGATACATGACTGAGCGAAC 503
Db 84 IleMetValIleTrpAsnLeuValGlnValGlyValIleLysCysLysTyrTrpPro--- 102
Oy 504 CGTGGACCGAGACCTGTGCGCTTATTCAGGTGACCCCTGTGTGACACAGTGAAGTGGAC 563
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Db      103  ASPTFTGRIuIleTyrLysAspIleLysValThrLeuIleGluThrGluLeuLeuAla 122
QY      564  ACATACACTGTGGCGCCTTCGCACCTCCACAGAGTGGCTCCAGTGAGAGAGCGTAGCTG 623
Db      123  GIuTYValIle-----PheAlaValGIuLysArgGIuValHisGIuIleLeuArgGIuIle 140
QY      624  CGCATTCATTCATGTGGCGTGGCCAGACCATGAGTTCCTGAGTACCACCATCCCATC 683
Db      141  ATGGLIPheHisPheThrGluTyrProAspHisGIuValProTyrHisAlaThrGIuLeu 160
QY      684  CTGGCGCTTCATACGAGCGGTCAAGCGCTCAACCCCTCAGACGACGAGCGCCATGTGTG 743
Db      161  LeuGIYPheValArgIleValLysSerLysSerProProSerAlaGIuProLeuVal 180
QY      744  CACTGACGGCGGGCGCTGGCGCCGACCGCGCTGCTCATGTGATGTGATGCCATGTGGAG 803
Db      181  HisCysSerAlaGIuLysArgIleGluTyrHisPheIleValIleAspIleMetLeuAsp 200
QY      804  CGGATGAACGACGAGAGAGCGGTGCATGTAGTGCACATGACCTGCATGCCATCACAG 863
Db      201  MetAlaGIuArgGIuLysValValAlaAspIleTyrAsnCysValArgIuLeuArgSerArg 220
QY      864  AGCAACTACATGATGTGCAGACGAGACGACATGCTTCATCCATGAGCGCTGCTGAG 923
Db      221  ArgValAsnMetValGIuThrGIuLysArgIleTyrValPheIleHisAlaIleLeuGIu 240
QY      924  GCTGCCACGTGGCGGCCACACAGAGGTG 950
Db      241  AlaCysLeuCysGIuLysPheThrSerVal 249

```

## RESULT 9

```

US-09-788-626-10
; Sequence 10, Application US/09788626
; Patent No. US2002009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-10

```

```

Alignment Scores:
Pred. No.: 2,07e-41 Length: 310
Score: 725.00 Matches: 140
Percent Similarity: 71.48% Conservative: 43
Best Local Similarity: 54.69% Mismatches: 67
Query Match: 11.25% Indels: 6
DB: 10 Gaps: 2

```

US-09-743-492-1 (1-3467) x US-09-788-626-10 (1-310)

```

QY      195  CAGTTCACCTGGGAGAAATTCAAACCTGGAGGTGACACCAAGACCGCTATGGCAAT 254
Db      1  GlnAlaThrCysGIuAlaIleAspLysGIuLysAsnArgTyrValAsn 20
QY      255  GTCATCGCTACGACCACTCTGAGTCACTTACCTCATGAGTGGCGCTCCCGGAGT 314
Db      21  IleLeuProTyrAspHisSerArgValHisLeuThrProValGIuLysValProAspSer 40
QY      315  GACTATCATGAATGCACTACATCATGATGGCTACCGGACAGAGATGCTCATATGCCACG 374
Db      41  AspTyrIleAsnAlaSerPheIleAsnGIuTyrGIuLysAsnLysPheIleAlaIle 60

```

```

QY      375  CAGGCGCCCTCCCGGAGACCATGGCGGAPTTCTGAGATGGTGGGAGACGCGCAG 434
Db      61  GlnGIYProLysGIuGIuThrValAsnAspPheTyrPheMetIleThrGIuGlnAsnThr 80
QY      435  GCCACTGTGGTGCATGATGACACGCGTGGAGAGAGAACTCCCGGATAAATGTATCAGTAC 494
Db      81  AlaThrIleValMetValThrAsnLeuLysGIuArgLysGIuLysCysAlaGIuTyr 100
QY      495  TGGCCAGCCCGTGGAGACCGACCATGCTGGCTTATTCAGGTGACCTGTGGACACAGTG 554
Db      101  TyrProAspGIuLysTyrThrTyrGIuAsnIleArgValSerValGIuAspValIThr 120
QY      555  GAGCTGGCAACATACACTGTGGCGCCACCTTGGCATCCCAAGAGTGGCGTCCAGTAGAG 614
Db      121  ValLeuValAspTyrThrVal-----PheCysIleGIuGlnValGIuLysPheThrAsn 138
QY      615  CGTGAG-----CTGGCTCACTTTCAGTTTCATGTCGCGCCGACACCATGAGATT 662
Db      139  ArgLysProGIuArgLeuIleThrGlnPheHisPheThrSerTyrProAspPheGIuVal 158
QY      663  CCTGATACCCAACTCCATCTCGGCTTCTTCAAGAGGGGTCAAGGCTGCAACCCCTTA 722
Db      159  ProPheThrProIleGIuMetLeuLysPheLeuLysValLysValLysAlaCysAsnProGIu 178
QY      723  GACGCGAGGCGCCATGTGTGGTGCATGCGACCGCGCGGTGGCGCCACCGGCTTCATC 782
Db      179  TyrAlaGIuAlaIleValAlaHisCysSerAlaGIuValGIuLysThrGIuThrPheVal 198
QY      783  GTGATGATGCCATGTTGGAGCGGATGAAGACGAGACAGCATCATGTATGGCCAC 842
Db      199  ValIleAspAlaMetLeuAspMetMetHisThrGIuArgLysValAlaIleTyrGIuPhe 218
QY      843  GTGACCTGCATGCCATCAGACAGAGAACTACATGTGTGACAGGAGGACCATGATGTTTC 902
Db      219  ValSerArgIleArgAlaGIuArgLysCysGlnMetValGIuThrAspMetGIuTyrValPhe 238
QY      903  ATCCATGAGCGCGCTGTGGAGCGTGCACGTGGCGCCACACAGAGTGTG 950
Db      239  IleTyrGlnAlaLeuLeuGIuHisTyrLeuTyrGIuAspThrGIuLeu 254

```

## RESULT 10

```

US-09-788-626-6
; Sequence 6, Application US/09788626
; Patent No. US2002009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-6

```

```

Alignment Scores:
Pred. No.: 5.85e-40 Length: 319
Score: 703.50 Matches: 140
Percent Similarity: 65.57% Conservative: 39
Best Local Similarity: 51.28% Mismatches: 79
Query Match: 10.92% Indels: 15
DB: 10 Gaps: 3

```

US-09-743-492-1 (1-3467) x US-09-788-626-6 (1-319)

```

QY      201  ACCTGGAGAAATTCAAACCTGGAGGTGAAAGACCCCAAGACCGCTATGCAATGCATC 260
Db      3  ThrAlaGIuHisSerHisThrProGIuAsnLysHisLysAsnArgTyrIleAsnIleLeu 22

```

```

OY 261 GCCTACGACACCTCTGAGCTATCTTACCTTATCATGATGCGCTCCCGG-----AGT 314
    |||||||
Db 23 AATGTAASPHISSErArGVallyLeuArProLeuProGlyLysAspserLyshSer 42
OY 315 GACTCATCATGCAATGCAATACATGCTGCTACCCCAAGCAGAAATGCTTACATCCCGCAG 374
    |||||||
Db 43 AspYrTLeAsnAlaAsnYrValAspGlyYrAsnLysAlaLysAlaTyrLLeAlaTTr 62
OY 375 CAGGCGCCCTGCGCCGAGACCATGGCGATTTCTGAGAAATGATGTGGAGACAGCGCAG 434
    |||||||
Db 63 GlnGlyProLeuLysSerThrPheGluAspPheTrpArgMetLLeTrpGlnAsnThr 82
OY 435 GCCACTGGTCATGATGACAGCTGAGAGAGAGATCCCGGGTAAATGTGATCAGTAC 494
    |||||||
Db 83 GlyLLeIleValMetLLeThrAsnLeuValGluLysGlyArgArgLysCysAspLntYr 102
OY 495 TGGCCAGCCCGGCGACCGAGACCTGTGGCTTATTCAGAGTACCTGTGGACACAGTG 554
    |||||||
Db 103 TrpProThrGluAsnSerLLeuLntYrGlyAsnLLeIleValThrLeuLysSerThrLys 122
OY 555 GAGTGGCCACATACATGCTGGCGACCTTCCGCACTCCACAAGAT----- 599
    |||||||
Db 123 IleAsnIaLcysTyrThrVal-----PheSerLLeArgAsnThrLysValLysLysGly 140
OY 600 -----GCTCCAGTAGAGAGAGCTGAGCTGAGCTGCTGACATTTCAGTTTCATG 641
    |||||||
Db 141 GlnLysGlyAsnProLysGlyArgGlnAsnGlnuArgValAlaLLeGlnLntYrHisTyrThr 160
OY 642 GCGTGGCCAGACCATGAGAGTTCTCTAGTACCACTCCCATCTGCTGCTTCCAGCAGG 701
    |||||||
Db 161 GlnTrpProAspMetGlyValProGlnLntYrAlaLeuProValLLeThrPheValAlaArg 180
OY 702 GTCAAGGCTGCAACCCCTAGACGAGGCCCATGCTGCTGCTGCTGACGAGCGGCGTG 761
    |||||||
Db 181 SerSerAlaIaArgMetProGlnThrGlyProValLLeuValHisCysSerLLeAlaLys 200
OY 762 GGGCGACCGGCTGCTTACATGCTGATGATGATGATGATGATGATGATGATGATGATG 821
    |||||||
Db 201 GlyArgThrGlyThrTyrLLeValLLeAspSerMetLLeuGlnLntYrLLeLysAspLysSer 220
OY 822 ACGGAGCAATCTATGCGACGCTGACGCTGATGATGATGATGATGATGATGATGATGATG 881
    |||||||
Db 221 ThrValAsnValLeuGlyPheLeuLysHisLLeArgThrGlnArgAsnTyrLLeuValGln 240
OY 882 ACGGAGCAAGTACATGCTTCCATGCTGAGCGCTGCTGAGAGCTGAGAGCTGAGCGGCGC 941
    |||||||
Db 241 ThrGlnGluGlnTyrLLePheLLeHisAspAlaLLeuLLeuGlnAlaLLeuGlnLysGlu 260
OY 942 ACAGAGTGCCTGCCCGCAACCTGTATGCCACATCCAG 980
    |||||||
Db 261 ThrGluValValLLeAspSerMetLLeuGlnGlnLntYrLys 273

RESULT 11
US-09-788-626-7
: Sequence 7, Application US/09788626
: Patent No. US20020009762A1
: GENERAL INFORMATION:
: APPLICANT: Flint, Andrew J.
: APPLICANT: Cool, Deborah E.
: TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
: FILE OF INVENTION: PHOSPHATES
: FILE REFERENCE: 200125.401
: CURRENT APPLICATION NUMBER: US/09/788.626
: CURRENT FILING DATE: 2001-02-13
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 7
: LENGTH: 313
: TYPE: PRT
: ORGANISM: Drosophila melanogaster
US-09-788-626-7

```

```

Alignment Scores:
Pred. No.: 9,26e-40 Length: 313
Score: 700.50 Matches: 131
Percent Similarity: 69.32% Conservative: 52
Best Local Similarity: 49.62% Mismatches: 76
Query Match: 10.87% Indels: 5
Db: 10 Gaps: 3

US-09-743-492-1 (1-3467) x US-09-788-626-7 (1-313)
OY 207 GAGAAATCAAAACCTGAGAGTGAACGCCAAGACCCGATGCAATGCTATCGCGCTAC 266
    |||||||
Db 5 GlnHisSerGlnHisProGluAsnLysArgLysAsnArgTyrLLeuAsnLLeThrLAlaTTr 24
OY 267 GACCACTCTCGAGTATCTTACTCTTATGCAATGGCGCTGCCCGGAGT--GACTACATC 323
    |||||||
Db 25 AspHisSerArgValHisLLeuHisProThrProGlnGlnLysLysAsnLeuAspYrTLe 44
OY 324 AATGCCAATCATGATGATGCTTACCCGCAAGCAGAAATGCTTACATGCGCACAGGCGCC 383
    |||||||
Db 45 AsnAlaAsnPheLLeAspGlyTyrGlnLysGlnHisAlaPheLLeGlyThrGlnGlnLPro 64
OY 384 CTGCCCCGAGACCATGGCGGATTTCTGAGAAATGCTGTGGAGACAGCGACGCGCACTGTG 443
    |||||||
Db 65 LeuProAspThrPheAspCysPheTrpArgMetLLeTrpGlnGlnArgValAlaLLeLLe 84
OY 444 GTCATGATGACACGCGCTGAGAGAGAGTCCCGGATGAAATGATGATGATGATGATGATGATG 503
    |||||||
Db 85 ValMetLLeThrAsnLeuValGlnuArgGlyArgArgLysCysAspMetLLeTrpProLys 104
OY 504 CGTGGCACCGACAGCTGTGGCTTATTCAGTGTGACGCTGTGGAGACAGAGTGGAGCTGGCC 563
    |||||||
Db 105 AspGlyValGlnThrTyrGlyLLeValLLeGlnValLLeuLLeGlnGlnLntYrLLeuLLeSer 124
OY 564 ACATGACACTGTG-----CGCACCTTGGCAGCTCCCAAGAGTGGCTCCAGTAGAGAG 614
    |||||||
Db 125 ThrTyrThrValLLeuGlnLLeLysHisLLeuLysLysLysLysLysLysLysLysLys 144
OY 615 CGTGAAGTG---CGTCAATTTTCAGTTTCATGAGCTGCGCCAGACAGCATGAGATTCGTGATAC 671
    |||||||
Db 145 GlnLysLLeuValTyrGlnLntYrHisTyrThrAsnTrpProAspHisGlyThrProAspHis 164
OY 672 CCAACTCCCAATCTGCGCTTCTCTACGAGCGGTCAAGGCTGCAACCCCTGACAGCGGCG 731
    |||||||
Db 165 ProLeuProValLLeuAsnPheValLysLysSerSerAlaAlaAsnProAlaGlnLLeLys 184
OY 732 CCCATGTTGGAGCGATGAGACGACGAGAGAGAGTGTGACATCTATGACCTGACCTGC 851
    |||||||
Db 205 AlaMetLLeuLysGlnLLeGlnGlnLntYrAsnLLeValAsnValPheGlnPheLeuArgHis 224
OY 852 ATGCGATCAGACAGAGACTTACATGCTGTCAGACAGGAGACAGTACAGTTCATCATGAG 911
    |||||||
Db 225 IleArgAlaGlnArgAsnPheLeuValGlnThrGlnGlnGlnTyrLLePheLeuHisAsp 244
OY 912 GCGGTGCTGAGAGCGGCGCACAGTGTGCGCACAGAGAGTGTGCGCGCGCGCAACCTGATGCC 971
    |||||||
Db 245 AlaLeuValGlnAlaLLeAlaLLeAspSerGlyLntThrAsnLeuValLLeuAspAlaMetLLeuLys 264
OY 972 CACATCCAGAG 983
    |||||||
Db 265 GlnLLeGlnGln 268

RESULT 12
US-09-788-626-11
: Sequence 11, Application US/09788626
: Patent No. US20020009762A1
: GENERAL INFORMATION:
: APPLICANT: Flint, Andrew J.
: APPLICANT: Cool, Deborah E.

```



```

; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-11

```

## Alignment Scores:

```

Pred. No.: 1.08e-39 Length: 309
Score: 699.50 Matches: 136
Percent Similarity: 70.20% Conservative: 43
Best Local Similarity: 53.33% Mismatches: 71
Query Match: 10.86% Indels: 5
DB: Gaps: 2

```

US-09-743-492-1 (1-3467) x US-09-788-626-11 (1-309)

```

OY 195 CAGTTCAGTGGGAAATTCAAACCTGGAGTGAACAAGCCAGAACCGCTATGCGAT 254
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GlnGlyThrPheGluLeuAlaAsnLysGluGlnAsnArgLysAsnAlaGlyTyrProAsn 20
OY 255 GTCATCGCCATGACGACGACCTGCGAGTCATCTTACCTGTATGATGGCGCGGAGT 314
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 21 IleLeuProAsnAspHisSerArgValIleLeuSerGlnLeuAspGlyIleProCysSer 40
OY 315 GACTACATCATGCACTATCATGATGCTACCGCAAGCAAGATGCTTACATGCGACG 374
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 41 AspTyrIleAsnAlaSerTyrIleAspGlyTyrLysGluLysAsnLysPheIleAlaAla 60
OY 375 CAGGCGCCCTGCGCCGACCATGGGCGATTTCTGAGAAATGGTGGAACACGCGACG 434
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GlnGlyProLysGlnGluThrValAsnAspPheThrArgMetValITrPgluGlnLysSer 80
OY 435 GCCACTGTGTATGATGACAGCGGCTGGAGAGAGAGTCCGGGTAATGTGATCACTAC 494
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 81 AlaThrIleValMetLeuThrAsnLeuLysGluThrArgLysGluLysCysHisGlnTyr 100
OY 495 TGGCCAGCCCGTGGCCACGACGCTGGGCTTATTCAGGTGACCCCTGTGGACACAGTG 554
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 101 TrpProAspGlnGlySerTrpThrTyrGlyAsnIleArgValLysValGluAspCysVal 120
OY 555 GACCTGGCCACATACACTGTGGCGACCTTGGCACTCCAC-----AAGAGTGGGCTCC 605
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 ValLeuValAspTyrThrIle-----PheCysIleGlnProGlnLeuProAspGlyCys 138
OY 606 AGTGAGAGCGGTAGCTGCTGCTGATTCAGTTCATGCTGCGCCAGACCATGAGTTCCT 665
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 139 LysAlaProArgLeuValSerGlnLeuHisPheThrSerTrpProAspPheGlyValPro 158
OY 666 GAGTACCCAACTCCCATCTCGGCTTCTTACGACGGGTCAAGGCTCAACCCCTAGAC 725
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 159 PheThrProIleGlyMetLeuLysPheLeuLysValLysThrLeuAsnProValHis 178
OY 726 GCAGGGCCATGTGTGGTCACTGTCAGCGCGGCTGGCGCGACCGGCTGTTCACTGTTG 785
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 AlaGlyProIleValValHisCysSerAlaGlyAlaGlyArgThrGlnThrPheIleVal 198
OY 786 ATTGATGCATGTGTGAGCGGATGACACAGAGAGAGCGGTGACATCTATGGCCACGTG 845
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 199 IleAspIleMetMetAlaMetMetHisAlaGlnGlnLysValAspValPheGluPheVal 218
OY 846 ACCTGATGGGATCAGAGAGAACTACATGCTGACAGCGAGGACCGAGTACGTTTATC 905
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 219 SerArgIleArgAsnGlnArgProGlnMetValGlnThrAspMetGlnTyrThrPheIle 238
OY 906 CATGAGCGCTGTGTGAGGCTGCCACGTCGGCGCCACACAGAGGTC 950
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Db 239 TyrGlnAlaLeuLeuGluTyrTyrTyrLeuTyrGlyAspThrGluLeu 253

## RESULT 13

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US-09-788-626-5
; Sequence 5, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-5

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## Alignment Scores:

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Pred. No.: 4.73e-39 Length: 316
Score: 690.00 Matches: 138
Percent Similarity: 63.74% Conservative: 36
Best Local Similarity: 50.55% Mismatches: 91
Query Match: 10.71% Indels: 8
DB: Gaps: 2

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US-09-743-492-1 (1-3467) x US-09-788-626-5 (1-316)

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OY 201 ACGTGGAGAAATTCAAACCTGGAGTGAACAAGCCAGAACCGCTATGCGAATGTCATC 260
    ||| : : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 ThrAlaAspSerSerAsnHisProAspAsnLysHisLysAsnArgTyrIleAsnIleVal 22
OY 261 GCCATGACGACCTGCGAGTCATCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 314
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 AlaTyrAspHisSerArgValLysLeuAlaGlnLeuAlaGlnLysAspGlyLysLeuThr 42
OY 315 GACTACATCATGCACTATCATGATGCTACCGCAAGCAAGATGCTTACATGCGACG 374
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 43 AspTyrIleAsnAlaAsnTyrValAspGlyTyrLysAsnArgProLysAlaTyrIleAlaAla 62
OY 375 CAGGCGCCCTGCGCCGACCATGGGCGATTTCTGAGAAATGGTGGAACACGCGACG 434
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63 GlnGlyProLeuLysSerThrAlaGlnAspPheThrArgMetIleTrpGlnHisAsnVal 82
OY 435 GCCACTGTGTATGATGACAGCGGCTGGAGAGAGAGTCCGGGTAATGTGATCACTAC 494
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 GluValIleValMetIleThrAsnLeuValGlnLysGluArgLysCysAspGlnTyr 102
OY 495 TGGCCAGCCCGTGGCCACGACGCTGGGCTTATTCAGGTGACCCCTGTGGACACAGTG 554
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 103 TrpProAlaAspGlySerGlnGluTyrGlyAsnPheLeuValITrGlnLysSerValGln 122
OY 555 GACCTGGCCACATACACTGTGGCGACCTTGGCACTCCACAG-----596
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 123 ValLeuAlaTyrTyrThrValPheThrLeuArgAsnThrLysIleLysGlySerGln 142
OY 597 AGTGGCTCCCACTGAGAACCGGTGACGCTGCTTACAGTTCATGATGCGCTGGCCAGACAT 656
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 LysGlyArgProSerGlyArgValValThrGlnTyrHisTyrThrGlnITrProAspMet 162
OY 657 GGAATTCCTGAGTACCCCACTCCCATCTGGCTTCTTACAGCGGTCACAGGCTGCAAC 716
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 163 GlyValProGlnTyrSerLeuProValLeuThrPheValArgLysAlaIleTyrAlaLys 182
OY 717 CCCCTAAGCAGGCGCATGCTGCTGACATGACGCGCGGCTGGCGCCGACGCGCTGC 776
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 183 ArgHisAlaValGlyProValValHisCysSerAlaGlyValGlyArgThrGlyThr 202
OY 777 TTCATCGTGTATGATGCCATGTTGGAGCGGATGAAGACGAGAGACGGGTGACATCTAT 836

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Db 203 TyrIleValLeuAspSerMetLeuGlnIleGlnHisGluGlyThrValAsnIlePhe 222
QY 837 GGCACGTCGACCTGCATGGCATCACAGAGAACTACATGCTGAGACGAGACGACGATAC 896
Db 223 GlyPheLeuLysHisIleArgSerGlnArgAsnTyrLeuValGlnThrGluGlnTyr 242
QY 897 GTGTCATCATGAGCGCTGCTGAGGCTGCCACGCTGGCCACACAGAGTGCCTGCC 956
Db 243 ValPheIleHisAspThrLeuValGlnAlaIleLeuSerLysGluThrGluValValLeu 262
QY 957 CGCAACCTGTATGCCACATCCAGAAAGCTGGCGCAAGTG 995
Db 263 AspSerMetLeuGlnIleGlnHisGluGlyThrVal 275

RESULT 14
US-09-788-626-26
; Sequence 26, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788.626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-26

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Alignment Scores:
Pred. No.: 4.73e-39 Length: 316
Score: 690.00 Matches: 138
Percent Similarity: 63.74% Conservative: 36
Best Local Similarity: 50.55% Mismatches: 91
Query Match: 10.71% Indels: 8
DB: 10 Gaps: 2

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US-09-743-492-1 (1-3467) x US-09-788-626-26 (1-316)

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QY 201 ACGTGGAGAAATTCAAACTGGAGGTGAACAGCCCAAGACCCGATGCGATGTCATC 260
Db 3 ThrAlaAspSerSerAsnHisProAspAsnLysHisLysAsnArgTyrIleAsnIleVal 22
QY 261 GCCTACGACCACTGTCGATGTCATCCTTACCTTATGATGAGGCTGCCGCG-AGT 314
Db 23 AlaTyrAspHisSerArgValLysLeuAlaGlnLeuAlaGlnLysAspLysLeuThr 42
QY 315 GACTCATCAATAGCCAACTACATGCTACGCTACCCGACCAAGAAAGCCATCATCCGACAG 374
Db 43 AspTyrIleAsnAlaAsnTyrValAspArgTyrAsnArgProLysAlaTyrIleAla 62
QY 375 CAGGCCCCCTGCCGAGCATGTGGCGCATTTCTGGAGAAAGTGGGAGACAGCGCAGC 434
Db 63 GlnGlyProLeuLysSerThrAlaGlnAspPheTrpArgMetIleTrpLuhHisAsnVal 82
QY 435 GCCACTGTGTCATGATGATGACAGCGCTGAGAGAGATCCCGGGTAAATGATGATGATAC 494
Db 83 GluValIleValMetIleThrAsnLeuValGlnLysGlyArgArgLysAspGlnTyr 102
QY 495 TGGCAGCCCGCTGGCAGCAGACGACTGTGGCTTATTCAGGTGACCCCTGTTGACACAGTG 554
Db 103 TrpProAlaAspGlySerGlnGluTyrGlnAsnPheLeuValThrGlnLysSerValGln 122
QY 555 GAGCTGGGCACTACACGTCGGCAGCTTCGACATCCACAAAG----- 596
Db 123 ValLeuAlaTyrTyrThrValPheThrLeuArgAsnThrLysIleLysLysGlnSerGln 142

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QY 597 AGTGAGTCCAGTGAAGAGCGTGAAGCTGCTCACTTTCAGTTTCAGTGGCGTGGCAGCAAT 656
Db 143 LysGlyArgProSerGlnArgValValThrGlnTyrHisIleTyrThrGlnTrpProAspMet 162
QY 657 GGAGTTCCTGAGTACCCAACTCCATCTCGGCTTCTCTAGACAGGCTCAAGGCTGCAAC 716
Db 163 GlyValArgGluTyrSerLeuProValLeuThrPheValArgLysAlaArgLysAlaLys 182
QY 717 CCCCTGAGCAGCAGCCCAATGCTGCTGTCATGCTGAGCGCGCGGCTGGCGCCAGCGCTGC 776
Db 183 ArgHisAlaValAlaGlyProValValValHisCysSerAlaGlyAlaGlyArgThrGlyThr 202
QY 777 TTCATCTGATTCATGATCCATGTTTGAAGCGATGAAGACAGCAGAGCGTGATCATAT 836
Db 203 TyrIleValLeuAspSerMetLeuGlnIleGlnHisGluGlyThrValAsnIlePhe 222
QY 837 GGCACGTCGACCTGCATGGCATCACAGAGAACTACATGCTGAGACGAGACGACGATAC 896
Db 223 GlyPheLeuLysHisIleArgSerGlnArgAsnTyrLeuValGlnThrGluGlnTyr 242
QY 897 GTGTCATCATGAGCGCTGCTGAGGCTGCCACGCTGGCCACACAGAGTGCCTGCC 956
Db 243 ValPheIleHisAspThrLeuValGlnAlaIleLeuSerLysGluThrGluValValLeu 262
QY 957 CGCAACCTGTATGCCACATCCAGAAAGCTGGCGCAAGTG 995
Db 263 AspSerMetLeuGlnIleGlnHisGluGlyThrVal 275

RESULT 15
US-09-788-626-4
; Sequence 4, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788.626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-4

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Alignment Scores:
Pred. No.: 2.41e-38 Length: 317
Score: 679.50 Matches: 138
Percent Similarity: 63.50% Conservative: 36
Best Local Similarity: 50.36% Mismatches: 91
Query Match: 10.34% Indels: 9
DB: 10 Gaps: 3

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US-09-743-492-1 (1-3467) x US-09-788-626-4 (1-317)

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QY 201 ACGTGGAGAAATTCAAACTGGAGGTGAACAGCCCAAGACCCGATGCGATGTCATC 260
Db 3 ThrAlaAspSerSerAsnHisProAspAsnLysHisLysAsnArgTyrIleAsnIleVal 22
QY 261 GCCTACGACCACTGTCGATGTCATCCTTACCTTATGATGAGGCTGCCGCG-AGT 314
Db 23 AlaTyrAspHisSerArgValLysLeuAlaGlnLeuAlaGlnLysAspLysLeuThr 42
QY 315 GACTCATCAATAGCCAACTACATGCTACGCTACCCGACCAAGAAAGCCATCATCCGACAG 374
Db 43 AspTyrIleAsnAlaAsnTyrValAspArgTyrAsnArgProLysAlaTyrIleAla 62
QY 375 CAGGCCCCCTGCCGAGCATGTGGCGCATTTCTGGAGAAAGTGGGAGACAGCGCAGC 434
Db 63 GlnGlyProLeuLysSerThrAlaGlnAspPheTrpArgMetIleTrpLuhHisAsnVal 82

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OY	435	GCCACTGGGCGATGATGATACAGGGCTGGAGGAAAGCCCGGGTAAATGATGATAC	494
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OY	495	TGG---CCAGGCCCGGCGACCGAAGACCTGTGGCCCTTATTCAGAGGACCCGTGGACACA	5515
Dd	103	TrpProProlAlaAspGlySerGluGlnIuylArgLysnHleuValThrGlnLysSerVal	122
OY	552	GTGGAGCTGGCCACATACATACATGTGGGACCTTGCACCTCCACAAG-----	596
Dd	123	GlnValleuAlaIuylTryTyrThrValPheThrLeuArgsnThrLysIleLysGlySer	142
OY	597	---ACGGCTCCACGTAGAGAACCGTGACCTGGCTAGTTTCATGTCAGCCCTGGCCAGAC	653
Dd	143	GlnIuylsGlyArgProSerGlyArgValValAlaThrIleThrIuylsTryThrGlnTrpProAsp	1620
OY	654	CATGAGAGTCCCTGATGATACCACCAATCCCATCCCTGGCCCTTCATACAGCGGGTCAAGGCCCTGC	713
Dd	163	MetGlyValProGlnIuylTrySerLeuProValLeuThrPheValAlaArgLysAlaAlaIuylAla	182
OY	714	AACCCCCTAGACGAGGGCCCATGTGGTGTCATGTACAGCGCGGGCGCTGGGCCACACCGGC	773
Dd	183	LysArgHisAlaValGlyProValValValAlaHisCysSerIaGlyValGlyArgThrGly	2020
OY	774	TGCTTATCCGTGATGATGATGCCATTTGTGGAGCGGATGAAACACAGCAAGACGGGTGCATATC	833
Dd	203	ThrIuylIleValIleuAspSerMetLeuGlnIleIleGlnIleGluGlyThrIleValAsnIle	222
OY	834	TATGGCCACGTGACCTGCATGCATCCATCAGACAGAACTACATGTGGTCAGACGGAGACAG	893
Dd	223	PheGlyPheLeuLysHisIleArgSerGlnIaArgsnIuylIleuValGlnThrGlnIuylGln	242
OY	894	TACGTGTTTCATCATGAGAGCGCTGTGGAGGCTTGCACCTGGCGGCCACACAGAGTGCCCT	953
Dd	243	TyrValPheIleHisAspThrLeuValGluValIleLeuSerLysGluThrGlnValVal	262
OY	954	GCCCGCAACCTGTATGCCACATCCACAAAGCTGGGCCCAATG	995
Dd	263	LeuAspSerMetLeuGlnIleGlnHisGluIuylThrVal	276

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 17, 2003, 09:57:19 ; Search time 35.5 Seconds  
(without alignments)  
5747.001 Million cell updates/sec

Title: US-09-743-492-1

Perfect score: 6444

Sequence: 1 gatccgactgaagactcc.....attgaataatcagatttct 3467

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:  
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued\_Patents\_AA:\*  
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4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2880	44.7	1911	2	US-08-800-825A-5
3	2880	44.7	1911	4	US-09-158-657-5
4	2880	44.7	1911	5	PCr-US94-10166-5
5	2850	44.2	1501	2	US-08-447-464-3
6	2850	44.2	1501	2	US-08-716-679-3
7	1553	24.1	289	1	US-08-036-210-13
8	1553	24.1	289	2	US-08-449-609-13
9	1552	24.1	793	1	US-08-015-985-3
10	1551	24.1	802	1	US-08-015-985-1
11	1423	22.1	699	1	US-08-348-006B-7
12	1423	22.1	699	2	US-08-800-825A-7

13	1423	22.1	699	4	US-09-158-657-7	Sequence 7, Appl1
14	1334	20.7	250	2	US-08-685-992-7	Sequence 7, Appl1
15	1334	20.7	250	2	US-09-144-923-7	Sequence 7, Appl1
16	1307	20.3	1452	2	US-08-652-971-4	Sequence 4, Appl1
17	1307	20.3	1452	2	US-08-991-258A-4	Sequence 4, Appl1
18	1307	20.3	1452	2	US-08-769-399-4	Sequence 4, Appl1
19	1307	20.3	1452	3	US-08-991-953A-4	Sequence 4, Appl1
20	1306	20.3	1452	2	US-08-449-644-8	Sequence 8, Appl1
21	1306	20.3	1452	2	US-08-087-244A-8	Sequence 8, Appl1
22	1295	20.1	245	2	US-08-685-992-26	Sequence 26, Appl1
23	1295	20.1	245	2	US-09-144-925-26	Sequence 26, Appl1
24	1255	19.5	1439	2	US-08-449-644-2	Sequence 2, Appl1
25	1255	19.5	1439	2	US-08-087-244A-2	Sequence 2, Appl1
26	1243	19.3	1457	2	US-08-652-971-3	Sequence 3, Appl1
27	1243	19.3	1457	2	US-08-449-644-1	Sequence 1, Appl1
28	1243	19.3	1457	2	US-08-087-244A-1	Sequence 1, Appl1
29	1243	19.3	1457	2	US-08-991-258A-3	Sequence 3, Appl1
30	1243	19.3	1457	2	US-08-769-399-3	Sequence 3, Appl1
31	1243	19.3	1457	3	US-08-991-953A-3	Sequence 3, Appl1
32	1168	18.1	1445	1	US-08-015-986A-2	Sequence 2, Appl1
33	1168	18.1	1445	2	US-08-446-363-2	Sequence 2, Appl1
34	1162	18.0	1442	1	US-08-015-986A-3	Sequence 3, Appl1
35	1162	18.0	1442	2	US-08-446-363-3	Sequence 3, Appl1
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37	1150.5	17.9	1436	2	US-08-991-258A-2	Sequence 2, Appl1
38	1150.5	17.9	1436	2	US-08-769-399-2	Sequence 2, Appl1
39	1150.5	17.9	1436	3	US-08-991-953A-2	Sequence 2, Appl1
40	1120	17.4	2308	1	US-08-015-973-1	Sequence 1, Appl1
41	1120	17.4	2308	2	US-08-448-164-1	Sequence 1, Appl1
42	1120	17.4	2308	4	US-08-081-929-2	Sequence 2, Appl1
43	1117.5	17.3	2314	4	US-09-816-703A-2	Sequence 2, Appl1
44	1048.5	16.3	1237	1	US-08-241-853-2	Sequence 2, Appl1
45	1048.5	16.3	1237	2	US-08-850-917-2	Sequence 2, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-348-006B-5  
Sequence 5, Application US/08348006B  
Patent No. 5658756  
GENERAL INFORMATION:  
APPLICANT: RODAN, GIDEON A.  
APPLICANT: SCHMIDT, AZRIEL  
APPLICANT: RUTLEDGE, SU JANE  
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: J. MARK HAND  
STREET: 126 E. LINCOLN AVE., P. O. BOX 2000  
CITY: RAHWAY  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/348,006B  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/122,032  
FILING DATE: 14-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: HAND, J., MARK  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 189921A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-594-3905

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; TELEFAX: 908-594-4720
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1911 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
OS-08-348-006b-5

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Alignment Scores:

Pred. No.:	5, 03e240	Length:	191
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Percent Similarity:	94.328	Conservative:	35
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Query Match:	44.698	Indels:	0
DB:	1	Gaps:	0

US-09-743-492-1 (1-3467) x US-08-348-006B-5 (1-1911)

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QY	90	CACCCACCATCCCATCAATACACGCACCTGGGGGACAAATGACAGCGCTCAAAAGCCAAACAT	149
Db	1333	HisProProIleProIleAlaAsnMetLlaGlnHisThrGluArgLeuLysAlaAsnsp	1352
QY	150	GGCCTCAAGTTCTCCACAGAGATATGAGTCCATGACACCTGGACACAGCTTCACTGAGGAG	209
Db	1353	SerLeuLysLeuSerGlnGluArgLysSerIleAsnProGlyGlnGlnPhenThrProIu	1372
QY	210	AATTCAAACCTGGGAGGAGCAACGCCCAAGAACCCGTATGGCAATGTCATGGCCCTACAC	269
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QY	330	AACATCATCATGGCTACCGCAGACAGAAATGCCATATGCCACAGCGGCCCTGTGCC	389
Db	1413	AsnTyrValAspGlyTyrArgArgGlnAsnAlaTyrIleAlaThrGlnGlyProIleuPro	1432
QY	390	GAGACCACTGGGCGATTTTGGAGCAATGGTGGGAAACAGCGACGGCCACATGGTCAATG	449
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Db	1453	MetThrArgLeuGlnGluLysSerArgIleLysScyAspGlnTyrITrProAsnArgGly	1472
QY	510	ACCGAGACCTGTGGCTTATTCAGGTGACCCCTGTGGACACAGTGGACCTGGCCACATAC	569
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QY	570	ACGTGGGCACTCTTGCGACATCCCAAGAGTGGGTCCACAGAAACCGAGCATGGGTGAC	629
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Db	1513	PheGlnPheThrAlaITrProAspHisGlyValITrProGluTyrProThrProPheLeuAla	1532
QY	690	TTCTCTACAGCGGGTCAAGGCTGTCAACCCCTTAGACGACAGGGCCCATGTGGTGCATGC	749
Db	1533	PheLeuArgArgValLysThrCysAsnProProAspAlaGlyProIleValValHisCys	1552
QY	756	AGCGCGGCGCTGGGCGCACCGGCTCTCAATCGATGTGAATGCCATGTGGACGGAGTG	809
Db	1553	SerIleAlaLysAlaITrArgThrGlyCysPheIleValIleAspAlaMetLeuGlnArgIle	1572
QY	810	AAGACAGAAAGCGGTGACATCTTGGCCACAGTACCTGATGCATGCATCACAGAGAAC	869



OY 1530 CCAAGACAGCGGAGGATTCATTGATTCATCGCGCAGGTGCATTAAGACCAAGAGCAG 1589  
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 Db 1813 ProlysserGlyGluGlyPheIleAspPheIleGlyGlnValHisLysThrLysGluGln 1832  
 OY 1590 TTGGACAGGATGGGCGATACAGCGTGCATCGAGTGGCGGCGCGGCGGCGG 1649  
 |||||.....  
 Db 1833 PheGlyGlnAspGlyProIleSerValHisCysSerAlaGlyValGlyArgThrGlyVal 1852  
 OY 1650 TTCATCACTGAGCATGCTCCTGGAGCGCATGCGCTATGAGGGCGGTGCATGTTT 1709  
 |||||.....  
 Db 1853 PheIleThrIleSerIleValIleGlnIleuArgMetArgTyrGlyGlyValValAspIlePhe 1872  
 OY 1710 CAGACGGTGAAGACCCCTCGTACACAGCGTCTCGCATGGTGCACAGAGCAGCATAT 1769  
 |||||.....  
 Db 1873 GlnThrValLysMetIleuArgThrGlnArgProAlaMetValGlnThrGlnAspGlyTyr 1892  
 OY 1770 CAGGTGCTACCGGCGGCGCTGAGTACCTGCGACGTTTGACCATATGCAAG 1826  
 |||||.....  
 Db 1893 GlnPheCysTyrGlnAlaIleuGlnIleuGlySerPheAspHisTyrAlaThr 1911

RESULT 3

US-09-158-657-5  
 : Sequence 5, Application US/09158657  
 : Patent No. 6214564

GENERAL INFORMATION:

APPLICANT: RODAN, GIDEON A.  
 APPLICANT: SCHMIDT, AZRIEL  
 APPLICANT: RUTLEDGE, SU JANE  
 TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: J. MARK HAND - MERCK & CO., INC.  
 STREET: 126 E. LINCOLN AVE., P.O. BOX 2000  
 CITY: RAHWAY  
 STATE: NEW JERSEY  
 COUNTRY: USA  
 ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/158,657  
 FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/800,825  
 FILING DATE: 14-FEB-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HAND, J. MARK  
 REGISTRATION NUMBER: 36,545  
 REFERENCE/DOCKET NUMBER: 18992DA  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 732-594-3905  
 TELEFAX: 732-594-4720  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1911 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-158-657-5

Alignment Scores:

Pred. No.: 5,03e-240 Length: 1911  
 Score: 2880.00 Matches: 530  
 Percent Similarity: 94.32% Conservative: 35  
 Best Local Similarity: 88.48% Mismatches: 34  
 Query Match: 44.69% Indels: 0

DB:	4	Gaps:	0
US-09-743-492-1 (1-3467) x US-09-158-657-5 (1-1911)			
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Db 1313 HisProIleProIleValIleuMetArgIleAsnProIleThrProGlyMetLeuSer 1332	.....		
OY 90 CACCCACCCATCCCATCAGCCAGCTGGCGGCAACATGAGCGGCTCAAGCCAGAT 149	.....		
Db 1333 HisProIleProIleValIleuMetArgIleAsnProIleThrProGlyMetLeuSer 1352	.....		
OY 150 GGCCTCAAGTTCCTCCAGAGATGATGTCATGCAATGCCCTGGACACAGTTCACGTGGAG 209	.....		
Db 1333 SerLeuLysLeuSerGlnIleuTyrGlnIleuSerIleuSerProGlyGlnIleuThrProGly 1372	.....		
OY 210 AATCAACCTGAGAGTGAACAGCCCAAGAACCTGTATGCAATGTATGCTGCTAGCAG 269	.....		
Db 1373 HisSerAsnLeuGlnValAsnLysProLysAsnAlaGlyTyrAlaAsnValIleAlaTyrAsp 1392	.....		
OY 270 CACTCTGAGTCATCTTACCTTATGATGAGCGTCCCGGAGTGAATACATCAATGCC 329	.....		
Db 1393 HisSerArgValIleIleuGlnProIleGlnIleuMetGlySerAspTyrIleAsnAla 1412	.....		
OY 330 AACTATCATGATGCTTACCCGACAGAGATGCTTACATGCGCCAGCGGCGCTGCC 389	.....		
Db 1413 AsnTyrValAspGlyTyrArgArgGlnAsnAlaTyrIleAlaThrGlnGlyProLeuPro 1432	.....		
OY 390 GAGACATGGGGGATTTCTGGAGATGGTGGGAACAGCGGCGGACCTGCTGTCATG 449	.....		
Db 1433 GlnThrPheGlyAspPheThrArgMetValIleuGlnAlaArgSerAlaThrIleValMet 1452	.....		
OY 450 ATGACACGGCTGGAGAGAGTCCCGGGTAAATGTATGATGCTGAGCCAGCCCGCTGGC 509	.....		
Db 1453 MetThrArgLeuGlnIleuLysSerArgIleuLysCysAspGlnTyrTrpProAsnArgGly 1472	.....		
OY 510 ACCGAGACCTGTGGCTTATTCAGGTGAACCTGTGACACAGTGGAGCTGGCCATAC 569	.....		
Db 1473 ThrGlnThrTyrGlyPheIleGlnValThrLeuAspThrIleGlnIleuAlaThrPhe 1492	.....		
OY 570 ACTGTGGCACCCTTGCACCTCCACAGAGTGGCTGACGAGAACGAGAGCTGGTGG 629	.....		
Db 1493 CysValArgThrPheSerLeuHisLysAsnGlySerSerGlnLysArgGlnValArgGln 1512	.....		
OY 630 TTTCAGTTCATGGCTGGCCACAGACCATGAGTCTCTGAGTACCAACTCCCATCTGGCC 689	.....		
Db 1513 PheGlnPheThrAlaThrProAsnIleGlyValProGlyTyrProThrProPheLeuAla 1532	.....		
OY 690 TTTCATGACAGGGGTAAAGGCTGGCAACCCCTAGACGACAGGGCCATGAGTGCATGCC 749	.....		
Db 1533 PheLeuArgArgValLysThrCysAsnProProAsnAlaGlyProIleValValHisCys 1552	.....		
OY 750 AGCGGGCGTGGGGCGGACCGGCTTCATCGATGATGATGATGATGATGATGATGATG 809	.....		
Db 1553 SerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeuGlnArgGlyIle 1572	.....		
OY 810 AAGCAGAGAGAGAGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 869	.....		
Db 1573 LysProGlyLysThrValAspValTyrGlnHisValThrLeuMetArgSerGlnArgGln 1592	.....		
OY 870 TACATGTCGACAGCGAGAGACAGTACGTGTCATGCAATGAGCGGCTCTGGAGGCTGCC 929	.....		
Db 1593 TyrMetValGlnThrGlnAspGlnTyrGlnSerPheIleHisGlnAlaLeuGlnValVal 1612	.....		
OY 930 ACGTGGCGGCACACAGAGAGTGGCTGGCGGCAACCTGTATGCGCCATGACAGAGTGGCG 989	.....		
Db 1613 GlyCysGlyAsnThrGlnValProAlaArgSerLeuTyrAlaTyrIleGlnHisLeuAla 1632	.....		
OY 990 CAAGTGCCTCCAGGAGAGATGTGACCCGATGAGAGTGCATGATGATGATGATGATGATG 1049	.....		
Db 1633 GlnValGlnProGlyGlnHisValThrGlnIleuMetGlnLeuGlnPheLysArgLeuAlaAsn 1652	.....		
OY 1050 TCCAAGGCCCAACAGTCCCGCTTCAATCAGCGGCAACCTGCGCCTGCAACAAGTTCAAGAAC 1109	.....		



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Db      1653 SerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysLysPheLysAsn 1672
      1110 CGGCTGGTGAACATCATGCCCTACGAATTGACCCGCTGTCTGTGACAGCCCATCCGTGT 1169
      1673 ArgLeuValAsnIleMetProTyrGluSerThrArgValCysLeuGlnProIleArgGly 1692
      1170 GTGGAGGGCTCTACTACATCAATGCCAGCTTCTGTGATGTTATGACAGCAGAGAGGCC 1229
      1693 ValGlnGlySerAspTyrIleAsnAlaSerPheIleAspIlyTyrArgGlnGlnLysAla 1712
      1230 TACATAGCTACACAGGGGCTGTGGCAGAGACAGCAGAGACTTGGGGCCATGCTATGG 1289
      1713 TyrIleAlaThrGlnGlnProLeuAlaGluThrThrGlnAspPheThrPargMetLeuTyr 1732
      1290 GAGCACAATTCCACATCATCTCATCTGATCCAGCAAGCTTCGGAGATGGAGAGAGAGAAA 1349
      1733 GluAsnAsnSerThrIleValValMetLeuThrLysLeuArgGluMetGlyArgGlnLys 1752
      1350 TGGCACCAGTACTGGCCAGCAGAGCCGCTGTGCTGCTACCAAGTACTTGTGTGACCCG 1409
      1753 CysHisGlnIlyTyrProAlaGluArgSerAlaArgTyrGlnTyrPheValAlaAspPro 1772
      1410 ATGGCTGAGTACAAATGCCCGCATATCTGCGTGGAGTTCAGAGGTCCAGAGTCCCGCG 1469
      1773 MetAlaGluTyrAsnMetProGlnTyrIleLeuArgGlnPheLysValThrAspAlaArg 1792
      1470 GATGGCAGTCAAGACAATCCGCGAGTTCACAGTTCACAGATGCGCCAGAGAGGCGGTG 1529
      1793 AspGlyGlnSerArgThrValArgGlnPheGlnPheThrAspThrProGlnGlnGlyVal 1812
      1530 CCCAACAAGGCGAGGATTCATTGACTTATCGGCGAGGTGCATTAAGACCAAGAGCAG 1589
      1813 ProLysSerGlyGlnLysPheIleAspPheIleGlyAlaHisLysThrLysGlnGln 1832
      1590 TTGGACAGATGGGCTATACAGCGTGCATGAGTGCAGTGGCGTGGGCGCCACCGGGGTG 1649
      1833 PheGlnGlnAspIlyProIleSerValHisCysSerAlaGlyAlaGlyArgThrGlyVal 1852
      1650 TTCATCACTGTGAGCATGCTGTGAGCGCATGCGGTATGAGGGCGGTGTGCATGTTT 1709
      1853 PheIleThrLeuSerIleValIleuGluArgMetArgTyrGlnLysValAlaAspIlePhe 1872
      1710 CAGACCGTGAAGACCTGCTTACACAGCTTCTGCGCATGCTGCAGACAGAGAGACAGTAT 1769
      1873 GlnThrValLysMetLeuArgThrGlnArgProAlaMetValGlnThrGlnAspGlnTyr 1892
      1770 CAGCTGTGCTACCGTGGCGGCGGTGAGTACCTGCGCAGCTTGGACCATGGAACG 1826
      1893 GlnPheCysTyrGlnAlaAlaLeuGlnTyrLeuGlySerPheAspHisTyrAlaThr 1911

RESULT 4
PCT-US94-10166-5
: Sequence 5, Application PC/TUS9410166
: GENERAL INFORMATION:
: APPLICANT: RODAN, GIDEON A
: APPLICANT: SCHMIDT, AZRIEL
: APPLICANT: RUTLEDGE, SU JANE
: TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
: TITLE OF INVENTION: TYROSINE PHOSPHATASE
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: JOHN W. WALLEN III
: STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.
: CITY: RAHWAY
: STATE: NJ
: COUNTRY: USA
: ZIP: 07065
: COMPUTER READABLE FORM:
: MEDIUM TYPE: FLOPPY disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/10166
: FILING DATE: 09-SEPT-1994
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/122,032
: FILING DATE: 14-SEP-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: WALLEN, JOHN W III
: REGISTRATION NUMBER: 35403
: REFERENCE/DOCKET NUMBER: 18992
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 908-594-3905
: TELEFAX: 908-594-4720
: TELEX: 138825
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1911 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US94-10166-5

Alignment Scores:
Pred. No.: 5.03e-240 Length: 1911
Score: 2880.00 Matches: 530
Percent Similarity: 94.32% Conservative: 35
Best Local Similarity: 88.48% Mismatches: 34
Query Match: 44.69% Indels: 0
DB: 5 Gaps: 0

US-09-743-492-1 (1-3467) x PCT-US94-10166-5 (1-1911)
      30 CACTCTGCTGACCTGTGGAGATGCGGAGGCTCACTACACAGACCCAGGATGCGAGAC 89
      1313 HisProLysAspProValGluMetArgArgIleAsnPheGlnThrProGlnMetLeuSer 1332
      90 CACCCACCATCCCATCACCGACCTGGCGAGCAACAATCGAGGCGCTCAAGCCAAAGAT 149
      1333 HisProIleProIleAlaAspMetAlaGlnHisThrGlnArgLeuLysAlaAsnAsp 1352
      150 GCGCTCAAGTTCCTCCAGAGATGATGATCCATGACCTTGACAGCAGCTTACGTGGAG 209
      1353 SerLeuLysLeuSerGlnGlyTyrGluSerIleAspProGlnGlnPheThrProGln 1372
      210 AATTCAACCTGGAGGAGCAAGCCCAAGACCGGTATGCAATGATCGCTACGAC 269
      1373 HisSerAsnLeuGlnValAsnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAsp 1392
      270 CACTCTGAGTCACTCTTACCTGATCGATGGCGTCCCGGAGTGCATCATCAATGCC 329
      1393 HisSerArgValIleLeuGlnProIleGlnGlyIleMetGlySerAspTyrIleAsnAla 1412
      330 AACTACTCATGCTGCTACCCCAAGCAGAAATGCTCACTATCCGACGAGGCGCCCTGCC 389
      1413 AsnTyrValAspGlyTyrArgArgGlnAsnAlaIlyThrIleAlaThrGlnGlyProLeuPro 1432
      390 GAGACCATGGCGATTTCTGAGAAATGCTGGAGACGCGCAGCGCATGTTGTCATG 449
      1433 GluThrPheGlnAspPheThrPargMetValTyrGlnIleArgSerAlaThrIleValMet 1452
      450 ATGACAGCGCTGAGAGAGATCCCGGTAATAATGTGATCAGTACGACGCGCCGTGGC 509
      1453 MetThrArgLeuGlnGluLysSerArgIleLysCysAspGlnTyrTyrProAsnArgGly 1472
      510 ACCGAGACCTGTGGCTTATTCAGAGTACCCCTGTGGACACAGTGGAGCTGGCCACATAC 569
      1473 ThrGlnThrTyrGlnPheIleGlnValThrLeuLeuAspThrIleGlnLeuAlaThrPhe 1492
      570 ACTGTGGCAGCTTGGCAGTCCACAGAGTGGCGCTGAGTGAAGAGCTGAGCGTGGCGTAC 629
      1493 CysValArgThrPheSerLeuHisLysAsnGlySerSerGlnLysArgGlnValArgGln 1512

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QY 630 TTTCAGTTCAGGCTGCGCCAGACCATGAGTTCTGAGTACCCAACTCCATCTGCGC 689
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Db 1513 PheGlnPheThrAlaTrpProAspHisGlyVal1ProGluTyrProThrProPheLeuAla 1532
QY 630 TTTCACAGAGGGGTAAAGGCTGCAACCCCTAGACAGCAGGGCCCATGGTGTGCACTGC 749
    |||||
Db 1533 PheLeuAlaGlyVal1ThrGlySerHisAsnProProAspAlaGly1ProLeuVal1HisCys 1552
QY 750 AGCGCGGCGTGGCGCGCCAGCCGCTTCATCGTATGATGATGATGATGATGATGATGATG 809
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Db 1553 SerAlaGlyVal1GlyArgThrGlyCysPheLeuAla1LeuAspAlaMetLeuAlaGlyLe 1572
QY 810 AAGCAGAGAGAGCGGTGACATCTATGCGCAGCTGACCTGATGCGATGCGATGACAGAGA 869
    |||||
Db 1573 LysProGluTyrThrVal1AspVal1GlyHisVal1ThrLeuMetAlaGlySerGlnArgAsn 1592
QY 870 TACATGGTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 929
    |||||
Db 1593 TyrMetVal1GlnThrGluAspGlnTyrSerPheLeuHisGluAlaLeuLeuGluAlaVal 1612
QY 930 ACGTGGCGCCACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 989
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Db 1613 GlyCysGlyAsnThrGluVal1ProAlaArgSerLeuTyrAlaTyr1LeuGlnHisLeuAla 1632
QY 990 CAAGTCCCTCCAGGAGGAGAGTGTGAACCCCATGAGAGCTGAGTTCAAGTTGCTGGCCAGC 1049
    |||||
Db 1633 GlnVal1GlnProGlyGlnHisVal1ThrGlyMetGlnLeuGlnPheLysArgLeuAlaAsn 1652
QY 1050 TCCAGAGGCGCCACAGCTCCCGCTTCATCAGCGGCAACCTGCGCTGCAACAGTTCAAGAAC 1109
    |||||
Db 1653 SerLysAlaHis1ThrSer1ArgPheLeuSerAlaAsnLeuProCysLys1SerPheLysAsn 1672
QY 1110 CGGCTGTGTAACATCATGATCCCTACAGAAATGACCCGTGTGTCTGTCAGCCCATCCGTGT 1169
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Db 1673 ArgLeuVal1Asn1LeuMetProTyrGlnLeuSerThrArgVal1CysLeuGlnPro1LeuArgGly 1692
QY 1170 GTGAGGAGCTGTGATACATCATGATCCAGCTTCCTGATGATGATGATGATGATGATGATG 1229
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Db 1693 ValGlnGlySerAspTyr1LeuAsn1AspPheLeuAspGlyTyrArgGlnGlnLysAla 1712
QY 1230 TACATAGTACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1289
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Db 1713 Tyr1LeuAla1ThrGlnGly1ProLeuAlaGln1ThrGlnLysAspPhe1TrpArgMetLeuTyr 1732
QY 1290 GAGCACAATTCACCATCATGCTCATGCTGACCAAGCTTCGGAGAGTGGCGAGGAGAAA 1349
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Db 1733 GlnAsnAsnSerThr1LeuVal1MetLeuThrLysLeuArgGlnMetGlyArgGlnLys 1752
QY 1350 TGCCACCACTACGTCGCGCAGCAGAGCGCTGCTGCTACCACTACTTGTGTTGACCCG 1409
    |||||
Db 1753 CysHisGlnTyrTrpProAlaGlnArgSerAlaArgTyrGlnTyrPheVal1ValAspPro 1772
QY 1410 ATGGCTGATGATCAACATGAGCCCATGATATCCGCTGCTGATGATGATGATGATGATGATG 1469
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Db 1773 MetAlaGlnTyrAsnMetProGlnTyr1LeuLeuArgGlnPheLysVal1ThrAspAlaArg 1792
QY 1470 GATGGGAGTAAAGAGACATCCGAGCTTCAGTTCACAGACTGGCCAGAGAGCGCGTG 1529
    |||||
Db 1793 AspGlyGlnSerArgThrVal1ArgGlnPheGlnPheThrAspTyrProGlnGlnLysVal 1812
QY 1530 CCCAAGACAGCGAGGATTCATGACTTCATGCGGCAAGGTGCATTAAGACCAAGAGCAG 1589
    |||||
Db 1813 ProLysSerGlyGlnGlyPhe1LeuAspPhe1LeuGlnVal1HisLysThrLysGln 1832
QY 1590 TTTCGACAGGATGGGCGCTCATACGCTGACATGCTGCTGCGTGGCGCGCAGCGGGGTG 1649
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Db 1833 PheGlyGlnAspGlyPro1LeuSerVal1HisCysSerAlaGlyVal1GlyArgThr1Val 1852
QY 1650 TTTCATCACTTGAGCATGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1709
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Db 1853 Phe1LeuThrLeuSer1LeuVal1LeuGlnArgMetArgTyrGlnGlyVal1ValAsp1LeuPhe 1872

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QY 1710 CAGACCGTGAAGACCTGCGGTACACAGCGTCTGCGCATGCTGAGAGAGAGACCATAT 1769
    |||||
Db 1873 GlnThrVal1MetLeuThrArgThrGlnArgProAlaMetVal1GlnThrGlnAspGlyTyr 1892
QY 1770 CAGCTTGCTACCGTGGCGGCGCTGGAGTACCTGCGCAGCTTTGACCATATGCAACG 1826
    |||||
Db 1893 GlnPheCysTyrGlnAla1AlaLeuGlnTyrLeuGlySerPheAspHisTyrAlaThr 1911

RESULT 5
US-08-447-464-3
; Sequence 3, Application US/08447464
; Patent No. 5840842
; GENERAL INFORMATION:
; APPLICANT: Schlessinger, Joseph
; APPLICANT: van, Hai
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN
; TITLE OF INVENTION: PHOSPHOTYROSINE PHOSPHATASE-SIGMA
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,464
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/130,570
; FILING DATE: 01-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7683-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEO ID NO.: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1501 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-447-464-3

Alignment Scores:
Pred. No.: 1,73e-237 Length: 1501
Score: 2850.00 Matches: 523
Percent Similarity: 93.99% Conservative: 40
Best Local Similarity: 87.31% Mismatches: 36
Query Match: 44.23% Indels: 0
Gaps: 0

US-09-743-492-1 (1-3467) x US-08-447-464-3 (1-1501)
QY 30 CACTCTCTGACCGCTGGAGATGGGAGGAGCTCACTACAGACCCAGCTATGGAGAC 89
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Db 903 HisProLysAspProVal1GlnMetArgTyrGln1LeuAsn1PheGlnThrProGlyMetLeuSer 922
QY 90 CACCACCACTCCCATCATCAGCACTGGCGGAGCAACATCAGAGCGCTCAACCAACGAT 149
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Db 923 HisProPro1LeuPro1LeuThrAspMetAlaGlnHisMetGlnArgLeuLysAlaAsnAsp 942
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Db 943 SerLeuLysLeuSerGlnGluTyrGluSerIleAspProGlnGlnInpHeThrTrpGlu 962  
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Db 963 HisSerAsnLeuGlnAlaAsnLysProLysAsnArgTyrGlnAlaAsnValIleAlaTyrAsp 982  
QY 270 CACTTCGAGTACATCCCTTACCTCATGAGGCGCTCCCGGAGTGACTACATCAATGCC 329  
Db 983 HisSerArgValIleLeuGlnProLeuGlnGlyIleMetelYserAspTyrIleAsnAla 1002  
QY 330 AACTACATGATGGCTACCGCAAGACAGATGCTACATGCGCCACGAGGCCCGCTGCC 389  
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QY 390 GAGACATGGCGCATTTCTGAGAAATGGTGGAAACAGGCGACCGCATCTGGTATG 449  
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QY 570 ACGTGGCGGCTGGACCTCCACAGAGAGTGGCTCCAGTGAAGAGCTGAGCTGGCAG 629  
Db 1083 CysValArgThrPheSerLeuHisLysAsnGlySerSerLysArgGlnValAlaArgHis 1102  
QY 630 TTTCAGTTCATGGCTGGCCAGACACATGAGTTCCTGAGTACCACATCCATCTGGC 689  
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QY 690 TTCTCAAGACGGGTCAAGGCTCAACCCCTCAAGACGAGGCCCATGAGTGGTGCAC 749  
Db 1123 PheLeuAlaArgValLysThrCysAsnProProAsnPalGlyProValIleHisCys 1142  
QY 750 AGCGCGGCGCTGGCCGACCGGCTGCTCATGCTGATTCATGCGATGGAGCGATG 809  
Db 1143 SerAlaGlyValGlyArgThrGlyCysPheIleValIleAsnPalMetLeuGlnArgIle 1162  
QY 810 AACGACGAGAGAGCGGTGATCATTCAGCTGACCTGACATGGCATGACAGAGAAC 869  
Db 1163 ArgThrGlnLysThrValAspValTyrGlyHisValThrLeuMetArgSerGlnAlaAsn 1182  
QY 870 TACATGGTGAGAGGAGGACAGTACAGTGTTCATCCATGAGCGCTGAGAGCTGCC 929  
Db 1183 TyrMetValGlnThrGlnAspGlnTyrSerPheIleHisGlnAlaLeuGlnAlaVal 1202  
QY 930 ACGTGGCGGCGACAGAGGTGCTGCCCGCAACCTGTATGCCACATCCAGAACTGGGC 989  
Db 1203 GlyCysGlyAsnThrGlnValProAlaArgSerLeuTyrThrTyrIleGlnLysLeuAla 1222  
QY 990 CAAGTGGCTCCAGGGGAGTGTGACCGGCTGAGTGGAGTTCAGTTCAGTGGCGGAC 1049  
Db 1223 GlnValGlnProGlyGlnHisValThrGlyMetGlnLeuGlnPheLysArgLeuAlaSer 1242  
QY 1050 TCCAGAGCCACAGCTCCGCTTCATCAGCGCCACACCTGCTGCACAAAGTTCAGAAC 1109  
Db 1243 SerLysAlaHisThrSerArgPheIleThrAlaSerLeuProCysAsnLysPheLysAsn 1262  
QY 1110 CGGCTGGTGAACATCATGCCCTACGAATTCACCGCTGTGTGTCGACGCCATCCGTGT 1169  
Db 1263 ArgLeuValAsnIleLeuProTyrGlnSerArgValLysLeuGlnProIleArgGly 1282  
QY 1170 GTGGAGGCGCTGACTACATACATGCGAGTTCCTGGATGGTATGAGAGCGAAGGCC 1229  
Db 1283 ValGlnGlySerAspTyrIleAsnAlaSerPheIleAspGlyTyrArgGlnGlnValAla 1302  
QY 1230 TACATAGCTACAGAGGCGCTGCGCAGAGAGACCGAGAGCTTGGCGCATGTATGG 1289  
Db 1303 TyrIleAlaThrGlnGlnGlyProLeuAlaGlnThrThrGlnLysPheTrpArgAlaLeuTrp 1322

QY 1290 GAGCACAATTCACCATCATGTCATGTACCAAGCTTCGGGAGATGGCGAGGAGAAA 1349  
Db 1323 GlnAsnAsnSerThrIleValValMetLeuThrLysLeuArgGlnMetGlyArgGlnLys 1342  
QY 1350 TGCCACGACTACTGGCCAGAGAGAGCGCTGCTGCTGCTACAGAGTACTTGTGTGACCG 1409  
Db 1343 CysHisGlnTyrTrpProIleGlnArgSerAlaArgTyrGlnTyrPheValAlaAspPro 1362  
QY 1410 ATGGCTAGTACAAATGCCCCAGTATATCCCTGCTGAGTTCAGAGTTCACGAGATGCCCG 1469  
Db 1363 MetAlaGlnTyrAsnMetProGlnTyrIleLeuArgGlnPheLysValThrAspAlaArg 1382  
QY 1470 GATGGAGAGCAAGCAATCCCGGACTGTCATGCTCAAGCTGCAGACGCGAGCGGCTG 1529  
Db 1383 AspGlyIleSerArgThrValArgGlnPheGlnPheThrAspTyrProGlnGlnGlyAla 1402  
QY 1530 CCCAAGACAGCGGAGGATTCATTCATGCTGATCGGAGAGTGCATTAAGACCAAGAGCAG 1589  
Db 1403 ProLysSerGlyGlnGlyPheIleAspPheIleGlyGlnValHisLysThrLysGlnGln 1422  
QY 1590 TTTCGACAGATGGCGCTATTCACGCTGCTGACGTGCTGCGCTGGCGCGAGGCTG 1649  
Db 1423 PheGlyGlnAspGlyProIleSerValHisCysSerAlaGlyValGlyArgThrGlyVal 1442  
QY 1650 TTTCATCCTGACATGCTGCTGCTGAGCGCATGGCTATAGAGGCGCTGCTGACATGTT 1709  
Db 1443 PheIleThrLeuSerIleValLeuGlnArgMetArgTyrGlnGlyValIleAspIlePhe 1462  
QY 1710 CAGACCGTGAAGACCTGCTGCTACACAGCGTCTGCTGCTGCTGCTGCTGCTGCTGCT 1769  
Db 1463 GlnThrValLysValLeuArgThrGlnArgProAlaMetValGlnThrGlnAspGlnTyr 1482  
QY 1770 CAGCTGTCTACGCTGGCGCTGGAGTACCTGCGGACCTTTCACCACTATGCAAG 1826  
Db 1483 GlnPheCysPheGlnAlaIleAlaLeuGlnTyrLeuGlnTyrLeuGlnTyrLeuGlnTyr 1501

RESULT 6  
US-08-716-679-3  
Sequence 3, Application US/08716679  
Patent No. 5846800  
GENERAL INFORMATION:  
APPLICANT: Schlessler, Joseph  
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PROTEIN  
TITLE OF INVENTION: PHOSPHORYROSINE PHOSPHATASE-SIGMA  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Penile & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/716, 679  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/130, 570  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-043  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-866-9741

TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1501 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-716-679-3

Alignment Scores:  
 Pred. No.: 1,736-237 Length: 1501  
 Score: 2850.00 Matches: 523  
 Percent Similarity: 93.99% Conservative: 40  
 Best Local Similarity: 87.31% Mismatches: 36  
 Query Match: 44.23% Indels: 0  
 Gaps: 0

US-09-743-492-1 (1-3467) x US-08-716-679-3 (1-1501)

QY 30 CACTCTCTGACCTGTGGAGATGCGGAGGCTCAACTACCAAGCCCAAGTATGCCGAGAC 89  
 DB 903 HSProlYsAspProValIGluMetArGArgIleAsnPheGlnThrProGlyMetLeuSer 922  
 QY 90 CACCCACCATCCCATCAGCAGCTGGGGGACAAACATGAGCGCTCAAGCCAAACGAT 149  
 DB 923 HSProlProIleProIleThrAspMetAlaGluHisMetGluArgLeuLysAlaAsnAsp 942  
 QY 150 GGCCTCAAGTTTCCAGAGATGATGTCATGACCCCTGAGCAGAGATTCACGTTGAGGAG 209  
 DB 943 SerLeuLysLeuSerGlnIleuArgIleuSerIleAspProGlyGlnGlnIleuThrTrpGlu 962  
 QY 210 AATTCAACCTGGAGGTGAACAAGCCCAAGAACCGCTATGCCAATGCTACGCTACGAC 269  
 DB 963 HSProlAsnLeuGluAlaAsnLysProLysAsnArgTyrAlaAsnValIleAlaTyrAsp 982  
 QY 270 CACTCTGAGTATGCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 329  
 DB 968 HSProlAsnValIleLeuGlnIleuSerIleuGlnIleuMetGlySerAspTyrIleAsnAla 1002  
 QY 330 AACTCATCGATGCTTACCTGACGAGAGAGATGCTTACCTTACCTTACCTTACCTTACCT 389  
 DB 1003 AsnTyrValAspGlyTyrArgArgIleuAsnAlaTyrIleAlaThrGlnIleuProLeuPro 1022  
 QY 330 GAGACCATGGCGGATTTCTGAGAAATGCTGTGGAGAACGCGCAGCGCCACTGTGTCATG 449  
 DB 1023 GlnThrPheGlyAspPheThrArgMetValTyrGlnGlnArgSerAlaThrValIleMet 1042  
 QY 450 ATGACACGGCTGGAGAGAGATGCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 509  
 DB 1043 MetThrArgLeuGlnIleuLysSerArgValLysCysAspGlnTyrTrpProAsnArgGly 1062  
 QY 510 ACCGAGACCTGTGCTTATTCAGGTGACCTTGTGAGACACAGTGGAGAGTGGCCACATAC 569  
 DB 1063 ThrGlnThrTyrGlyPheIleGlnValIleuLeuAspThrMetGluLeuAlaThrPhe 1082  
 QY 570 ACTGTGGCAGCTTGGCAGCTCCACAGAGTGGCTCCAGTGAAGCGTGAAGCTGCTGACG 629  
 DB 1083 CysValArgTyrPheSerLeuHisLysAsnGlySerSerGlnLysArgGluValAlaArgHis 1102  
 QY 630 TTTCAGTTCATGCGCTGGCAGACCATGAGTTCCTGAGTACCAACCTCCATCCCTGGCGC 689  
 DB 1103 PheGlnPheThrAlaTrpProAsnHisGlyValAlaProGlnTyrProThrPheLeuAla 1122  
 QY 650 TTTCATGACGAGGTGAAGGCTGCAACCCCTGAGACAGGAGGCGCATGTGTCATGCTG 749  
 DB 1123 PheLeuArgArgValLysThrCysAsnProProAspAlaGlyProValValAlaHisCys 1142  
 QY 750 AGCGCGGCGTGGCGGCGACCGGCTTCATGCTGATGATGATGATGATGATGATGATGATG 809  
 DB 1143 SerAlaGlyValAlaGlyArgThrGlnLysPheIleValIleAspAlaMetLeuGlnIleuArg 1162  
 QY 810 AAGCAGGAGAGAGCGGTGACATCTATGCCACGTGACCTGATGATGATGATGATGATGATG 869

DB 1163 ArgThrGlnLysThrValAspValTyrGlnHisValThrLeuMetArgSerGlnArgAsn 1182  
 QY 870 TACATGGTCAGACGAGGAGACAGTACGTTTCATTCATGACGAGCGCTGGAGCGTGGC 929  
 DB 1183 TyrMetValGlnThrGlnLysPheGlnTyrSerPheIleHisGlnAlaLeuLeuGlnAlaVal 1202  
 QY 930 ACSTGGCGCCACACAGAGTGGCTGGCCGACACCTGTATGCCACATCCAGAACTGGCGC 989  
 DB 1203 GlnCysGlyAsnThrGlnValAlaProAlaArgSerLeuTyrThrTyrIleGlnLysLeuAla 1222  
 QY 990 CAAGTCCCTCCAGGAGGAGTGGAGCGGACCTGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1049  
 DB 1223 GlnValGlnProGlyGlnLysValIleuGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1242  
 QY 1050 TCCAAAGCCCAACAGCTCCCGCTTCATACAGCGCCACCTGCTGCAACAGTTCAGAAAC 1109  
 DB 1243 SerLysAlaHisThrSerArgPheIleThrAlaSerLeuProCysAsnLysPheLysAsn 1262  
 QY 1110 CGGCTGGTACATCATGCTTACGATTAATGACCCGTTGCTGTGACGCCATCCGCTGCT 1169  
 DB 1263 ArgLeuValAsnIleuLeuProTyrGlnSerSerArgValCysLeuGlnProIleArgGly 1282  
 QY 1170 GTGGAGGCTGTGACATCATGCTTACGATTAATGACCCGTTGCTGTGACGCCATCCGCTG 1229  
 DB 1283 ValGlnGlySerAspTyrIleAsnAlaSerPheIleAspGlyTyrArgGlnGlnLysAla 1302  
 QY 1230 TACATGATGATACAGAGGCGCTGTGAGAGAGACAGCAGAGCTTGTGGCATGTATG 1289  
 DB 1303 TyrIleAlaThrGlnIleuProLeuAlaGlnTyrThrGlnAspPheThrArgAlaLeuTrp 1322  
 QY 1290 GAGCACAATTCACATCATGCTTACGATTAATGACCCGTTGCTGTGAGCGAGAGAGAA 1349  
 DB 1323 GluAsnAsnSerThrIleValIleValMetLeuThrLysLeuArgGlnMetGlyArgGlnLys 1342  
 QY 1350 TGGCAGCAGTACCTGGCCAGCAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1409  
 DB 1343 CysHisGlnTyrTrpProAlaGlnIleuArgSerAlaArgTyrGlnTyrPheValAlaAspPro 1362  
 QY 1410 ATGCTGATGATACATGCTTACGATTAATGACCCGTTGCTGTGAGTTCAGGATGCCCG 1469  
 DB 1363 MetAlaGlnTyrAsnMetProGlnTyrIleLeuArgGlnPheLysValThrAspAlaArg 1382  
 QY 1470 GATGGCAGTCAAGCAATCCGCGCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 1529  
 DB 1383 AspGlyGlnSerArgThrValArgIleuGlnPheThrAspTyrProGlnGlnGlnAla 1402  
 QY 1530 CCCAAGACGCGGAGGAGTTCATGCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 1589  
 DB 1403 ProLysSerGlyGlnIleuLysPheIleAspPheIleGlnValHisLysThrLysGlnGln 1422  
 QY 1590 TTTCGACAGATGGCGCTTACGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 1649  
 DB 1423 PheGlyGlnAspGlyProIleSerValHisCysSerAlaGlyValGlnIleArgThrGlyVal 1442  
 QY 1650 TTTCATCTCTGAGCATGCTTCTGAGGCGCATGCGCTATGAGGCGGTGCTGCATGTTT 1709  
 DB 1443 PheIleThrLeuSerIleValLeuGlnIleuArgMetArgTyrGlnGlyValAlaAspIlePhe 1462  
 QY 1710 CAGACCGTGAAGCCCTGCTGACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1769  
 DB 1463 GlnThrValLysValLeuArgThrGlnArgProAlaMetValGlnIleuGlnLysPheGln 1482  
 QY 1770 CAGCTGTGCTACCGTGGCGGCTGAGTATGCTGAGGAGTTCGAGGAGTTCGAGGAGT 1826  
 DB 1483 GlnPheCysPheGlnAlaIleAlaLeuGlnIleuGlnLysSerPheAspHisTyrIleThr 1501

RESULT 7  
 US-08-036-210-13  
 Sequence 13, Application US/08036210  
 Patent No. 5585233  
 GENERAL INFORMATION:  
 APPLICANT: Moller, Niels P.H.  
 APPLICANT: Moller, Karin B.

APPLICANT: Ullrich, Axel  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08-036,210  
FILING DATE: 23-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistock, S. Leslie  
REGISTRATION NUMBER: 18, 872  
REFERENCE/DOCKET NUMBER: 7683-025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 289 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-036-210-13  
  
Alignment Scores:  
Pred. No.: 8, 01e-126 Length: 289  
Score: 1553.00 Matches: 289  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 24.10% Indels: 0  
Gaps: 0  
DB: 1  
  
US-09-743-492-1 (1-3467) x US-08-036-210-13 (1-289)  
QY 81 ATGCGAGACCCAGCCATCCCATCCAGCAGCAGCAGCAACATCGAGCGCTCAAA 140  
DB 1 MetArgAspHisProIleProIleThrAspLeuAlaAspAsnIleGluArgLeuLys 20  
QY 141 GCCAAGATGGCCTCAAGTCTCCAGAGATAGATCGATCGACCCCTGAGCAGATTG 200  
DB 21 AlaAsnAspGlyLeuLysPheSerGlnGluTyrGluSerIleAspProGlyGlnGlnIle 40  
QY 201 AGCTGGGAGAAATTCAACTCGAGGTGAGCAAGCCCAAGACCGCTATGCGATGTCATC 260  
DB 41 ThrTPrGlnAsnSerAsnLeuGluValAsnLysProLysAsnArgTyrIleAsnValIle 60  
QY 261 GCCTACGACCACTCTGAGATCATCTTACCTATGATGCGCTCCCGGAGATGACTAC 320  
DB 61 AlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyValProGlySerAspTyr 80  
QY 321 ATCAATGCCAATCTACTGATGGCTACCGCAGCAGCAATGCTTACATCGCCAGCAGGCG 380  
DB 81 IleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGly 100  
QY 381 CCCCTGCCGAGACCATGGGCGCATTTCTGGAGATGGTGTGGAAAGCGGACGGCCACT 440  
DB 101 ProLeuProGluThrMetGlyAspPheTPrArgMetValTPrGluGlnArgThrAlaThr 120  
QY 441 GTGGTCATGATGACAGCGCTGGAGGAGAAAGTCCGGGTAAAGTGATCATGATCTGGCCA 500  
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DB 121 ValValMetMetThrArgLeuGluGluLysSerArgValLysCysAspGlnTyrTrpPro 140  
QY 501 GCCCGTGGCAGCCAGACCTGTGGCTTATTCAGAGTACCTGTGGACACAGTGGAGCTG 560  
DB 141 AlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeuAspThrValGluLeu 160  
QY 561 GCCACATACACCTGTGGCAGCTTCGACATCCACAGAGTGGCTCCAGTGGAGAGCGTGAG 620  
DB 161 AlaThrTyrThrValArgThrPheAlaLeuHisLysSerIleYserGluLysArgGlu 180  
QY 621 CTGCGTCACTTCAGTTCATGAGCTGCGCTGCGCAGACCATGAGTCTCTGATACCACTGCC 680  
DB 181 LeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValProGluTyrProThrPro 200  
QY 681 ATCTGGGCTTCTTACGACGGGTCAAGGCTGCAACCCCTAGACGAGGCGCCATGTGTG 740  
DB 201 IleLeuAlaPheLeuArgValLysAlaCysAsnProLeuAspIleArgPrometVal 220  
QY 741 GTGCACTGCAGCGCGGCGGCGCGCCAGCGGCTGCTCATCGTGAATGATGCGCATGTG 800  
DB 221 ValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeu 240  
QY 801 GACCGATGAGCAGCAGAGAGAGCGTGGACATGATGCGCCAGCTGACCTGATCATGATCA 860  
DB 241 GluArgMetLysHisGluLysThrValAspIleTyrGlyHisValThrCysMetArgSer 280  
QY 861 CAGAGCACTACTAGTGTGTCAGACGAGCAGACCATGACGTGTTCATTCATGAGGCGTGTG 920  
DB 261 GlnArgAsnTyrMetValGlnThrGlnAspGlnTyrValPheIleHisGlnAlaLeuLeu 280  
QY 921 GAGGCTGCCACCTGCGGCCACACAGAG 947  
DB 281 GluAlaAlaThrCysGlyHisThrGlu 289  
  
RESULT 8  
US-08-449-609-13  
Sequence 13, Application US/08449609  
Patent No. 5952212  
GENERAL INFORMATION:  
APPLICANT: Moller, Niels P. H.  
APPLICANT: Moller, Karin B.  
APPLICANT: Ullrich, Axel  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,609  
FILING DATE: 24-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/036,210  
FILING DATE: 23-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistock, S. Leslie  
REGISTRATION NUMBER: 18, 872  
REFERENCE/DOCKET NUMBER: 7683-025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 13:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 289 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-449-609-13

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Alignment Scores:
Pred. No.:      8,01e-126      Length:      289
Score:          1553.00        Matches:      289
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     24.10%       Indels: 0
DB:              2            Gaps: 0

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US-09-743-492-1 (1-3467) x US-08-449-609-13 (1-289)

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QY 81 ATGCGAGACCAACCCATCCCATCAACGACCTGGCGGACACATCGAGCGCTCAAA 140
    |||||||
Db 1 MetArgAspHisProIleProIleThrAspLeuAlaAspAsnIleGluArgLeuLys 20

QY 141 GCCAAGCATGGCCCTCAATCTCCAGAGAGTATGATGCTCATGACCCTGGAGACAGATTTC 200
    |||||||
Db 21 AlaAsnAspGlyLeuLysPheSerGlnGluTyrGlnSerIleAspProGlyGlnGlnPhe 40

QY 201 ACGTGGAGAAATTCAAACCTGGAGGTGAACAAGCCCAAGAACCGCTATGCGAATGTCATC 260
    |||||||
Db 41 ThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArgTyrAlaAsnValIle 60

QY 261 GCCTACGACCACTCGAGTCATCCTTACCTGATGCGGCTCCCGGAGTACTAC 320
    |||||||
Db 61 AlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyValProGlySerAspTyr 80

QY 321 ATGCATGCCAATACATGATGATGCTACCGCAAGCAAGATGCTATAGTCCACCGACGGGC 380
    |||||||
Db 81 IleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleLeuThrGlnGly 100

QY 381 CCCCTGCCGAGACCATGGCGGATTCGTGAGAAATGCTGTGGAGACAGCGGCCACT 440
    |||||||
Db 101 ProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGluGlnArgThrAlaThr 120

QY 441 GTGCTCATGATGACACGGCTGGAGAGAAAGTCCCGGTAATAATGTGATCACTAGCGCCA 500
    |||||||
Db 121 ValValMetMetThrArgLeuGlnGluLysSerArgValLysCysAspGlnTyrTrpPro 140

QY 501 GCCCGTGGCAGCGAGACCTGTGGCTTATTCAGGTGACCCCTGTGGACACATGAGCTG 560
    |||||||
Db 141 AlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeuAspThrValGluLeu 160

QY 561 GCCACATGACACTGTGCGCACCTTGCACACTCCACAAGAGTGGCTCCAGTGAAGAGCTGAG 620
    |||||||
Db 161 AlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySerSerGluLysArgGlu 180

QY 621 CTGGCTGCAATTCAGTTTCATGGCTGGCCAGACACATGAGATTCTGAGTACCCAACTCCC 680
    |||||||
Db 181 LeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValArgProGluTyrProThrPro 200

QY 681 ATCTGGGCTTCCTTACACAGCGGTCAAGGCTCTGCAACCCCTTAGACGCGAGGCCCTGAGTG 740
    |||||||
Db 201 IleLeuAlaPheLeuArgValArgValLysAlaCysAsnProLeuAspAlaGlyProMetVal 220

QY 741 GTGCACTGACGCGGGGCTGGCGGCGACCGGCTTCATCGTGATGATGATGCCCTGTTG 800
    |||||||
Db 221 ValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleValIleAspIleMetLeu 240

QY 801 GAGCGGATGAAGCAAGCAAGAGCGGTGACATCTATGAGCCACCTGACCTGCATGCGATCA 860
    |||||||
Db 241-GluArgMetLysHisGluLysThrValAspIleTyrGlnLysValThrCysMetArgSer 260

QY 861 CAGAGGAATCTCATGTGTGCACAGAGGAGGACAGTACGTTTCATGCATGAGGCGCTGCTG 920
    |||||||
Db 261 GlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIleHisGluAlaLeuLeu 280

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QY 921 GAGCTGCCACGTGGCGGACACACAGAG 947
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Db 281 GluAlaAlaThrCysGlyHisThrGlu 289

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# RESULT 9

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US-08-015-985-3
; Sequence 3, Application US/08015985
; Patent No. 5538886
; GENERAL INFORMATION:
; APPLICANT: Schlessinger, Joseph
; APPLICANT: Sap, Jan M.
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
; TITLE OF INVENTION: PHOSPHATASE-ALPHA
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/015, 985
; FILING DATE: 10-FEB-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 793 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-015-985-3

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Alignment Scores:
Pred. No.:      1.65e-125      Length:      793
Score:          1552.00        Matches:      297
Percent Similarity: 67.69%    Conservative: 99
Best Local Similarity: 50.77% Mismatches: 183
Query Match:     24.08%       Indels: 6
DB:              1            Gaps: 3

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US-09-743-492-1 (1-3467) x US-08-015-985-3 (1-793)

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QY 84 CGAGACCAACCCATCCCATCAACGACCTGGCGGACACATCGAGCGCTCAAGCC 143
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Db 207 ArgLysTyrProProLeuProValAspLysLeuGluGlnGluIleAsnArgArgMetAla 226

QY 144 AACGATGGCCCTCAATCTCCAGAGATGATGCTCATGACGACCCCTGAGCAG--CAAGTTC 200
    |||
Db 227 AspAspAsnLysLeuPheArgGluGluPheAsnAlaLeuProAlaCysProIleGlnAla 246

QY 201 ACGTGGAGAAATTCAAACCTGGAGGTGAACAAGCCCAAGAACCGCTATGCGAATGTCATC 260
    |||
Db 247 ThrCysGluAlaAlaSerLysGluGluAsnLysGluLysAsnArgTyrValAsnIleLeu 266

QY 261 GCCTACGACCACTCGAGTCATCCTTACCTTATGATGCGGCTCCCGGAGTACTAC 320
    |||
Db 267 ProTyrAspHisSerArgValHisLeuThrProValGluGluValProAlaAspSerAspTyr 286

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[illegible]

```

Db      647  GlyspilrhtValGluLeuLysLysGluGluGluCysGluSerTyrThrValAlaGAsp 666
      |||::: ||| ||| ::|||:::
Qy      1449  TTCAGGTCACGGATGCCGGGATGGGACATGACAGGACATCCGGCAGTTCACGATTCACA 1508
      |||::: |||::: |||::: |||::: |||
Db      667  LeuLeuValThrAsnThrArGValuAnLysSerArGInLleArgGlnPheHisIshenHis 686
      |||::: |||::: |||::: |||::: |||
Qy      1509  GACTGGCCACAGACAGGGCGTGGCCCAACACAGCCGACGAGATTCATGATCACTCAATCCGACAG 1568
      |||::: |||::: |||::: |||::: |||
Db      687  GlyTrpProGluValGlyIleProSerAspGlyLysGlyMetLeuAsnIleLeuAla 706
      ||| ||| ::|||::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      1569  GTGCATTAAGAACCAAGAGACGATTGGACAGAGAGATGGGCGCTATCAGCTGCATCGACAGCTCT 1628
      ||| ||| ::|||::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      707  ValGlnLysGlnGlnGlnGlnSerGly--AsnHisProIleThrValHisIscysSerAla 725
      ||| ||| ::|||::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      1629  GCGCTGGGCGCGCACACCGCGGTGTTTCATCATCTGACATGCGATGCTGTCGAGCGCATCGGCTAT 1688
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      726  GlyValGlnAlaGlyThrGlyThrPheCysAlaLeuSerThrValLeuGlnAlaGlyAlaLysAla 745
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      1689  GAGGCGCGTGGTCGATGTTTCAGACCGGTGAGACCGTCCGTACACAGCGCTCCGCCATG 1748
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db      746  GluGlyIleLeuAspValPheGlnThrValLysSerLeuArgLeuGlnAlaGlyProHisMet 765
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Qy      1749  GTGACAGACAGAGACGACGTATCAGCTGCTGCTACCGTGGCGCCCTGGAGACTCGGCGACG 1808
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db      766  ValGlnThrLeuGlnGlnGlyIleGluPheCysTyrLysValValGlnGlnIleThrLeuAspAla 785
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      1809  TTTGACCACATATGCA 1823
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      786  PheSerAspTyrAla 790
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
US-08-015-985-1
Sequence 1, Application US/08015985
Patent No. 5538886
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Sap, Jan M.
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-ALPHA
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/015,985
FILING DATE: 10-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-015-985-1

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1  COUNTRY: USA
2  ZIP: 07065-0900
3
4  COMPUTER READABLE FORM:
5  MEDIUM TYPE: floppy disk
6  COMPUTER: IBM PC compatible
7  OPERATING SYSTEM: PC-DOS/MS-DOS
8  SOFTWARE: PatentIn Release #1.0, V
9  CURRENT APPLICATION DATA:
10 APPLICATION NUMBER: US/08/348,006B-1
11 FILING DATE:
12
13 CLASSIFICATION: 514
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: US 08/122,032
16 FILING DATE: 14-SEP-1993
17
18 ATTORNEY/AGENT INFORMATION:
19 NAME: HAND, J., MARK
20 REGISTRATION NUMBER: 36,545
21 REFERENCE/DOCKET NUMBER: 189921A
22
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: 908-594-3905
25 TELEFAX: 908-594-4720
26
27 INFORMATION FOR SEQ ID NO: 7:
28
29 SEQUENCE CHARACTERISTICS:
30
31 LENGTH: 699 amino acids
32 TYPE: amino acid
33 STRANDEDNESS: single
34 TOPOLOGY: linear
35
36 MOLECULE TYPE: peptide
37
38 US-08-348-006B-7

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Alignment Scores:	
Pred. NO.:	2,169,114
Score:	143.00
Percent Similarity:	64.49%
Best Local Similarity:	47.07%
Query Match:	22.08%
DB:	1
	Gaps: 4
	Length: 699
	Matches: 231
	Conservative: 104
	Mismatches: 102
	Indels: 10

US-09-743-492-1 (1-3467) x US-08-348-006B-7 (1-699)

QY	60	CTCAACATCCAGACGCCAGGATGACGAGACACCAACCCATGCCATCCACCAACGCCAGCTGGGG	113
Db	101	LeuSerArgSerProSerGlyProLysLysPhePheProIleProValGluHisIleGlu	120
QY	120	GACAACATCGAGCGCCTCAAGGCCAACGATGGCCTCAAGTTCTCCAGAGATATGATGCC	179
Db	121	GluGluIleArgValArgSerAlaAspScylsArgPheArgGluIleuPheAsnSer	140
QY	180	ATGCACCCCTGCACG---CAGTTCACGTGGGAGAGATTTCAACACTGGAGGTGAACAAGCCC	236
Db	141	LeuProSerGlyHisIleGlnGlyThrPheGluIleuAlaAsnLysGluGluAsnArgGlu	160
QY	237	AGAAGACGCTATGGCATGTCATACGCGCTACAGACCACCTCGAGTCAATCCTTACCTATAC	296
Db	161	LysAsnArgTyrProAsnIleLeuProAsnAspHisScylsArgValIleLeuSerGluVal	180
QY	297	GATGGCCTCCCCGGGAGTACTATCATCAATGCCAACTACATCGATGGCTACCGCAACGAG	356
Db	181	AspIlyIleProCysSerAspTyrIleAsnAlaSerTyrIleAspGlyTyrLysGluLys	200
QY	357	AATGCCATACATCGGCACGAGGGGCCCCCTCCCGAGACCATGGGCGGATTTCTGTGCAATAG	416
Db	201	AsnLysPheIleAlaIleAlaGlnGlyProLysGlnGluThrValAsnAspPheTrpMet	220
QY	417	GTTGGGGAACAGCGCACGGCCACTGTGTGTCATGATGATGACAGCGGTGAGGAAGATCCGG	476
Db	221	ValTrpCysGlnArgSerAlaThrIleValaMetLeuThrAsnLeuLysGluArgLysGlu	240
QY	477	GTAAGAATGTATCGATCGTCGGCCACCGCCGGGACGACGAGACCATCGTGCGCTTATTCAGGG	536
Db	241	GluLysCysTyrGlnTyrTrpProAspGlnGlyCysTrpThrTyrGlnLysIleArgVal	260
QY	537	ACCCTGTTGGACACATGAGGAGGTGGCCACATACACTGTGTGGCACCTTGGCACTCCAC---	593

D	261	CysValGluAspCysValValLeuValAspTyrThrThrIleArgLysPheCysIleHisPro	280
Q	594	-----AAGAGTGGCTCCAGTGGAGAGCGAGATCCGTCAGTTTCAGTTTCAGTTGGCTGG	647
D	281	GlnLeuProAspSerCysLysLysAlaProAlaProGluLeuValSerGlnLeuHisIshenThrTrp	300
Q	648	CCAGACCATGGAGTTCCTGTAGTACCCAACTCCCATCTGGCTTCCTACAGACGGGTCAAG	707
D	301	ProAspPheGlyValProPheThrProIleGlyMetLeuLysPheLeuLysValLys	320
Q	708	GGCTGCACACCCCTCAGACGGAGGGCCCATGGTGTGTACTGAGAGGGGGGTGGGGCC	767
D	321	ThrLeuAsnProSerHisAlaGlyProIleValValHisCysSerAlaGlyValGlyArg	340
Q	768	ACCGGCTGGCTTCATCGTGGATTGATGGCATTTGGATGGAGCGGATACAGACAGAAAGCGTGG	827
D	341	ThrIleYthrPheIleValIleAspAlaMetLeaPheMetIleHisSerGluGlnLysVal	360
Q	828	GACATCTATGGCCACGTGACCTCATGCGATCCACAGAGGAACTACATGGTGTGACAGCGAG	887
D	361	AspAlaPheGluPheValSerArgIleArgAsnGlnArgProGlnMetValGlnThrAsp	380
Q	888	GACCACTAGCTGTTCATTCATGAGGGCGTGTGGAGCGGTCCACGTGGGGCCACACAGAG	947
D	381	ValGlnTyrThrPheIleTyrGlnAlaLeuLeuGlnTyrTyrLeuTyrGlyAspPheGlu	400
Q	948	GTGGCTCCCGCCCAACCTGTATGCCCAATCCCAACAGCTGGGCGCAAGTGGCTCCAGGGAG	1007
D	401	LeuAspValSerSerLeuGluArgHisLeuGlnThrLeuHisSerThrAlaThrHisPhe	420
Q	1008	AGTGTGACCCGCAATGAGAGCGTGCAGTTCAAGTTGTCTGGCAGCTCCAGAGCCCAAGCTCC	1067
D	421	AspLysIleGlyLeuGluGlnGluPheArgLysLeuThrAsnValArgIleMetLysGlu	440
Q	1068	CGCTTCATCAGCGCCCAACTGCTCCCTGCACAACTTCAGAACCGCGCTGTGAATCATG	1127
D	441	AsnMetArgThrGlyAsnLeuProAlaAsnMetLysAlaArgValIleGlnIleIle	460
Q	1128	CCCTACCAATTGACCCGTGTGTGTGTGCAGACCCATCCCGTGTGTGTGAGGGCGTCTGACAC	1187
D	461	ProTyrAspPheAsnArgValIleLeuSerMetLysArgGlyGlnGlnPheThrAspTyr	480
Q	1188	ATCATATCCAGATCCCTCGATGTGTATAGACAGACAAAGCCCTACATAGCTACACAGGG	1247
D	481	IleAsnIleSerPheIleAspGlyTyrArgGlnLysAspTyrPheMetAlaThrGlnGly	500
Q	1248	CTTGTGGCAGAGACCCAGACCTTGTGGCGCATGTGGGACACAAATTCACCATC	1307
D	501	ProLeuIleHisThrValGlnAspPheThrArgMetValTyrGlnTyrLysSerHisThr	520
Q	1308	ATCTCATCTGTGCACCAAGCTTGGGAGATGGGAGAGGAATAATGCCACCACTAGTGGCCA	1367
D	521	IleValMetLeuThrIleGlnValGlnGlnArgGluGlnAspLysCysTyrGlnTyrTrpPro	540
Q	1368	GCAAGAGCGCTGTGGCTCCATCCAGTACTTGTGTGTGAGCCCATGGATGGATGACAAATG	1427
D	541	ThrIleuLyservaIleThrHisGlyAspIleThrIleGlnIleLysSerIAspThrIleuser	560
Q	1428	CCCCAGTATATCCGTGCGTGAATTCAGATGACG-----GATGCCCGGAT	1472
D	561	GluAlaIleSerValArgAspPheLeuValThrPheLysGlnProLeuAlaArgGlnGlu	580
Q	1473	GGGAGTGCAGAGACATCCGGCGATTCACAGTTCACAGACTGGCCAGAGAGGGGTGGCC	1532
D	581	GluIleValArgMetValArgGlnPheHisPheHisGlyTyrTrpGlnValaIleTyrPro	600
Q	1533	AAGACAGCGGAGGATCATGTGATTCATCCGGGAGGTGCATCAAGCAAGGAGGAGTTT	1592
D	601	AlaGluTyrLysGlyMetIleAspLeuIleAlaIleValaGlnLysGlnGlnGlnIleThr	620
Q	1593	GGACAGAGTGGGCTTATCAGATGACATGCTGCTGGCGTGGCGGACCGGGGTGTTTC	1652

Db 621 Gly---AsnHisProIleTherValHisCysSerAlaGlyAlaGlyArgThrclYThrPhe 639

QY 1653 ATCACTGTAGAGATGCTCTGTGAGGCGATGCGCTATGAGGGCGGTGCACATGTTTTCAG 1712

Db 640 IleAlaIleSerAsnIleLeuGlnIarGValValSalGluGlyLeuLeuAspValPheGln 659

QY 1713 ACCGTGAAGACCCCTGCTGATACAGCGCTGCTGCCATGCTGTCACAGAGACCATATCAG 1772

Db 660 AlaValIysSerLeuAlaGlnIarGProHisMetValGlnThrLeuGlnGlnTyGln 679

QY 1773 CTGTCTACCGTGGCGCCCTGTGATACCTGCGACGCTTGTACCATATGCA 1823

Db 680 PheCysTyIysValValGlnAspPheIleAspIlePheSerAspTyIa 696

RESULT 12

US-08-800-825A-7

: Sequence 7, Application US/08800825A

: Patent No. 5866397

: GENERAL INFORMATION:

: APPLICANT: RODAN, GIDEON A.

: APPLICANT: SCHMIDT, AZRIEL

: APPLICANT: RUTLEDGE, SU JANE

: TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN

: TITLE OF INVENTION: TYROSINE PHOSPHATASE

: NUMBER OF SEQUENCES: 7

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: J. MARK HAND - MERCK & CO., INC.

: STREET: 126 E. LINCOLN AVE., P.O. BOX 2000

: CITY: RAHWAY

: STATE: NEW JERSEY

: COUNTRY: USA

: ZIP: 07065-0900

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: PatentIn Release #1.0, Version #1.30

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/800, 825A

: FILING DATE: 14-FEB-1997

: CLASSIFICATION: 435

: ATTORNEY/AGENT INFORMATION:

: NAME: HAND, J. MARK

: REGISTRATION NUMBER: 36,545

: REFERENCE/DOCKET NUMBER: 189922DA

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 732-594-3905

: TELEFAX: 732-594-4720

: INFORMATION FOR SEQ ID NO: 7:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 699 amino acids

: TYPE: amino acid

: STRANDEDNESS: single

: TOPOLOGY: linear

: MOLECULE TYPE: peptide

US-08-800-825A-7

Alignment Scores:

Pred. No.: 2.16e-114 Length: 699

Score: 1423.00 Matches: 281

Percent Similarity: 64.49% Conservative: 104

Best Local Similarity: 47.07% Mismatches: 202

Query Match: 22.08% Indels: 10

DB: 2 Gaps: 4

US-09-743-492-1 (1-3467) x US-08-800-825A-7 (1-699)

QY 60 CTCACATCCAGACCCAGTATGAGAGACCCACCCATCCCATGACCGACCTGGCG 119

Db 101 LeuSerArgSerProSerGlyProlYsLysPhePheProIleProValGlnIleuGln 120

QY 120 GACAAATCGAGCGGCTCTAAAGCCACAGATGGCTTCAAGTTCTCCAGAGAGTAGTCC 179

Db 121 GluIuIleIarGValIarGSerAlaAspAspCysLysArgPheArgGluIuIleAsnSer 140

QY 180 ATGACCCCTGAGACAG---CAGTTCACTGGAGAAATTCACCACTGGAGTGAACAGCCC 236

Db 141 LeuProSerGlyHisIleGlnIlyThrPheGluIleuAlaAsnLysLysIuIuAsnArgGlu 160

QY 237 AAGAACCGTTATGACCATGCTACGCGCTGACACACCACTGCGATGCTTACCTTATC 296

Db 161 LysAsnArgTyIProAsnIleLeuProAsnAspHisCysArgValIleLeuSerGlnVal 180

QY 297 GATGGCGTCCCGGGAGTGCATGATGCAATGCAATGCAATGATGATGCGTACCGCAAGCAG 356

Db 181 AspGlyIleProCysSerAspTyIleAsnAlaSerTyIleAspIlyTyIysGluLys 200

QY 357 AATGCTCATGCGCCACAGCGGCGCCCTGCGCGAGACCATGCGGCGCATTTGTGAGAAAG 416

Db 201 AsnLysPheIleAlaIleGlnIlyProLysGlnIuIuThrValAsnAspPheThrArgMet 220

QY 417 GTGTGGAGACAGCGACGCGCCACTGTGATGATGACACAGCGCTGGAGAGATCCCGG 476

Db 221 ValTrpGluGlnArgSerAlaThrIleValMetLeuThrAsnLeuLysGluArgLysGlu 240

QY 477 GTAAATGTGATCAGTACG 536

Db 241 GluLysCysTyIyGlnTyIyTrpProAspGlnGlyCysTrpThrTyIyGlnIleArgVal 260

QY 537 ACCCTGTGGACACAGTGGAGCGTGGCGCCATGATGATGATGATGATGATGATGATGATGAT 593

Db 261 CysValGlnAspCysValIleuValAspTyIyThrIleArgLysPheCysIleHisPro 280

QY 594 -----AAGAGTGGCTCCAGTGAAGAGCGTGGCGCGCGCGCGCGCGCGCGCGCGCG 647

Db 281 GlnLeuProAspSerCysLysLysAlaProArgLeuValIleSerGlnIleuHisPheThr 300

QY 648 CCAAGCAATGAGATGCTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 707

Db 301 ProlAspPheGlyValProlPheThrProIleGlyMetLeuLysPheLeuLysLysValLys 320

QY 708 GCGTCACACCCCTGATGACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 767

Db 321 ThrLeuAsnProSerHisIleAlaIleProIleValHisCysSerAlaGlyValGlnArg 340

QY 768 ACCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 827

Db 341 ThrGlyThrPheIleValIleAspIleMetAspMetIleHisSerGlnIuLysVal 360

QY 828 GACATCTATGCG 887

Db 361 AspValPheGluPheValSerArgIleArgAsnGlnIarGProGlnMetValGlnThrAsp 380

QY 888 GACAGTACGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 947

Db 381 ValGlnIyThrPheIleTyIeGlnAlaLeuLeuGluTyIyTyIeLeuTyIyLysPheArg 400

QY 948 GTGCTGCG 1007

Db 401 LeuAspValSerSerLeuGlnIarGlnHisLeuGlnIyThrIleuHisSerThrAlaThrHisPhe 420

QY 1008 AGTGTGACCGCGCATGAGCGTGCATGATGATGATGATGATGATGATGATGATGATGATGAT 1067

Db 421 AspLysIleGlyLeuGlnIuGlnIleuPheArgLysLeuThrAsnValArgIleMetLysGlu 440

QY 1068 CGCTTCATGACG 1127

Db 441 AsnMetArgThrGlyAsnLeuProAlaAsnMetLysLysAlaArgValIleGlnIleIle 460

QY 1128 CCGTACGAATTGACCGGT 1187

Db 461 ProTyIarSpPheAsnArgValIleLeuSerMetLysArgGlyGlnIuIyPheThrAspTyI 480

QY 1188 ATCAATGCGAGTCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1247

Db 481 IleAsnAlaSerPheIleAspIlyTyIyTrArgLysAspTyIyPheMetAlaThrGlnGly 500

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OY 1248 CCTGTGCAGAGACGACCCGAGACTTCTGTGGCGATGCTATGGAGGACCAATTCACCATC 1307
      ||||||| : : ||||||| ||||||| ||||||| |||
Db 501 ProLeuAlaHisThrValGlnAspPheTrpAlaMetValTrpIlePlySerHisThr 520
OY 1308 ATGCTCATGTGCACCAAGCTTCGGAGATGGCGAGGAGAAATGCCACAGTACTGCCCA 1367
      ||||||| : : ||||||| ||||||| ||||||| |||
Db 521 lIeValMetLeuThrGlnValGlnGlnValArgGlnAspIleGlnIlePlyTrpPro 540
OY 1368 GCAGAGCGCTGTGCTGCTACACAGTACTTGTGTTGACCCCGATGGCTGACCAACATG 1427
      ||| ||| : : ||| : : ||| : : |||
Db 541 ThrGlnGlySerValThrHisGlyAspIleThrIleGlnIlePlySerAspThrLeuSer 560
OY 1428 CCGCAGTATATCTCGGTGAGTGCACAGTCACG-----GATGCCCGCGAT 1472
      : : ||| : : ||| |||||
Db 561 GluAlaIleSerValAlaTrpAspPheLeuValThrPheIleGlnIleProLeuAlaArgGlnIu 580
OY 1473 GGGCAGTCAAGACAAATCCGCGAGTTCAGATTCCACAGACTGGCCAGAGCGAGTGGCC 1532
      ||| ||| : : ||||||| ||| ||||||| |||
Db 581 GlnGlnValArgMetValArgGlnPheHisGlyTrpProGlnValGlyIlePro 600
OY 1533 AAGACAGCGGAGGATTCATGATTCATTCGCGGAGGTGCATAAAGACCAAGAGCATTT 1592
      ||| : : ||| ||||| ||| ||| : : |||
Db 601 AlaGlnGlyIleSerValIleAspPheIleAlaAlaValGlnIleGlnIleGlnIleThr 620
OY 1593 GGCAGAGATGGGCTATTCACGCGTGCACGTGAGTGTGGCGCGCGCGGCGGTTC 1652
      ||| : : ||||||| ||||||| ||||||| |||
Db 621 Gly--AsnHisProIleThrValHisCysSerIleGlyAlaGlyIleThrGlyIlePhe 639
OY 1653 ATCACTGTAGCATGCTGCTGCGAGCGCATGCGCTATGAGGCGGTGCTGCACATGTTTCA 1712
      ||| ||||| : : ||||||| : : ||| : : |||
Db 640 lIeAlaLeuSerAsnIleLeuGlnArgValIleGlyAlaGlnIleLeuIleAspValIlePheGln 659
OY 1713 ACCGTGAAGACCTGCTGCTACACAGCGTCTGCGATGTCGACAGACAGACAGATTCAG 1772
      ||||||| : : ||||| ||||||| ||||||| |||
Db 660 AlaValIleSerLeuArgIleGlnArgProHisMetValGlnThrLeuGlnIleGlyIle 679
OY 1773 CTGTGCTACCGTGGCGCGCTGAGTACCTGCGAGCTTTGACACATATGA 1823
      ||||||| : : ||| : : ||| |||||
Db 680 pheCysTyrIleValValGlnAspPheIleAspIlePheSerAspTyrAla 696

RESULT 13
US-09-158-657-7
: Sequence 7, Application US/09158657
: Patent No. 6214564
: GENERAL INFORMATION:
: APPLICANT: RODAN, GIDEON A.
: APPLICANT: SCHMIDT, AZRIEL
: APPLICANT: RUTLEDGE, SU JANE
: TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
: STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
: CITY: RAHWAY
: STATE: NEW JERSEY
: COUNTRY: USA
: ZIP: 07065-0900
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/158,657
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/800, 825
: FILING DATE: 14-FEB-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: HAND, J. MARK

```

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: REGISTRATION NUMBER: 36,545
: REFERENCE/DOCKET NUMBER: 18992DA
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 732-594-3905
: TELEFAX: 732-594-4720
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 699 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-09-158-657-7

Alignment Scores:
Pred. No.: 2,16e-114 Length: 699
Score: 1423.00 Matches: 281
Percent Similarity: 64.49% Conservative: 104
Best Local Similarity: 47.07% Mismatches: 202
Query Match: 22,088 Indels: 10
DB: Gaps: 4

US-09-743-492-1 (1-3467) x US-09-158-657-7 (1-699)
OY 60 CTCACTACACAGACCCAGGTATGCGAGACCCACCCATCCCATCAGCACTGGCG 119
      ||| : : ||| : : ||| ||||||| : : |||
Db 101 LeuSerArgSerProSerGlyProLysLysPhePheTrpIleProValGlnHisLeuGln 120
OY 120 GACCAATCGAGCGGCTCAAGACCAAGATGCGCTCAAGTTCGCCAGAGTATGATGTC 179
      : : ||| ||| : : ||| : : ||| |||
Db 121 GlnGlnIleArgValArgSerAlaAspAspCysLysArgPheArgGlnGlnIlePheAsnSer 140
OY 180 ATGACCCCTGGACAG---CAGTTCACGTGGGAGAAATTCAAACCTGGAAGTGAACAGCCC 236
      : : ||| ||| ||| : : ||| : : ||| |||
Db 141 LeuProSerGlyHisIleGlnGlyThrPheGlnIleValAsnIleGlnIleAsnArgGln 160
OY 237 AAGACCGCATGCGAATGCATGCATGCGCTACGACCACTGCTGAGTCATCTCATTC 296
      ||||||| ||| : : ||| ||||||| ||| : : |||
Db 161 LysAsnArgTyrProAsnIleLeuProAsnAspHisCysArgValIleLeuSerGlnVal 180
OY 297 GATGGCGTCCCGGAGGTGACTACATCAATGCAATGCAATGCAATGCAATGCAATGCAATG 356
      ||||||| : : ||| ||||||| ||||||| ||| : : |||
Db 181 AspGlyIleProCysSerAspTyrIleAsnAlaSerTyrIleAspGlyTyrIleGlnLys 200
OY 357 AATGCTATACATGCGACGCGAGGCGCGCTGCGCGAGACCATGCGCATTTCTGAGAAATG 416
      ||| : : ||||| ||||||| ||||||| ||| : : |||
Db 201 AsnLysPheIleAlaGlnGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIle 220
OY 417 GTGTGGGACAGCGGACGCGCACTGTGTGTCATGATGACAGCGCTGGAGGAAAGTCCCG 476
      ||||||| ||| : : ||||||| : : ||| : : |||
Db 221 ValTrpGlnIleArgSerAlaThrIleValMetLeuThrAsnLeuGlnIleGlnIleGln 240
OY 477 GTAAATGTGATGATGACTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 536
      ||||||| ||||||| ||||||| ||| ||| ||| ||| ||| |||
Db 241 GlnLysCysTyrGlnIleTrpProAspGlnIleCysTrpThrIleGlnIleValGlnVal 260
OY 537 ACCCTGTGGACACAGTGAAGTGGCGACATACACTGTGGCGCACTTGGCACTCCAC--- 593
      : : ||| ||| ||| ||||||| ||| ||| : : |||
Db 261 CysValAlaAspCysValValIleValAspTyrIleLeuGlyPheCysIleHisPro 280
OY 594 -----AAGAGTGGCTCCCACTGAGAAAGCGTGAAGCTGCGTCACTTGAAGTTCAG 647
      : : ||| ||| : : ||| : : ||| : : |||
Db 281 GlnLeuProAspSerCysLysAlaProArgLeuValSerGlnIleHisIlePheThrSerTrp 300
OY 648 CCAGACCATGAGTCTCTGTGATGACCCACATCCCATCTGCGCTTGCAGAGGCGTCAAG 707
      ||||||| ||||||| ||| : : ||| ||||||| : : |||
Db 301 ProAspPheGlyValAlaProPheThrProIleGlyMetLeuLysPheLeuLysValLys 320
OY 708 GCGTGAACCCCTAGACGAGGCGCCATGTTGTCACATGCAAGCGCGGCGGTGGCGCG 767
      ||||||| ||||||| : : ||| : : ||| : : |||
Db 321 ThrLeuAsnProSerHisIleGlyProIleValIleHisCysSerAlaGlyValGlyArg 340
OY 768 ACCGCTGCTCATCTGCTGATGATGCGATGTTGAGACGCGATGAAGACAGGAGCGTG 827

```

[illegible]



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GenCore version 5.1.3  
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# OM protein - protein search, using sw model

Run on: January 17, 2003, 09:11:01 : Search time 16 Seconds  
(without alignments)  
72.101 Million cell updates/sec

Title: US-09-743-492-4  
Perfect score: 65  
Sequence: 1 VVHCSAGVGRG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

PIR-73:\*  
1: pirl:\*  
2: pirl:\*  
3: pirl:\*  
4: pirl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	198	2 T27722	hypothetical prote
2	65	100.0	256	2 A40169	protein-tyrosine-p
3	65	100.0	398	2 I56540	protein-tyrosine-p
4	65	100.0	483	2 T25992	hypothetical prote
5	65	100.0	582	2 A57068	protein-tyrosine-p
6	65	100.0	583	2 S17671	protein-tyrosine-p
7	65	100.0	699	2 JC6132	protein-tyrosine-p
8	65	100.0	700	2 SI2053	protein-tyrosine-p
9	65	100.0	796	1 JC1285	protein-tyrosine-p
10	65	100.0	802	1 A36065	protein-tyrosine-p
11	65	100.0	829	1 A47373	protein-tyrosine-p
12	65	100.0	1187	1 JC4155	protein-tyrosine-p
13	65	100.0	1189	1 JC2366	protein-tyrosine-p
14	65	100.0	1200	2 T43148	probable protein-t
15	65	100.0	1237	2 A54080	protein-tyrosine-p
16	65	100.0	1262	1 B48758	protein-tyrosine-p
17	65	100.0	1273	1 TDRFLT	leukocyte common a
18	65	100.0	1290	2 A56493	leukocyte common a
19	65	100.0	1291	1 A28334	protein-tyrosine-p
20	65	100.0	1301	1 A41622	protein-tyrosine-p
21	65	100.0	1304	1 A46546	leukocyte common a
22	65	100.0	1422	2 T42636	probable protein-t
23	65	100.0	1437	2 T31093	protein-tyrosine-p
24	65	100.0	1496	1 A48758	protein-tyrosine-p
25	65	100.0	1499	2 I50212	protein-tyrosine-p
26	65	100.0	1501	2 I58148	protein-tyrosine-p
27	65	100.0	1691	2 D54689	protein-tyrosine-p
28	65	100.0	1863	2 S46217	protein-tyrosine-p
29	65	100.0	1894	2 C54689	protein-tyrosine-p

30	65	100.0	1897	1 TDHULK	leukocyte antigen-
31	65	100.0	1898	2 S46216	leukocyte antigen-
32	65	100.0	1907	2 S50893	protein-tyrosine-p
33	65	100.0	1912	2 A56178	protein-tyrosine-p
34	65	100.0	1997	1 S12050	protein-tyrosine-p
35	65	100.0	2051	2 T30938	receptor tyrosine
36	65	100.0	2302	2 T14328	protein-tyrosine-p
37	65	100.0	2314	1 A46151	protein-tyrosine-p
38	64	98.5	135	2 H88683	protein-tyrosine-p
39	64	98.5	332	2 T06536	protein-tyrosine-p
40	64	98.5	335	1 A39862	protein-tyrosine-p
41	64	98.5	344	2 T32869	hypothetical prote
42	64	98.5	352	2 T20729	hypothetical prote
43	64	98.5	360	1 JH0692	protein-tyrosine-p
44	64	98.5	365	2 T25917	hypothetical prote
45	64	98.5	374	2 F88712	protein C17H12.3 {

## ALIGNMENTS

### RESULT 1

T27722

hypothetical protein ZK1251.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence #revision 15-Oct-1999 #text-change 15-Oct-1999

C:Accession: T27722

R:McMurray, A. submitted to the EMBL Data Library, December 1995

A:Reference number: Z20411

A:Accession: T27722

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-198 <MIL>

A:Cross-references: EMBL:Z68222; PIDN:CAA92501.1; GSPDB:GN00022; CESP:ZK1251.5

C:Genetics:

A:Gene: CESP:ZK1251.5

A:Map position: 4

A:Introns: 46/3; 101/2; 185/3

Query Match 100.0% Score 65; DB 2; Length 198;

Best Local Similarity 100.0%; Pred. NO. 0.00063; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0;

QY 1 VVHCSAGVGRG 12

Db 105 VVHCSAGVGRG 116

### RESULT 2

A40169

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type zeta - rat (fragment)

N:Alternate names: protein-tyrosine-phosphatase beta; protein-tyrosine-phosphatase PT

C:Species: Rattus norvegicus (Norway rat)

C>Date: 05-Jun-1992 #sequence #revision 05-Jun-1992 #text-change 24-Apr-1998

C:Accession: A40169

R:Guan, K.; Dixon, J.E. Science 249, 553-556, 1990

A>Title: Protein tyrosine phosphatase activity of an essential virulence determinant

A:Reference number: A40169; MUID:90341778; PMID:2166336

A:Accession: A40169

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-256 <GVAV>

C:Function:

A:Description: may be involved in the regulation of specific developmental processes

C:Superfamily: protein-tyrosine-phosphatase, receptor type zeta; carbonic anhydrase h

C:Keywords: brain; glycoprotein; phosphoprotein; phosphoric monoester hydrolase; rece

F;6-237/Domain: protein-tyrosine-phosphatase homology <PTP1>

F;189/Active site: Cys (phosphocysteine intermediate) #status predicted

F;195/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 2; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 0.00079;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12  
 |||||  
 DB 186 VVHCSAGVGRGTG 197

RESULT 3  
 I56540  
 protein-tyrosine-phosphatase (EC 3.1.3.48) cphpl - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 23-Jul-1999  
 C:Accession: I56540  
 R:Sahin, M.; Hockfield, S.  
 J. Neurosci. 13, 4968-4978, 1993  
 A:Title: Protein tyrosine phosphatases expressed in the developing rat brain.  
 A:Reference number: I56540; M0ID:94043925; PMID:8229209  
 A:Accession: I56540  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-398 <RES>  
 A:Cross-references: EMBL:003273; NID:9414996; PIDN:AAC52124.1; PID:9414997  
 C:Genetics:  
 A:Gene: cphpl  
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;  
 ogy  
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase  
 F:1-157/Domain: protein-tyrosine-phosphatase homology (fragment) <PTP>  
 F:1225-398/Domain: protein-tyrosine-phosphatase homology (fragment) <PTP>  
 F:109/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:115/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 2; Length 398;  
 Best Local Similarity 100.0%; Pred. No. 0.0012;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12  
 |||||  
 DB 106 VVHCSAGVGRGTG 117

RESULT 4  
 T25992  
 hypothetical protein ZK354.8 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T25992  
 R:Johnson, D.; Wamsley, P.; Bradshaw, H.  
 submitted to the EMBL Data Library, February 1997  
 A:Description: The sequence of C. elegans cosmid ZK354.  
 A:Reference number: Z20120  
 A:Accession: T25992  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-483 <JON>  
 A:Cross-references: EMBL:U88172; PIDN:ABA42260.1; GSPDB:GN00022; CESP:ZK354.8  
 A:Experimental source: strain Bristol N2; clone ZK354  
 C:Genetics:  
 A:Gene: CESP:ZK354.8  
 A:Map position: 4  
 A:Intons: 7/1; 70/3; 180/2; 256/2; 331/3; 386/2; 470/3

Query Match 100.0%; Score 65; DB 2; Length 483;  
 Best Local Similarity 100.0%; Pred. No. 0.0014;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12  
 |||||  
 DB 390 VVHCSAGVGRGTG 401

RESULT 5  
 A57068  
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type f - mouse (fragment)  
 N:Alternate names: Leukocyte antigen-related protein LAR  
 C:Species: Mus musculus (house mouse)  
 C:Date: 03-Oct-1995 #sequence\_revision 09-Mar-1996 #text\_change 23-Jul-1999  
 C:Accession: A57068; S40280  
 R:Schaapveld, R.Q.J.; van den Maagdenberg, A.M.J.M.; Schepens, J.T.G.; Olde Weghuis,  
 Genomics 27, 124-130, 1995  
 A:Title: The mouse gene Ptpfr encoding the leukocyte common antigen-related molecule  
 A:Reference number: A57068; M0ID:95394448; PMID:7665159  
 A:Accession: A57068  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-582 <SCH>  
 A:Cross-references: GB:Z37988; NID:9993005; PIDN:CAA6070.1; PID:9993006  
 R:Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.  
 submitted to the EMBL Data Library, June 1993  
 A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatase  
 A:Reference number: S40280  
 A:Accession: S40280  
 A:Molecule type: mRNA  
 A:Residues: 116-221 <HEN>  
 A:Cross-references: EMBL:Z23049; NID:9438135; PIDN:CAA80584.1; PID:9438136  
 C:Genetics:  
 A:Gene: Ptpfr  
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology  
 ogy  
 C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembra  
 F:1-582/Domain: leukocyte common antigen cytosolic domain homology (fragment) <LAC>  
 F:50-271/Domain: protein-tyrosine-phosphatase homology <PTP>  
 F:339-562/Domain: protein-tyrosine-phosphatase homology <PTP>  
 F:223/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:229/Binding site: substrate phosphate (Arg) #status predicted  
 F:514/Active site: Cys (phosphocysteine intermediate) #status predicted  
 F:520/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 2; Length 582;  
 Best Local Similarity 100.0%; Pred. No. 0.0017;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12  
 |||||  
 DB 220 VVHCSAGVGRGTG 231

RESULT 6  
 S17671  
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type beta - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 22-Nov-1993 #sequence\_revision 15-Mar-1996 #text\_change 23-Jul-1999  
 C:Accession: S17671; S40287  
 R:Gebpink, M.F.B.G.; van Etten, I.; Hatober, G.; Suikerbuijk, R.; Beljersbergen, R.  
 FEBS Lett. 290, 123-130, 1991  
 A:Title: Cloning, expression and chromosomal localization of a new putative receptor-  
 A:Reference number: S17671  
 A:Accession: S17671  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-583 <CEB>  
 A:Cross-references: EMBL:X58289  
 R:Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.  
 submitted to the EMBL Data Library, June 1993  
 A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatase  
 A:Reference number: S40280  
 A:Accession: S40287  
 A:Molecule type: mRNA  
 A:Residues: 377-483, 'T', 485-486 <HEN>  
 A:Cross-references: EMBL:Z23056; NID:9438149; PIDN:CAA80591.1; PID:9438150  
 C:Superfamily: protein-tyrosine-phosphatase, receptor type beta; fibronectin type III  
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane p  
 F:311-536/Domain: protein-tyrosine-phosphatase homology <PTP>  
 F:488/Active site: Cys (phosphocysteine intermediate) #status predicted



F:494/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 2; Length 583;  
Best Local Similarity 100.0%; Pred. No. 0.0017;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRGTG 12  
|||||  
DB 485 VVHCSAGVGRGTG 496

# RESULT 7

JC6132

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type epsilon precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 16-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 21-Jun-2002

C:Accession: J06132

R:Schmidt, A.; Rutledge, S.J.; Endo, N.; Opas, E.E.; Tanaka, H.; Wesolowski, G.; Leu, C.

Proc. Natl. Acad. Sci. U.S.A. 93, 3068-3073, 1996

A:Title: Protein-tyrosine phosphatase activity regulates osteoclast formation and function in the bone marrow cell

A:Reference number: JC6132; MUID:96181534; PMID:8610169

A:Contents: bone marrow cell

A:Accession: J06132

A:Molecule type: mRNA

A:Residues: 1-699 <SCCH>

A:Cross-references: GB:040280; NID:q1373052; PIDN:AAB02190.1; PID:q1373053

C:Comment: This enzyme plays an important role in osteoclast formation and function in the bone marrow cell

C:Genetics:

A:Gene: ptp

C:Superfamily: protein-tyrosine-phosphatase, receptor type alpha; leukocyte common antigen

C:Keywords: phosphoprotein; phosphoric monoester hydrolase; transmembrane protein; tyrosine

F:77-697/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:158-382/Domain: protein-tyrosine-phosphatase homology <PTP1>

F:334/Active site: Cys (phosphocysteine intermediate) #status predicted

F:340/Binding site: substrate phosphate (Arg) #status predicted

F:629/Active site: Cys (phosphocysteine intermediate) #status predicted

F:635/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 2; Length 699;  
Best Local Similarity 100.0%; Pred. No. 0.002;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRGTG 12  
|||||  
DB 331 VVHCSAGVGRGTG 342

# RESULT 8

S12053

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type epsilon precursor - human

C:Species: Homo sapiens (man)

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: S12053

R:Knueger, N.X.; Streuli, M.; Saito, H.

EMBO J. 9, 3241-3252, 1990

A:Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatases

A:Reference number: S12049; MUID:91006018; PMID:2170109

A:Accession: S12053

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-700 <RNU>

A:Cross-references: GB:X54134; NID:g35791; PIDN:CAA38069.1; PID:g35792

C:Genetics:

A:Gene: GDB:PTPRE

A:Cross-references: GDB:131385; OMIM:600926

A:Map position: 10q26-10q26

C:Function: catalyzes the hydrolysis of peptidyl-phosphotyrosine to release phosphate

C:Superfamily: protein-tyrosine-phosphatase, receptor type alpha; leukocyte common antigen

C:Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane protein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-700/Product: protein-tyrosine-phosphatase, receptor type epsilon #status predicted

F:47-63/Domain: transmembrane #status predicted <TM>

F:78-696/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:159-383/Domain: protein-tyrosine-phosphatase homology <PTP1>

F:335/Active site: Cys (phosphocysteine intermediate) #status predicted

F:341/Binding site: substrate phosphate (Arg) #status predicted

F:630/Active site: Cys (phosphocysteine intermediate) #status predicted

F:636/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 1; Length 700;  
Best Local Similarity 100.0%; Pred. No. 0.002;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRGTG 12  
|||||  
DB 332 VVHCSAGVGRGTG 343

# RESULT 9

JC1285

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type alpha precursor - rat

N:Alternate names: protein-tyrosine-phosphatase LRP

C:Species: Rattus norvegicus (Norway rat)

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: J01285; S23253; JH0450

R:Moriyama, T.; Fujiwara, Y.; Imai, E.; Takenaka, M.; Kawanishi, S.; Inoue, T.; Noguc

Biochem. Biophys. Res. Commun. 188, 34-39, 1992

A:Title: cDNA cloning of rat LRP, a receptor like protein tyrosine phosphatase, and e

A:Reference number: J01285; MUID:93038682; PMID:1417854

A:Accession: J01285

A:Molecule type: mRNA

A:Residues: 1-796 <MOR>

A:Experimental source: kidney

A:Note: the authors translated the codon TCC for residue 788 as Ala

R:Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.

Biochem. J. 284, 569-576, 1992

A:Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by t

A:Reference number: S23126; MUID:92287069; PMID:1599438

A:Accession: S23253

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 254-267, 'I', 269-354, 'T', 356-501 <HAS>

R:Zhang, W.R.; Goldstein, B.J. Commun. 178, 1291-1297, 1991

A:Title: Identification of skeletal muscle protein-tyrosine phosphatases by amplifica

A:Reference number: JH0450; MUID:91337074; PMID:1651716

A:Accession: JH0450

A:Molecule type: mRNA

A:Residues: 324-354, 'T', 356-434 <HAS>

A:Experimental source: skeletal muscle, strain Sprague-Dawley

C:Function:

A:Description: catalyzes the hydrolysis of peptidyl-phosphotyrosine to release phosph

C:Superfamily: protein-tyrosine-phosphatase, receptor type alpha; leukocyte common an

C:Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane p

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-706/Product: protein-tyrosine-phosphatase, receptor type alpha #status predicted

F:149-165/Domain: extracellular #status predicted <EXT>

F:166-796/Domain: transmembrane #status predicted <TM>

F:178-794/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:259-484/Domain: protein-tyrosine-phosphatase homology <PTP1>

F:552-774/Domain: protein-tyrosine-phosphatase homology <PTP2>

F:436/Active site: Cys (phosphocysteine intermediate) #status predicted

F:442/Binding site: substrate phosphate (Arg) #status predicted

F:726/Active site: Cys (phosphocysteine intermediate) #status predicted

F:732/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 1; Length 796;  
Best Local Similarity 100.0%; Pred. No. 0.0023;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHCASAGVGRGTG 12  
 |||  
 Db 433 VHCASAGVGRGTG 444

RESULT 10  
 A36065

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type alpha precursor - human

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: A36065; S12049; S12905; S13085

R:Kaplan, R.; Morse, B.; Huebner, K.; Croce, C.; Howk, R.; Ravera, M.; Ricca, G.; Jaye, Proc. Natl. Acad. Sci. U.S.A. 87, 7000-7004, 1990

A:Title: Cloning of three human tyrosine phosphatases reveals a multigene family of receptors

A:Reference number: A36065; MUID:90384936; PMID:2169617

A:Accession: A36065

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-802 <NAP>

A:Cross-references: GB:M34668; NID:q190738; PIDN:AAA36528.1; PID:q190739

R:Kruenger, N.X.; Streuli, M.; Saito, H.

EMBO J. 9, 3241-3252, 1990

A:Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatases

A:Reference number: S12049; MUID:91006018; PMID:2170109

A:Accession: S12049

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-138,148-802 <KR0>

A:Cross-references: GB:X54130; NID:q35785; PIDN:CAA38065.1; PID:q35786

R:Jirik, F.R.; Janzen, N.M.; Melhado, I.G.; Harder, K.W.; Leslie, K.B.

submitted to the EMBL Data Library, June 1990

A:Description: Isolation of a cDNA encoding a novel protein-tyrosine phosphatase from thymocytes

A:Reference number: S17371

A:Accession: S17371

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-121, 'P', 123-138, 148-199, 'G', 201-203, 'C', 205-802 <JIR>

A:Cross-references: EMBL:X53364

R:Jirik, F.R.; Janzen, N.M.; Melhado, I.G.; Harder, K.W.

FEBS Lett. 273, 239-242, 1990

A:Title: Cloning and chromosomal assignment of a widely expressed human receptor-like protein-tyrosine phosphatase

A:Reference number: S12905; MUID:91032191; PMID:2172030

A:Accession: S12905

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-61, 'V', 62-82, 84-121, 'P', 123-138, 148-199, 'G', 201-203, 'C', 205-802 <JIR>

R:Ohagi, S.; Nishii, M.; Steinle, D.F.

Nucleic Acids Res. 18, 7159, 1990

A:Title: Sequence of a cDNA encoding human LRP (leukocyte common antigen-related peptide)

A:Reference number: S13085; MUID:91088320; PMID:2175890

A:Accession: S13085

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113, 'W', 115-138, 148-288, 'E', 290-366, 'A', 368-492, 'S', 494-785, 'E', 787-802 <C>

A:Cross-references: EMBL:X54890; NID:q32312; PIDN:CAA38662.1; PID:q32313

C:Genetics:

A:Gene: GDB:PTPRA; PTPA

A:Cross-references: GDB:126732; OMIM:176884

A:Map position: 20p13-20p13

C:Function:

A:Description: catalyzes the hydrolysis of peptidyl-phosphotyrosine to release phosphate

A:Note: allows recovery from insulin stimulation by dephosphorylating insulin receptor

A:Superfamily: protein-tyrosine-phosphatase, receptor type alpha; leukocyte common antigen

C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; receptor

F:1-19/Domain: signal sequence #status predicted <S>

F:20-802/Product: protein-tyrosine-phosphatase, receptor type alpha #status predicted <W>

F:448/Binding site: substrate phosphate (Arg) #status predicted

F:732/Active site: Cys (phosphocysteine intermediate) #status predicted

F:738/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 1; Length 802;

Best Local Similarity 100.0%; Pred. No. 0.0023;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VHCASAGVGRGTG 12  
 |||  
 Db 433 VHCASAGVGRGTG 450

RESULT 11  
 A47373

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type alpha precursor - mouse

N:Alternate names: leukocyte common antigen-related protein LRP; PTPR28; receptor pr

C:Species: Mus musculus (house mouse)

C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text\_change 21-Jan-2000

C:Accession: A47373; B35501; PS0367; S40285; S40286; A36004; D61180

R:Mong, E.C.; Mullersman, J.E.; Thomas, M.L.

Genomics 17, 33-38, 1993

A:Title: Leukocyte common antigen-related phosphatase (LRP) gene structure: conservat

A:Reference number: A47373; MUID:94010906; PMID:8406469

A:Accession: A47373

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-829 <MON>

A:Cross-references: GB:L13607

R:Matthews, R.J.; Cahill, E.D.; Thomas, M.L.

Proc. Natl. Acad. Sci. U.S.A. 87, 4444-4448, 1990

A:Title: Identification of a novel murine non-receptor protein tyrosine phosphatase

A:Reference number: A35501; MUID:90280391; PMID:2162042

A:Accession: B35501

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-829 <MA2>

A:Cross-references: GB:M36033; GB:M33671

R:den Hertog, J.; Pals, C.E.G.M.; Jonk, L.J.C.; Kruijer, W.

Biochem. Biophys. Res. Commun. 184, 1241-1249, 1992

A:Title: Differential expression of a novel murine non-receptor protein tyrosine phosphatase

A:Reference number: JH0609; MUID:92272714; PMID:1590786

A:Accession: PS0367

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 322-325, 'G', 327-356 <DEN>

A:Experimental source: embryonal carcinoma cell, p19 cell

R:Hendriks, W.; Brugman, C.; Zeewen, P.; Schepens, J.; Wieringa, B.

submitted to the EMBL Data Library, June 1993

A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatase

A:Reference number: S40280

A:Accession: S40280

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 358-467 <HEN>

A:Cross-references: EMBL:Z23054; NID:q438145; PIDN:CAA80589.1; PID:q438146

A:Accession: S40286

A:Molecule type: mRNA

A:Residues: 651-756 <HB2>

A:Cross-references: EMBL:Z23055; NID:q438147; PIDN:CAA80590.1; PID:q438148

R:Sap, J.; D'Eustachio, P.; Givol, D.; Schlesinger, J.

Proc. Natl. Acad. Sci. U.S.A. 87, 6112-6116, 1990

A:Title: Cloning and expression of a widely expressed receptor tyrosine phosphatase.

A:Reference number: A36004; MUID:90349565; PMID:2166945

A:Accession: A36004

A:Molecule type: mRNA

A:Residues: 1-230, 'L', 232-267, 'Y', 305-410, 'S', 412-829 <NAP>

A:Cross-references: GB:M34668

R:Yi, T.; Cleveland, J.L.; Ihle, J.N.

Blood 78, 2222-2228, 1991

A:Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells by  
A:Reference number: A61180; MUID:92032882; PMID:1932742  
A:Accession: D61180  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 358-467 <YIA>  
C:Genetics:  
A:Map position: 2  
C:Function:  
A:Description: catalyzes the hydrolysis of peptidyl-phosphotyrosine to release phosphate  
A:Note: allows recovery from insulin stimulation by dephosphorylating insulin receptor  
C:Superfamily: protein-tyrosine-phosphatase, receptor type alpha; leukocyte common antigen  
C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-829/Product: protein-tyrosine-phosphatase, receptor type alpha #status predicted <W  
F:20-14/Domain: extracellular #status predicted <EXT>  
F:143-166/Domain: transmembrane #status predicted <TM>  
F:167-829/Domain: intracellular #status predicted <INT>  
F:175-827/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:585-807/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:21-47, 51, 68, 80, 86, 104, 124/Binding site: carbohydrate (Asn) (covalent) #status predicte  
F:469/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:475/Binding site: substrate phosphate (Arg) #status predicted  
F:759/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:765/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 1; Length 829;  
Best Local Similarity 100.0%; Pred. No. 0.0024;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12  
Db 466 VVHCSAGVGRG 477

RESULT 12  
JC4155  
N:Alternate names: Ptz protein; protein-tyrosine-phosphatase/ezrin-like protein  
C:Species: Homo sapiens (man)  
C:Date: 27-Aug-1995 #sequence\_revision 23-Feb-1996 #text\_change 21-Jul-2000  
C:Accession: JC4155  
R:Smith, A.L.; Mitchell, P.J.; Shipley, J.; Gusterson, B.A.; Rogers, M.V.; Crompton, M.F.  
Biochem. Biophys. Res. Commun. 209, 959-965, 1995  
A:Title: Ptz: a novel human cDNA encoding protein tyrosine phosphatase-and ezrin-like dom  
A:Reference number: JC4155; MUID:95251727; PMID:7733990  
A:Accession: JC4155  
A:Molecule type: mRNA  
A:Residues: 1-1187 <SMID>  
A:Cross-references: EMBL:X82676; NID:93929753; PIDN:CA57993.1; PID:9809029  
A:Experimental source: Breast  
C:Genetics:  
A:Gene: GDB:PTPN14  
A:Cross-references: GDB:454485  
A:Map position: 1q32.2-1q32.2  
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-t  
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas  
F:23-302/Domain: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-t  
F:566-575/Region: proline-rich  
F:709-716/Region: acidic  
F:933-1169/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:1121/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1127/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 1; Length 1187;  
Best Local Similarity 100.0%; Pred. No. 0.0033;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12  
Db 1118 VVHCSAGVGRG 1129

RESULT 13  
JC2366  
N:Alternate names: Ptz protein; protein-tyrosine-phosphatase PTP36; protein-tyrosine-  
C:Species: Mus musculus (house mouse)  
C:Date: 24-Feb-1995 #sequence\_revision 23-Feb-1996 #text\_change 21-Jul-2000  
C:Accession: JC2366  
R:Sawada, M.; Ogata, M.; Fujino, Y.; Hamoka, T.  
Biochem. Biophys. Res. Commun. 203, 479-484, 1994  
A:Title: cDNA cloning of a novel protein tyrosine phosphatase with homology to cytosol  
A:Reference number: JC2366; MUID:94354845; PMID:8074693  
A:Accession: JC2366  
A:Molecule type: mRNA  
A:Residues: 1-1189 <SNM>  
A:Cross-references: GB:D51842; NID:9507330; PIDN:BA06628.1; PID:9507331  
A:Experimental source: thymus  
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membran  
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosph  
F:23-302/Domain: protein 4.1 membrane-binding domain homology <BA1>  
F:566-575/Region: proline-rich  
F:712-718/Region: acidic  
F:933-1171/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:1123/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1129/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 1; Length 1189;  
Best Local Similarity 100.0%; Pred. No. 0.0033;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12  
Db 1120 VVHCSAGVGRG 1131

RESULT 14  
T43148  
N:Alternate names: CD45 homolog  
C:Species: Heterodontus francisci (horn shark)  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000  
C:Accession: T43148  
R:Okumura, M.; Matthews, R.J.; Robb, B.; Bork, P.; Thomas, M.L.  
submitted to the EMBL Data Library, August 1995  
A:Reference number: Z22317  
A:Accession: T43148  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1200 <OKU>  
A:Cross-references: EMBL:U34750; NID:91304393; PID:91335805; PIDN:AA01087.1  
C:Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain ho  
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphat

Query Match 100.0%; Score 65; DB 2; Length 1200;  
Best Local Similarity 100.0%; Pred. No. 0.0033;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12  
Db 748 VVHCSAGVGRG 759

RESULT 15  
A54080  
N:Alternate names: Ptz protein; protein-tyrosine-phosphatase PTP36; protein-tyrosine-  
C:Species: Gallus gallus (chicken)  
C:Date: 02-Aug-1994 #sequence\_revision 02-Aug-1994 #text\_change 21-Jan-2000  
C:Accession: A54080; I50592  
R:Fang, K.S.; Barker, K.; Sudol, M.; Hanafusa, H.  
J. Biol. Chem. 269, 14056-14063, 1994  
A:Title: A transmembrane protein-tyrosine phosphatase contains spectrin-like repeats  
A:Reference number: A54080; MUID:94245724; PMID:8188686  
A:Accession: A54080  
A:Status: preliminary

A;Molecule type: mRNA  
A;Residues: 1-1237 <PAN>  
A;Cross-references: EMBL:Z21960; NID:9510510; PID:CAA79972.1; PID:9510511; GB:L13285  
C;Superfamily: leukocyte common antigen; leukocyte common antigen cytosolic domain homol  
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas  
F:528-1170/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:610-834/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:786/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:792/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 65; DB 2; Length 1237;  
Best Local Similarity 100.0%; Pred. No. 0.0034;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12  
|||||||  
Db 783 VVHCSAGVGRGTG 794

Search completed: January 17, 2003, 09:12:21  
Job time : 17 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 17, 2003, 09:10:56 ; Search time 10 Seconds  
(without alignments)  
49.772 Million cell updates/sec

Title: US-09-743-492-4  
Perfect score: 65  
Sequence: 1 VVHCSAGVGRGTG 12

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	65	100.0	PTPE_MOUSE	P49446 mus musculu
2	65	100.0	PTPE_HUMAN	P23469 homo sapien
3	65	100.0	PTRA_RAT	Q03348 rattus norv
4	65	100.0	PTRA_HUMAN	P18433 homo sapien
5	65	100.0	PTRA_MOUSE	P18052 mus musculu
6	65	100.0	CD45_MOUSE	P06800 mus musculu
7	65	100.0	PTNE_HUMAN	Q15678 homo sapien
8	65	100.0	PTNE_MOUSE	Q62130 mus musculu
9	65	100.0	CD45_RAT	P4157 rattus norv
10	65	100.0	PTP9_DROME	P35832 dtrosophila
11	65	100.0	CD45_HUMAN	P08575 homo sapien
12	65	100.0	PTPG_CHICK	Q38936 gallus gall
13	65	100.0	PTPD_HUMAN	P10566 homo sapien
14	65	100.0	PTPD_HUMAN	P23468 homo sapien
15	65	100.0	PTPB_HUMAN	P23471 homo sapien
16	65	100.0	PTP2_HUMAN	Q62636 rattus norv
17	65	100.0	PTP2_RAT	Q62636 rattus norv
18	65	100.0	PTP1_YEAST	P25044 saccharomyc
19	64	98.5	PTN7_RAT	P49445 rattus norv
20	64	98.5	PTN7_HUMAN	P35236 homo sapien
21	64	98.5	PTP1_DICDI	P4137 dictyostell
22	64	98.5	PTP1_SCHPO	P27574 schizosacch
23	64	98.5	PTNB_MOUSE	P35235 mus musculu
24	64	98.5	PTN3_MOUSE	P43378 mus musculu
25	64	98.5	PTNB_HUMAN	Q06124 homo sapien
26	64	98.5	PTNB_RAT	Q1459 rattus norv
27	64	98.5	PTN4_HUMAN	P29074 rattus norv
28	64	98.5	PTP1_CAEEL	P28101 caenorhabdi
29	64	98.5	LAR_DROME	P16621 dtrosophila
30	63	96.9	PTN5_RAT	P35234 rattus norv
31	63	96.9	PTN5_HUMAN	P34829 homo sapien
32	63	96.9	PTN5_MOUSE	P24830 mus musculu
33	63	96.9	PTN6_HUMAN	P29350 homo sapien

34	63	96.9	595	1	PTN6_MOUSE	P29351 mus musculu
35	62	95.4	1174	1	PTNL_HUMAN	Q16825 homo sapien
36	62	95.4	1175	1	PTNL_RAT	Q62728 rattus norv
37	62	95.4	1176	1	PTNL_MOUSE	Q62136 mus musculu
38	62	95.4	1238	1	PTPJ_MOUSE	Q64455 mus musculu
39	62	95.4	1337	1	PTPJ_HUMAN	Q12913 homo sapien
40	62	95.4	1442	1	PTPG_MOUSE	Q05909 mus musculu
41	62	95.4	1445	1	PTPG_HUMAN	P23470 homo sapien
42	62	95.4	1462	1	PTP6_DROME	P16620 dtrosophila
43	62	95.4	1705	1	PTP6_MOUSE	P70289 mus musculu
44	62	95.4	1711	1	PTP6_RAT	Q64612 rattus norv
45	61	93.8	711	1	PYP2_SCHPO	P32586 schizosacch

## ALIGNMENTS

```

RESULT 1
PTPE_MOUSE          STANDARD:      PRT:    699 AA.
ID PTPE_MOUSE
AC P49446: Q62134; Q62444; Q64496;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase epsilon precursor (EC 3.1.3.48) (R-PTP-
DE epsilon).
GN PTPE OR PTPE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RX MEDLINE=96064677; PubMed=7592814;
RA Elson A., Leder P.;
RT "Protein-tyrosine phosphatase epsilon. An isoform specifically
RT expressed in mouse mammary tumors initiated by v-Ha-ras OR neu.";
RL J. Biol. Chem. 270:26116-26122(1995).
RN
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RX Mukoyama Y.;
RA Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain, and lung;
RX Hou E.W., Li S.L.;
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN
[4]
RP SEQUENCE OF 224-332 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=93086603; PubMed=1454056;
RA Schepens J., Zeeuwen P., Wieringa B., Hendriks W.;
RT "Identification and typing of members of the protein-tyrosine
RT phosphatase gene family expressed in mouse brain.";
RL Mol. Biol. Rep. 16:241-248(1992).
RN
[5]
RP SEQUENCE OF 224-332 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=95134232; PubMed=7832766;
RA Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.;
RT "A novel receptor-type protein tyrosine phosphatase with a single
RT catalytic domain is specifically expressed in mouse brain.";
RL Biochem. J. 305:499-504(1995).
-1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
-1- tyrosine + phosphate.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
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CC -----
DR EMBL: U35368; AAC52281.1; -
DR EMBL: D83484; BAA11927.1; -
DR EMBL: U62387; AAB04553.1; -
DR EMBL: Z23052; CAA80587.1; -
DR EMBL: Z23053; CAA80588.1; -
DR HSSP: P18052; 1YFO.
DR MGD: MGI:97813; PTPRE.
DR InterPro: IPR000387; TYR_phosphatase.
DR Pfam: PF00102; Y_phosphatase; 2.
DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
DR Glycoprotein: Transmembrane; Hydrolase; Phosphorylation; Repeat;
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 699 PROTEIN-TYROSINE PHOSPHATASE EPSILON.
FT TRANSMEM 20 45 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 46 68 POTENTIAL.
FT DOMAIN 69 699 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 153 392 PROTEIN-TYROSINE PHOSPHATASE 1.
FT DOMAIN 393 699 PROTEIN-TYROSINE PHOSPHATASE 2.
FT ACT_SITE 334 334 BY SIMILARITY.
FT ACT_SITE 629 629 BY SIMILARITY.
FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 500 500 G -> A (IN REF. 2).
FT CONFLICT 506 506 G -> V (IN REF. 2).
FT CONFLICT 521 522 IV -> ML (IN REF. 1).
FT CONFLICT 606 606 IV -> I (IN REF. 1).
SQ SEQUENCE 699 AA; 80645 MW; 4D04467438017FEB CRC64;

Query Match 100.0%; Score 65; DB 1; Length 699;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12
   |||||||
Db 331 VVHCSAGVGRG 342

RESULT 2
PTPE_HUMAN
ID PTPE_HUMAN STANDARD; PRT; 700 AA.
AC P23469;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase epsilon precursor (EC 3.1.3.48) (R-PTP-
DE epsilon).
GN PTPRE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=91006018; PubMed=2170109;
RA Krueger N.X., Streuli M., Saito H.;
RA "Structural diversity and evolution of human receptor-like protein
RT tyrosine phosphatases";
RT EMBO J. 9:3241-3252(1990).
CC -i- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -i- SUBCELLULAR LOCATION: Type I membrane protein.
```

```
CC -i- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
CC -----
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CC -----
DR EMBL: X54134; CAA38069.1; -
DR PIR: S12053; 512053.
DR HSSP: P18052; 1YFO.
DR Genew: HGNC:9669; PTPRE.
DR MIM: 600926; -
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00102; Y_phosphatase; 2.
DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
DR Glycoprotein: Transmembrane; Hydrolase; Phosphorylation; Repeat;
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 700 PROTEIN-TYROSINE PHOSPHATASE EPSILON.
FT TRANSMEM 20 46 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 47 69 POTENTIAL.
FT DOMAIN 70 700 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 154 393 PROTEIN-TYROSINE PHOSPHATASE 1.
FT DOMAIN 394 700 PROTEIN-TYROSINE PHOSPHATASE 2.
FT ACT_SITE 335 335 BY SIMILARITY.
FT ACT_SITE 630 630 BY SIMILARITY.
FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 700 AA; 80641 MW; D096BCADCEA65708 CRC64;

Query Match 100.0%; Score 65; DB 1; Length 700;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12
   |||||||
Db 332 VVHCSAGVGRG 343

RESULT 3
PTPE_RAT
ID PTPE_RAT STANDARD; PRT; 796 AA.
AC O03348;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase alpha precursor (EC 3.1.3.48) (R-PTP-
DE alpha).
GN pTPRA OR LRP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93038682; PubMed=1417854;
RA Moriyama T., Fujiwara Y., Imai E., Takenaka M., Kawanishi S.,
RA Inoue T., Noguchi T., Tanaka T., Kamada T., Ueda N.;
RA "CDNA cloning of rat LRP, a receptor like protein tyrosine
RT phosphatase, and evidence for its gene regulation in cultured rat
RT mesangial cells.";
RT Biochem. Biophys. Res. Commun. 188:34-39(1992).
CC -i- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
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CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
CC -----
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CC -----
DR EMBL: L01702; AAA1983.1; -.
DR HSSP: P18052; 1YFO.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PF00102; T-phosphatase; 2.
DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART: SM00194; PTPc; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Transmembrane; Hydrolase; Phosphorylation; Repeat;
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 796 PROTEIN-TYROSINE PHOSPHATASE ALPHA.
FT DOMAIN 20 145 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 146 169 POTENTIAL.
FT DOMAIN 170 796 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 234 494 PROTEIN-TYROSINE PHOSPHATASE 1.
FT DOMAIN 495 796 PROTEIN-TYROSINE PHOSPHATASE 2.
FT ACT_SITE 436 436 BY SIMILARITY.
FT ACT_SITE 726 726 BY SIMILARITY.
FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 51 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 68 80 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 80 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 796 AA; 90260 MW; 4793796191056920 CRC64;

Query Match 100.0%; Score 65; DB 1; Length 796;
Best Local Similarity 100.0%; Pred. NO. 0.00071;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVHCSAGVGRGTG 12
Db 433 VVHCSAGVGRGTG 444

RESULT 4
PTRA_HUMAN
ID PTRA_HUMAN STANDARD; PRT; 802 AA.
AC P18433; 014513;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase alpha precursor (EC 3.1.3.48) (R-PTP-
DE alpha).
GN PTPRA OR PTPA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Sap J., D'Eustachio P., Givol D., Schlessinger J.;
RT "Cloning and expression of a widely expressed receptor tyrosine
RT phosphatase.";
RT Proc. Natl. Acad. Sci. U.S.A. 87:6112-6116(1990).

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RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90384936; PubMed=2169617;
RA Kaplan R., Morse B., Huebner K., Croce C., Howk R., Ravera M.,
RA Ricca G., Jaye M., Schlessinger J.;
RT "Cloning of three human tyrosine phosphatases reveals a multigene
RT family of receptor-linked protein-tyrosine-phosphatases expressed in
RT brain.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:7000-7004(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91006018; PubMed=2170109;
RA Krueger N.X., Streuli M., Saito H.;
RT "Structural diversity and evolution of human receptor-like protein
RT tyrosine phosphatases.";
RL EMBO J. 9:3241-3252(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RA MEDLINE=91088320; PubMed=2175890;
RA Ohagi S., Nishi M., Steiner D.F.;
RT "Sequence of a cDNA encoding human LRP (leukocyte common antigen-
RT related peptide).";
RL Nucleic Acids Res. 18:7159-7159(1990).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=91032191; PubMed=2172030;
RA Jirik F.R., Janzen N.M., Melhado I.G., Harder K.W.;
RT "Cloning and chromosomal assignment of a widely expressed human
RT receptor-like protein-tyrosine phosphatase.";
RL FEBS Lett. 273:239-242(1990).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA DeJoukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagquley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Cordy N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Kay M.P., Kimberley A.M., King A., Knights K., Johnson C.M., Johnson D.,
RA Key M.P., Kimberley A.M., King A., Knights K., Laird G.K., Lawlor S.,
RA Leivasialho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachle L.J., McEay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [7]
RP CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
RP tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
CC -----
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CC -----
DR EMBL: M34668; AAA36528.1; -
DR EMBL: X54130; CAA38065.1; -
DR EMBL: X54890; CAA38662.1; -
DR EMBL: X53364; CAA37447.1; -
DR EMBL: AL121905; CAC10337.1; -
DR PIR: A36065; A36065.
DR PIR: S12049; S12049.
DR HSSP: P18052; 1YFO.
DR Genew: HGNC:9664; PTPRA.
DR MIM: 176884; -
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00102; Y_phosphatase_2.
DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
DR Glycoprotein: Transmembrane; Hydroxylase; Phosphorylation; Signal;
KW Repeat; Alternative splicing.
FT SIGNAL 1 19
FT CHAIN 20 802
FT DOMAIN 20 142
FT TRANSMEM 143 165
FT DOMAIN 166 802
FT DOMAIN 241 500
FT DOMAIN 401 802
FT ACT_SITE 732 732
FT ACT_SITE 732 732
FT CARBOHYD 21 21
FT CARBOHYD 36 36
FT CARBOHYD 68 68
FT CARBOHYD 80 80
FT CARBOHYD 86 86
FT CARBOHYD 104 104
FT CARBOHYD 124 124
FT VARSLIC 139 147
FT CONFLICT 114 114
FT CONFLICT 122 122
FT CONFLICT 138 138
FT CONFLICT 179 179
FT CONFLICT 289 289
FT CONFLICT 367 367
FT CONFLICT 493 493
FT CONFLICT 786 786
SQ SEQUENCE 802 AA; 90599 MW; 8E964C3B56B5B32 CRC64;

Query Match 100.0%; Score 65; DB 1; Length 802;
Best Local Similarity 100.0%; Pred. No. 0.00072;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12
Db 439 VVHCSAGVGRG 450

RESULT 5
PTPR_MOUSE STANDARD; PRT; 829 AA.
AC P18052; 061808;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein-tyrosine phosphatase alpha precursor (EC 3.1.3.48) (R-PTP-
DE alpha) (LCA-related phosphatase).
OS PTPRA OR LRP OR PTPA.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.

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RC STRAIN-G57BL/6 X DBA/2;
RA MEDLINE=90280391; Pubmed=2162042;
RX Matthews R.J., Cahir E.D., Thomas M.L.;
RT "Identification of an additional member of the protein-tyrosine-
RT phosphatase family: evidence for alternative splicing in the tyrosine
RT phosphatase domain."
RT Proc. Natl. Acad. Sci. U.S.A. 87:4444-4448(1990).
RN [2]
RP SEQUENCE OF 358-467 FROM N.A.
RC STRAIN-BALB/c; TISSUE=Brain;
RX MEDLINE=95134232; Pubmed=7837266;
RA Hendriks W., Schepens J., Bruygan C., Zeeuwen P., Wieringa B.;
RT "A novel receptor-type protein tyrosine phosphatase with a single
RT catalytic domain is specifically expressed in mouse brain."
RT Biochem. J. 305:499-504(1995).
RN [3]
RP SEQUENCE OF 651-756 FROM N.A.
RC STRAIN-BALB/c; TISSUE=Brain;
RX MEDLINE=93086603; Pubmed=1454056;
RA Schepens J., Zeeuwen P., Wieringa B., Hendriks W.;
RT "Identification and typing of members of the protein-tyrosine
RT phosphatase gene family expressed in mouse brain."
RT Mol. Biol. Rep. 16:241-248(1992).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 202-503.
RX MEDLINE=96320562; Pubmed=8700232;
RA Bilwes A.M., den Hertog J., Hunter T., Noel J.P.;
RT "Structural basis for inhibition of receptor protein-tyrosine
RT phosphatase-alpha by dimerization."
RT Nature 382:555-559(1996).
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND
CC A SHORT FORM. ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
-----
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-----
DR EMBL: M36033; AAA39448.1; -
DR EMBL: M36034; AAA39449.2; -
DR EMBL: Z23054; CAA80589.1; -
DR EMBL: Z23055; CAA80590.1; -
DR PIR: A35501; A35501.
DR PIR: B35501; B35501.
DR PDB: 1YFO; 01-APR-97.
DR MGD; MGI:97808; Ptpra.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00102; Y_phosphatase_2.
DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Glycoprotein; Transmembrane; Hydroxylase; Phosphorylation; Signal;
KW Repeat; Alternative splicing; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 829
FT DOMAIN 20 142
FT TRANSMEM 143 166
FT DOMAIN 167 829
FT DOMAIN 232 527
FT DOMAIN 528 829
FT ACT_SITE 469 469
FT ACT_SITE 759 759
FT ACT_SITE BY SIMILARITY.

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CC FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT VASAPLIC 268 303 MISSING (IN SHORT ISOFORM).
CC SO SEQUENCE 829 AA; 93697 MW; 7B1E335D4CCEB09B CRC64;

Query Match 100.0%; Score 65; DB 1; Length 829;
Best Local Similarity 100.0%; Pred. No. 0.00074;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VVHCSAGVGRG 12
Db 466 VVHCSAGVGRG 477

RESULT 6
CD45_MOUSE STANDARD; PRT; 1152 AA.
ID CD45_MOUSE
AC P06800;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Leukocyte common antigen precursor (EC 3.1.3.48) (L-CA) (Lymphocyte
DE common antigen Ly-5) (CD45) (T200).
GN PRPC OR Ly-5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=66313686; PubMed=2944116;
RA Saga Y., Tung J.-S., Shen F.-W., Boyse E.A.;
RT "Sequences of Ly-5 cDNA: Isoform-related diversity of Ly-5 mRNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:6940-6944(1986).
RN [2]
RP REVISIONS.
RA Saga Y., Tung J.-S., Shen F.-W., Boyse E.A.;
RL Proc. Natl. Acad. Sci. U.S.A. 84:1991-1991(1987).
RN [3]
RP SEQUENCE OF 10-124 FROM N.A.
RX TISSUE=T-cell;
RA MEDLINE=66042665; PubMed=3864163;
RX Shen F.-W., Saga Y., Littman G., Freeman G., Tung J.-S., Cantor H.,
RA Boyse E.A.;
RT "Cloning of Ly-5 cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7360-7363(1985).
RN [4]
RP SEQUENCE OF 822-1152 FROM N.A.
RX MEDLINE=87092355; PubMed=2948186;
RA Raschke W.C.;
RT "Cloned murine T200 (Ly-5) cDNA reveals multiple transcripts within
RT B- and T-lymphocyte lineages.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:161-165(1987).
CC -1- FUNCTION: REQUIRED FOR T-CELLS ACTIVATION THROUGH THE ANTIGEN
CC RECEPTOR. THE FIRST PRPASE DOMAIN HAS ENZYMATIC ACTIVITY, WHILE
CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
CC FIRST ONE.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF ISOFORMS ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION IS RESTRICTED TO THE HEMATOPOIETIC
CC COMPARTMENT OF DEVELOPMENT.
CC -1- PIM: HEAVILY N- AND O-GLYCOSYLATED.
CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC or send an email to license@sib-sib.ch).
CC -----
CC DR EMBL; M14342; AAA39458.1; -
CC DR EMBL; M11934; AAA39461.1; -
CC DR EMBL; M15174; AAA40161.1; -
CC DR PIR; A29381; A29381.
CC DR HSSP; P18052; LYPO.
CC DR MGD; MGI:97810; Ptpnc.
CC DR InterPro; IPR003961; FM_III.
CC DR InterPro; IPR000387; TYR_phosphatase.
CC DR InterPro; IPR000242; Tyr_pp.
CC DR Pfam; PF00041; fn3; 3.
CC DR Pfam; PF00102; Y_phosphatase; 2.
CC DR PRINTS; PR00700; PRTYPHPTASE.
CC DR SMART; SM00194; PTPc; 2.
CC DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
CC DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
CC DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
CC KW Glycoprotein. Transmembrane; Phosphorylation; B-cell; T-cell; Repeat;
CC Alternative splicing; Hydrolase; Signal.
CC FT SIGNAL 1 23
CC FT CHAIN 24 1152 LEUCOCYTE COMMON ANTIGEN.
CC FT DOMAIN 24 425 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 426 447 POTENTIAL.
CC FT DOMAIN 448 1152 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 233 329 FIBRONECTIN TYPE-III 1.
CC FT DOMAIN 330 421 FIBRONECTIN TYPE-III 2.
CC FT DOMAIN 520 769 PROTEIN-TYROSINE PHOSPHATASE 1.
CC FT DOMAIN 811 1084 PROTEIN-TYROSINE PHOSPHATASE 2.
CC FT ACT_SITE 701 701 BY SIMILARITY.
CC FT ACT_SITE 1016 1016
CC FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 318 318 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 379 379 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SO SEQUENCE 1152 AA; 130421 MW; BAD956B4E32DEA812 CRC64;

Query Match 100.0%; Score 65; DB 1; Length 1152;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VVHCSAGVGRG 12
Db 698 VVHCSAGVGRG 709

RESULT 7
PTNE_HUMAN STANDARD; PRT; 1187 AA.
ID PTNE_HUMAN
AC Q15678;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein tyrosine phosphatase.
DE (Protein-tyrosine phosphatase pez).
GN PTN14 OR PEZ.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast carcinoma;
RX MEDLINE=9521727; Pubmed=7733990;
RA Smith A.L., Mitchell P.J., Shipley J., Gusterson B.A., Rogers M.V.,
RT Crompton M.R.;
RT "Pez: a novel human cDNA encoding protein tyrosine phosphatase- and
RT ezrin-like domains.";
RU Biochem. Biophys. Res. Commun. 209:959-965(1995).
CC CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF HUMAN TISSUES
CC INCLUDING KIDNEY, SKELETAL MUSCLE, LUNG AND PLACENTA.
CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
-----
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-----
DR EMBL: X83676; CAA57993.1; -
DR HSSP: P29350; 1GMZ.
DR Genew: HGNC:9647; PTPN14.
DR MIM: 603155; -
DR InterPro: IPR000299; Band_4.1.
DR InterPro: IPR000387; TYR_P.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PF00102; Y-phosphatase; 1.
DR Pfam: PF00373; Band_4.1; 1.
DR PRINTS: PR00935; BAND4.1.
DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART: SM00295; B41; 1.
DR SMART: SM00194; PTPC; 1.
DR PROSITE: PS00660; BAND_4.1; 1.
DR PROSITE: PS00661; BAND_4.1.2; 1.
DR PROSITE: PS0057; BAND_4.1.3; 1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR Structural protein; Cytoskeleton; Hydrolyase.
KW Structural protein; Cytoskeleton; Hydrolyase.
FT DOMAIN 75 239 BAND 4.1-LIKE.
FT DOMAIN 933 1187 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 1121 1121 BY SIMILARITY.
FT DOMAIN 566 573 POLY-PRO.
FT DOMAIN 709 716 POLY-GLU.
FT DOMAIN 712 718 POLY-GLY.
SQ SEQUENCE 1187 AA; 135239 MW; 015760B75E3574E3 CRC64;

Query Match 100.0%; Score 65; DB 1; Length 1187;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12
Db 1118 VVHCSAGVGRG 1129
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DE (Protein-tyrosine phosphatase ptp36).
GN PTPN14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CB-17-SCID; TISSUE=Thymus;
RX MEDLINE=94354845; Pubmed=8074693;
RA Sawada M., Ogata M., Fujino Y., Hamaoka T.;
RT "cDNA cloning of a novel protein tyrosine phosphatase with homology
RT to cytoskeletal protein 4.1 and its expression in T-lineage cells.";
RU Biochem. Biophys. Res. Commun. 203:479-484(1994).
CC FUNCTION: MAY BE INVOLVED IN THE REGULATION OF T CELL DEVELOPMENT.
CC CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC TISSUE SPECIFICITY: THYMUS; IN CELLS OF BOTH HEMATOPOIETIC AND
CC NON-HEMATOPOIETIC ORIGINS.
CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
-----
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-----
DR EMBL: D31842; BAA06628.1; -
DR HSSP: O06124; ZSHP.
DR MGD: MGI:102467; Ptpn14.
DR InterPro: IPR000299; Band_4.1.
DR InterPro: IPR000387; TYR_P.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PF00102; Y-phosphatase; 1.
DR Pfam: PF00373; Band_4.1; 1.
DR PRINTS: PR00935; BAND4.1.
DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART: SM00295; B41; 1.
DR SMART: SM00194; PTPC; 1.
DR PROSITE: PS00660; BAND_4.1; 1.
DR PROSITE: PS00661; BAND_4.1.2; 1.
DR PROSITE: PS0057; BAND_4.1.3; 1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR Structural protein; Cytoskeleton; Hydrolyase.
KW Structural protein; Cytoskeleton; Hydrolyase.
FT DOMAIN 75 239 BAND 4.1-LIKE.
FT DOMAIN 935 1189 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 1123 1123 BY SIMILARITY.
FT DOMAIN 566 573 POLY-PRO.
FT DOMAIN 635 639 POLY-GLY.
FT DOMAIN 712 718 POLY-GLU.
SQ SEQUENCE 1189 AA; 135030 MW; 2B85BE5F9C723303 CRC64;

Query Match 100.0%; Score 65; DB 1; Length 1189;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12
Db 1120 VVHCSAGVGRG 1131
|||||

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RESULT 8
ID PTNE_MOUSE STANDARD; PRT; 1189 AA.
AC 062130;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)

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RESULT 9
ID CD45_RAT STANDARD; PRT; 1255 AA.
AC P04157;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1988 (Rel. 08, Last sequence update)

```

DT 15-JUN-2002 (Rel. 41, last annotation update)  
 DE Leukocyte common antigen variant 4 precursor (EC 3.1.3.48) (L-CA)  
 GN (CD45) (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Barclay A.N., Jackson D.I., Willis A.C., Williams A.F.;  
 RL Submitted (MAY-1987) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE OF 190-1255 FROM N.A.  
 RX MEDLINE=85201691; PubMed=3158393;  
 RA Thomas M.L., Barclay A.N., Gagnon J., Williams A.F.;  
 RT "Evidence from cDNA clones that the rat leukocyte-common antigen  
 RT (T200) spans the lipid bilayer and contains a cytoplasmic domain of  
 RT 80,000 Mr.";  
 RL Cell 41:83-93(1985).  
 RN [3]  
 RP ALTERNATIVE SPLICING.  
 RX MEDLINE=87275817; PubMed=2440674;  
 RA Barclay A.N., Jackson D.I., Willis A.C., Williams A.F.;  
 RT "Lymphocyte specific heterogeneity in the rat leukocyte common  
 RT antigen (T200) is due to differences in polypeptide sequences near  
 RT the NH2-terminus".  
 RL EMBO J. 6:1259-1264(1987).  
 CC -1- FUNCTION: REQUIRED FOR T-CELLS ACTIVATION THROUGH THE ANTIGEN  
 CC RECEPTOR. THE FIRST PTASE DOMAIN HAS ENZYMAIC ACTIVITY, WHILE  
 CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE  
 CC FIRST ONE.  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: A number of isoforms are produced by  
 CC alternative splicing.  
 CC -1- TISSUE SPECIFICITY: VARIANTS 4 AND 3 ARE FOUND IN THE LYMPH NODE,  
 CC VARIANTS 1 AND 2 ARE FOUND IN THYMOCYTE AND LYMPH NODE.  
 CC -1- PTM: HEAVILY N- AND O-GLYCOSYLATED.  
 CC -1- PTM: THE CYTOPLASMIC DOMAIN CONTAINS POTENTIAL PHOSPHORYLATION  
 CC SITES.  
 CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
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 CC  
 CC EMBL: Y00065; CAA68272.1; -  
 CC EMBL: Y00065; CAA68273.1; -  
 CC EMBL: Y00065; CAA68274.1; -  
 CC EMBL: Y00065; CAA68275.1; -  
 CC EMBL: M25820; AAA41518.1; -  
 CC EMBL: M25821; AAA41519.1; -  
 CC EMBL: M25822; AAA41520.1; -  
 CC EMBL: M25823; AAA41521.1; -  
 CC PIR: A60241; TRDTLT.  
 CC HSSP: P18052; LYPO.  
 CC InterPro: IPR003961; FN\_III.  
 CC InterPro: IPR000387; Tyr\_P Kinase.  
 CC InterPro: IPR000242; Tyr\_PP.  
 CC Pfam: PF00041; fn3; 2.  
 CC Pfam: PF00102; Y\_phosphatase; 2.  
 CC SMART: SM00060; FN3; 2.  
 CC SMART: SM00194; PTPc; 2.  
 CC PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
 CC PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 2.  
 CC PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 2.

KW glycoprotein; Transmembrane; Phosphorylation; B-cell; T-cell; Repeat;  
 KM Alternative splicing; Hydrolase; Signal.  
 FT SIGNAL 1 1  
 FT NON\_TER 1 1  
 FT CHAIN 1 1  
 FT DOMAIN 6 1255  
 FT TRANSMEM 529 528  
 FT DOMAIN 551 550  
 FT DOMAIN 551 1255  
 FT DOMAIN 341 432  
 FT DOMAIN 433 524  
 FT DOMAIN 623 872  
 FT DOMAIN 914 1187  
 FT ACT\_SITE 804 804  
 FT ACT\_SITE 1119 1119  
 FT CARBOHYD 44 44  
 FT CARBOHYD 124 124  
 FT CARBOHYD 135 135  
 FT CARBOHYD 146 146  
 FT CARBOHYD 160 160  
 FT CARBOHYD 182 182  
 FT CARBOHYD 227 227  
 FT CARBOHYD 232 232  
 FT CARBOHYD 253 253  
 FT CARBOHYD 264 264  
 FT CARBOHYD 309 309  
 FT CARBOHYD 315 315  
 FT CARBOHYD 353 353  
 FT CARBOHYD 356 356  
 FT CARBOHYD 453 453  
 FT CARBOHYD 484 484  
 FT VARSPPLIC 12 53  
 FT VARSPPLIC 12 102  
 FT VARSPPLIC 53 143  
 FT VARSPPLIC 103 143  
 FT CONFLICT 38 38  
 SQ SEQUENCE 1255 AA; 141208 MW; C257CBD2A355BCEA CRC64;  
 Query Match 100.0%; Score 65; DB 1; Length 1255;  
 Best Local Similarity 100.0%; Pred. No. 0.0011;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VVHCSAGVGRTG 12  
 DB 801 VVHCSAGVGRTG 812  
 RESULT 10  
 ID PTP9\_DROME STANDARD; PRT; 1301 AA.  
 AC P35832;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Protein-tyrosine phosphatase 99A precursor (EC 3.1.3.48) (Receptor-  
 DE linked protein-tyrosine phosphatase 99A).  
 GN PTP99A.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A. (LONG ISOFORM).  
 RC TISSUE=Eye Imaginal disk;  
 RX MEDLINE=92107930; PubMed=1662390;  
 RA Hartharain I.K., Chuang P.-T., Rubin G.M.;  
 RT "Cloning and characterization of a receptor-class phosphotyrosine  
 RT phosphatase gene expressed on central nervous system axons in  
 RT Drosophila melanogaster".  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:11266-11270(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RC TISSUE=Embryo;

RA MEDLINE-92034989; PubMed-1657402;  
 RA Tian S.-S., Tsoulfas P., Zinn K.;  
 RT "Three receptor-linked protein-tyrosine phosphatases are selectively  
 RT expressed on central nervous system axons in the Drosophila embryo.";  
 RL Cell 67:675-685(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE-Embryo;  
 RX MEDLINE-92034988; PubMed-1657401;  
 RA Yang X., Seow K.T., Bahri S.M., Oon S.H., Chia W.;  
 RT "Two Drosophila receptor-like tyrosine phosphatase genes are  
 RT expressed in a subset of developing axons and pioneer neurons in the  
 RT embryonic CNS.";  
 RL Cell 67:661-673(1991).  
 CC -1- FUNCTION: MAY PLAY A KEY ROLE IN SIGNAL TRANSDUCTION AND GROWTH  
 CC CONTROL.  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a  
 CC short form; are produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED IN A SUBSET OF AXONS AND  
 CC PIONEER NEURONS IN THE EMBRYO.  
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.  
 CC -----  
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 CC -----  
 DR EMBL: M81795; AAA28483.1; -  
 DR EMBL: M80539; AAA28485.1; -  
 DR EMBL: M80464; AAA28486.1; -  
 DR PIR: A41622; A41622.  
 DR PIR: A41214; A41214.  
 DR PIR: B41214; B41214.  
 DR PIR: B41215; B41215.  
 DR HSP: P18052; TYPO.  
 DR Flybase: FBgn0004369; Ptp99A.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR003962; FNIII\_repeat.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR InterPro: IPR000242; Tyr\_PP.  
 DR Pfam: PF00102; Y-phosphatase; 2.  
 DR PRINTS: PR00014; ENTPETII.  
 DR PRINTS: PR00700; PRTPHPTASE.  
 DR SMART: SM00060; FNS; 2.  
 DR SMART: SM00194; PTPc; 2.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Transmembrane; Hydrolase; Repeat; Signal; Alternative splicing.  
 FT SIGNAL 1 29  
 FT CHAIN 30 1301  
 FT DOMAIN 30 394  
 FT TRANSMEM 395 415  
 FT DOMAIN 416 1301  
 FT DOMAIN 169 268  
 FT DOMAIN 269 368  
 FT DOMAIN 467 747  
 FT DOMAIN 748 975  
 FT ACT\_SITE 682 682  
 FT DOMAIN 1076 1091  
 FT CARBOHYD 33 33  
 FT CARBOHYD 176 176  
 FT CARBOHYD 212 212  
 FT CARBOHYD 278 278

FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPIC 1050 1119 MISSING (IN SHORT ISOFORM).  
 FT CONFLICT 586 586 P -> R (IN REF. 2 AND 3).  
 FT CONFLICT 1205 1205 N -> H (IN REF. 3).  
 SQ SEQUENCE 1301 AA: 145336 MW: 8241E3E19A4CA5BD CRC64;  
 Query Match 100.0%; Score 65; DB 1; Length 1301;  
 Best local Similarity 100.0%; Pred. No. 0.0011;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VVHCSAGVGRGT 12  
 Db 679 VVHCSAGVGRGT 690  
 RESULT 11  
 ID CD45\_HUMAN STANDARD; PRT; 1304 AA.  
 AC P08575;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Leukocyte common antigen precursor (EC 3.1.1.3.48) (L-CA) (CD45 antigen)  
 DE (T200).  
 GN PTPRC OR CD45.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI:Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Lymphocytes;  
 RX MEDLINE-88061067; PubMed-2824653;  
 RA Streuli M., Hall L.R., Saga Y., Schlossman S.F., Saito H.;  
 RT "Differential usage of three exons generates at least five different  
 RT mRNAs encoding human leukocyte common antigens.";  
 RL J. Exp. Med. 166:1548-1566(1987).  
 RN [2]  
 RP FUNCTION.  
 RX MEDLINE-89017162; PubMed-2845400;  
 RA Charbonneau H., Tonks N.K., Walsh K.A., Fischer E.H.;  
 RT "The leukocyte common antigen (CD45): a putative receptor-linked  
 RT protein tyrosine phosphatase";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186(1988).  
 RN [3]  
 RP MUTAGENESIS.  
 RX MEDLINE-90316093; PubMed-1695146;  
 RA Streuli M., Krueger N.X., Thal T., Tang M., Saito H.;  
 RT "Distinct functional roles of the two intracellular phosphatase like  
 RT domains of the receptor-linked protein tyrosine phosphatases LCA and  
 RT LAR";  
 RL EMBO J. 9:2399-2407(1990).  
 CC -1- FUNCTION: REQUIRED FOR T-CELLS ACTIVATION THROUGH THE ANTIGEN  
 CC RECEPTOR. THE FIRST PTASE DOMAIN HAS ENZYMTIC ACTIVITY, WHILE  
 CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE  
 CC FIRST ONE.  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 8 ISOFORMS ARE PRODUCED BY  
 CC ALTERNATIVE SPLICING.  
 CC -1- PTM: HEAVILY N- AND O-GLYCOSYLATED.  
 CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD45 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd45.htm".  
 CC -----  
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CC -----

DR EMBL: Y00638; CAA6669.1; -.

DR HSP: P18052; 1YFO.

DR GlycosultedB: P08575; -.

DR Genew: HGNC:9666; PTPRC.

DR MIM: 151460; -.

DR InterPro: IPR003961; FN\_III.

DR InterPro: IPR000387; Tyr\_P.

DR InterPro: IPR00242; Tyr\_PP.

DR Pfam: PF00041; fn3; 2.

DR Pfam: PF00102; Y-phosphatase; 2.

DR PRINTS: PR00700; PRTYPHPTASE.

DR SMART: SM00060; FN3; 2.

DR SMART: SM00194; PTPC; 2.

DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.

DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 2.

DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 2.

DR Glycoprotein: Transmembrane: Phosphorylation; B-cell; T-cell; Repeat; Alternative splicing; Hydrolase; Signal.

KW SIGNAL

FT CHAIN 1 23

FT DOMAIN 24 575

FT TRANSMEM 576 597

FT DOMAIN 598 1304

FT DOMAIN 387 479

FT DOMAIN 480 571

FT DOMAIN 670 919

FT DOMAIN 961 1235

FT ACT\_SITE 851 851

FT ACT\_SITE 1167 1167

FT CARBOHYD 90 90

FT CARBOHYD 95 95

FT CARBOHYD 184 184

FT CARBOHYD 190 190

FT CARBOHYD 197 197

FT CARBOHYD 232 232

FT CARBOHYD 260 260

FT CARBOHYD 270 270

FT CARBOHYD 335 335

FT CARBOHYD 378 378

FT CARBOHYD 419 419

FT CARBOHYD 468 468

FT CARBOHYD 488 488

FT CARBOHYD 529 529

FT MUTAGEN 851 851

SEQ 1304 AA; 147253 MW; 1F357BC5632618B2 CRC64;

Query Match 100.0%; Score 65; DB 1; Length 1304;

Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12

Db 848 VVHCSAGVGRG 859

RESULT 12

PTPG\_CHICK

AC 098936; STANDARD; PRT; 1422 AA.

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Protein-tyrosine phosphatase gamma precursor (EC 3.1.3.48) (R-PTP-gamma).

DE PTPRC.

GN Gallus gallus (Chicken).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

CC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney, and Brain;

RA Qinghua X., Xiaojun G., Cong S., Zong S.M., Jong Y.J., Chan J., Wang L.-H.;

RU Submitted (Oct-1995) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).

CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE EUKARYOTIC-TYPE CARBONIC ANHYDRASE FAMILY.

CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.

CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.

CC -----

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CC -----

DR EMBL: U38349; AAB16910.1; -.

DR HSP: P18052; 1YFO.

DR InterPro: IPR001148; Euk\_COanhd.

DR InterPro: IPR003961; FN\_III.

DR InterPro: IPR000387; Tyr\_P.

DR InterPro: IPR00242; Tyr\_PP.

DR Pfam: PF00041; fn3; 1.

DR Pfam: PF00102; Y-phosphatase; 2.

DR Pfam: PF00194; Carb\_anhdase; 1.

DR PRINTS: PR00700; PRTYPHPTASE.

DR PRODOM: PD000865; Euk\_COanhd; 1.

DR SMART: SM00060; FN3; 1.

DR SMART: SM00194; PTPC; 2.

DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.

DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 2.

DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 2.

DR Glycoprotein: Transmembrane; Hydrolase; Repeat; Signal.

FT SIGNAL 1 19

FT CHAIN 20 1422

FT DOMAIN 20 742

FT TRANSMEM 743 768

FT DOMAIN 769 1422

FT DOMAIN 56 322

FT DOMAIN 347 441

FT DOMAIN 846 1102

FT DOMAIN 1103 1422

FT ACT\_SITE 1037 1037

FT SITE 1328 1328

FT CARBOHYD 109 109

FT CARBOHYD 113 113

FT CARBOHYD 156 156

FT CARBOHYD 359 359

FT CARBOHYD 444 444

FT CARBOHYD 620 620

FT CARBOHYD 632 632

FT CARBOHYD 640 640

FT CARBOHYD 728 728

SEQ 1422 AA; 159766 MW; DD48405593DA74F CRC64;

Query Match 100.0%; Score 65; DB 1; Length 1422;

Best Local Similarity 100.0%; Pred. No. 0.0012;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12

Db 1034 VVHCSAGVGRG 1045

RESULT 13

PTPF\_HUMAN STANDARD: PRT: 1897 AA.  
 ID PTPF\_HUMAN PRT: 1897 AA.  
 AC P10586;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE LAR protein precursor (Leukocyte antigen related) (EC 3.1.3.48).  
 GN PTPF OR LAR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Tonsil;  
 RA MEDLINE=89035978; PubMed=2972792;  
 RA Streuli M., Krueger N.X., Hall L.R., Schlossman S.F., Saito H.;  
 RT "A new member of the immunoglobulin superfamily that has a  
 RT cytoplasmic region homologous to the leukocyte common antigen.";  
 RL J. Exp. Med. 168:1523-1530(1988).  
 RN [2]  
 RP MUTAGENESIS.  
 RA MEDLINE=90046860; PubMed=2554325;  
 RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;  
 RT "A family of receptor-linked protein tyrosine phosphatases in humans  
 RT and Drosophila.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).  
 RN [3]  
 RP MUTAGENESIS.  
 RA MEDLINE=90316093; PubMed=1695146;  
 RA Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;  
 RT "Distinct functional roles of the two intracellular phosphatase like  
 RT domains of the receptor-linked protein tyrosine phosphatases LCA and  
 RT LAR.";  
 RL EMBO J. 9:2399-2407(1990).  
 CC -1- FUNCTION: IT IS POSSIBLE THAT LAR IS A CELL ADHESION RECEPTOR.  
 CC IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY  
 CC (PTPASE).  
 CC -1- FUNCTION: THE FIRST PTPASE DOMAIN HAS ENZYMATIC ACTIVITY, WHILE  
 CC THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE  
 CC FIRST ONE.  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 8 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: Y00815; CAA68754.1; -  
 CC PIR: S03841; TDHULK.  
 CC HSSP: P18052; IYPO.  
 CC GeneW: HGNC:9670; PTPRF.  
 CC MIM: 179590; -  
 CC InterPro: IPR003961; FN\_III.  
 CC InterPro: IPR003962; FNIII\_repeat.  
 CC InterPro: IPR003006; Iq\_MHC.  
 CC InterPro: IPR003598; Iq\_C2.  
 CC InterPro: IPR000387; TYR\_phosphatase.  
 CC InterPro: IPR000242; Tyr\_Pp.  
 CC Pfam: PF00041; fn3; 7.  
 CC Pfam: PF00047; Iq; 3.  
 CC Pfam: PF00102; Y\_phosphatase; 2.  
 CC PRINTS: PR00014; ENTPERTIII.  
 CC PRINTS: PR00700; PRTPHPTASE.  
 CC SMART: SM00060; FN3; 5.

DR SMART: SM00408; IGC2; 3.  
 DR SMART: SM00194; PTPC; 2.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE: PS00056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE: PS00055; TYR\_PHOSPHATASE\_PTP; 2.  
 KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;  
 KW Cell adhesion; Immunoglobulin domain; Repeat.  
 FT SIGNAL 1  
 FT CHAIN 17  
 FT DOMAIN 17 1897  
 FT TRANSMEM 1251 1274  
 FT DOMAIN 1275 1887  
 FT DOMAIN 1360 1606  
 FT DOMAIN 1649 1897  
 FT ACT\_SITE 1538 1538  
 FT ACT\_SITE 1829 1829  
 FT CARBOHYD 107 107  
 FT CARBOHYD 240 240  
 FT CARBOHYD 285 285  
 FT CARBOHYD 711 711  
 FT CARBOHYD 956 956  
 FT MUTAGEN 1538 1538  
 SQ SEQUENCE 1897 AA; 211844 MW; 439850F1D50C31EF CRC64;  
 Query Match 100.0%; Score 65; DB 1; Length 1897;  
 Best Local Similarity 100.0%; Pred. No. 0.0017;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VVHCSAGVGRGTG 12  
 DB 1535 VVHCSAGVGRGTG 1546  
 RESULT 14  
 PTPD\_HUMAN  
 ID PTPD\_HUMAN STANDARD: PRT: 1912 AA.  
 AC P23468;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Protein-tyrosine phosphatase delta precursor (EC 3.1.3.48) (R-PTP-  
 DE delta).  
 GN PTPRD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.  
 RA MEDLINE=95204468; PubMed=7896816;  
 RA Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;  
 RT "Molecular characterization of the human transmembrane protein-  
 RT tyrosine phosphatase delta. Evidence for tissue-specific expression of  
 RT alternative human transmembrane protein-tyrosine phosphatase delta  
 RT isoforms.";  
 RL J. Biol. Chem. 270:6722-6728(1995).  
 RN [2]  
 RP SEQUENCE OF 390-1912 FROM N.A.  
 RC TISSUE=Placenta;  
 RA MEDLINE=91006018; PubMed=2170109;  
 RA Krueger N.X., Streuli M., Saito H.;  
 RT "Structural diversity and evolution of human receptor-like protein  
 RT tyrosine phosphatases.";  
 RL EMBO J. 9:3241-3252(1990).  
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein  
 CC tyrosine + phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: A number of isoforms are produced by  
 CC alternative splicing.  
 CC -1- PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN  
 CC FROM THE TRANSMEMBRANE SEGMENT.  
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 8 FIBRONECTIN TYPE III-LIKE DOMAINS.



FT	DOMAIN	993	1082	FIBRONECTIN TYPE-III 12.
FT	DOMAIN	1083	1170	FIBRONECTIN TYPE-III 13.
FT	DOMAIN	1171	1268	FIBRONECTIN TYPE-III 14.
FT	DOMAIN	1269	1352	FIBRONECTIN TYPE-III 15.
FT	DOMAIN	1353	1442	FIBRONECTIN TYPE-III 16.
FT	DOMAIN	1722	1997	PROTEIN-TYROSINE PHOSPHATASE.
FT	ACT_SITE	1904	1904	BY SIMILARITY.
FT	CARBOHYD	28	28	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	53	53	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	75	75	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	172	172	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	198	198	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	267	267	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	321	321	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	414	414	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	421	421	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	479	479	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	544	544	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	574	574	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	598	598	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	652	652	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	721	721	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	829	829	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1040	1040	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1096	1096	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1163	1163	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1185	1185	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1212	1212	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1274	1274	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1367	1367	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1470	1470	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1474	1474	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1518	1518	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	1997	AA: 224267	MW: 691E99BA7A1515DD CRC64;

Query Match 100.0%; Score 65; DB 1; Length 1997;  
 Best Local Similarity 100.0%; Pred. No. 0.0017;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12  
 |||||  
 DB 1901 VVHCSAGVGRGTG 1912

Search completed: January 17, 2003, 09:11:59  
 Job time : 11 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 17, 2003, 09:36:13 : Search time 29 Seconds  
(without alignments)  
85.261 Million cell updates/sec

Title: US-09-743-492-4  
Perfect score: 65  
Sequence: 1 VVHCSAGVGRGTG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPREMBL\_21:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.podent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriaph:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	24	11 088570	088570 mus musculus
2	65	100.0	24	11 088571	088571 mus musculus
3	65	100.0	112	11 09JLJ6	09JLJ6 mus musculus
4	65	100.0	198	5 023433	023433 caenorhabditis
5	65	100.0	253	13 09NLU0	09NLU0 cephalopoda
6	65	100.0	358	11 062604	062604 ratius norv
7	65	100.0	460	11 062917	062917 ratius norv
8	65	100.0	468	13 09NLU6	09NLU6 eptaretus
9	65	100.0	468	13 09TBA5	09TBA5 potamotrygo
10	65	100.0	468	13 09TBA2	09TBA2 potamotrygo
11	65	100.0	468	13 09TBA0	09TBA0 potamotrygo
12	65	100.0	469	5 09NLI4	09NLI4 branchiosteo
13	65	100.0	469	13 09NLU8	09NLU8 eptaretus
14	65	100.0	470	5 09NLI5	09NLI5 branchiosteo
15	65	100.0	471	5 09YIX6	09YIX6 ephydria f
16	65	100.0	471	13 09TBA3	09TBA3 potamotrygo

17	65	100.0	473	13 09NLU5	09NLU5 eptaretus
18	65	100.0	473	13 09TBA7	09TBA7 potamotrygo
19	65	100.0	483	5 09TBA6	09TBA6 caenorhabditis
20	65	100.0	487	5 09NLI3	09NLI3 branchiosteo
21	65	100.0	488	5 09NLI2	09NLI2 branchiosteo
22	65	100.0	497	13 09TBA8	09TBA8 potamotrygo
23	65	100.0	505	13 09TBA9	09TBA9 potamotrygo
24	65	100.0	508	13 09TBA5	09TBA5 potamotrygo
25	65	100.0	511	13 09NLU7	09NLU7 eptaretus
26	65	100.0	536	4 08TBA8	08TBA8 homo sapien
27	65	100.0	579	11 09JLJ7	09JLJ7 mus musculus
28	65	100.0	582	11 064696	064696 mus musculus
29	65	100.0	615	13 09TBA8	09TBA8 xenopus lae
30	65	100.0	642	4 096K06	096K06 homo sapien
31	65	100.0	642	11 060986	060986 mus musculus
32	65	100.0	659	11 063477	063477 ratius norv
33	65	100.0	699	11 061042	061042 mus musculus
34	65	100.0	749	11 08R169	08R169 mus musculus
35	65	100.0	793	11 09TBA3	09TBA3 mus musculus
36	65	100.0	802	4 096T09	096T09 homo sapien
37	65	100.0	807	13 09TBA9	09TBA9 gallus gall
38	65	100.0	822	13 09TBA6	09TBA6 xenopus lae
39	65	100.0	832	13 090947	090947 gallus gall
40	65	100.0	833	13 090957	090957 brachydanio
41	65	100.0	849	11 09JLJ8	09JLJ8 mus musculus
42	65	100.0	1114	4 09H076	09H076 homo sapien
43	65	100.0	1143	4 016614	016614 homo sapien
44	65	100.0	1200	13 09TBA4	09TBA4 heterodontu
45	65	100.0	1214	5 09VAL3	09VAL3 drosophila

## ALIGNMENTS

RESULT 1	088570	PRELIMINARY:	PRT:	24 AA.
ID	088570			
AC	088570			
DT	01-NOV-1998 (TREMBLrel. 08, Created)			
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Protein tyrosine phosphatase, rPTP-GMCI (Fragment).			
CN	PTPase.			
OC	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI_TaxID	10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J;			
RX	MEDLINE=98395110; PubMed=9727007;			
RA	Wright M.B., Hugo C., Seifert R., Distche C.M., Bowen-Pope D.F.;			
RT	"Proliferating and migrating mesangial cells responding to injury			
RT	express a novel receptor protein-tyrosine phosphatase in experimental			
RT	mesangial proliferative glomerulonephritis.";			
RL	J. Biol. Chem. 273:23929-23937(1998).			
DR	EMBL: AF073998; AAC34822.1; -.			
DR	MGI: 1096349; Ptpyg.			
DR	InterPro: IPR000387; TYR_phosphatase.			
DR	PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.			
DR	PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.			
KW	Hydrolase.			
FT	NON_TER			
FT	NON_TER			
FT	NON_TER			
SO	SEQUENCE	24 AA;	2483 MW;	7E81A5FBF2BC2E2B CRC64;
QY	1 VVHCSAGVGRGTG 12	100.0%;	Score 65;	DB 11; Length 24;
DB	9 VVHCSAGVGRGTG 20	Best Local Similarity	100.0%;	Pred. No. 7.2e-05;
		Matches 12; Conservative	0;	Mismatches 0;
			Indels	0; Gaps 0;

## RESULT 2

```

088571 ID 088571 PRELIMINARY: PRT; 24 AA.
AC 088571:
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Protein tyrosine phosphatase rppp-GMCI (Fragment).
GN PTPRO.
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98395110; PubMed=9727007;
RT Wright M.B., Hugo C., Seifert R., Distèche C.M., Bowen-Pope D.F.;
RT "Proliferating and migrating mesangial cells responding to injury
RT express a novel receptor protein-tyrosine phosphatase in experimental
RT mesangial proliferative glomerulonephritis.";
RL J. Biol. Chem. 273:23929-23937(1998).
DR EMBL: AF073999; AAC34823.1; -.
DR MGD: MGI:1096349; PcpPq.
DR InterPro: IPR000387; TYR_phosphatase.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
KW Hydrolase.
FT NON_TER 1 1
FT NON_TER 24 24
SQ SEQUENCE 24 AA; 2483 MW; 7E81A5FBE2BC2E2B CRC64;

Query Match 100.0%; Score 65; DB 11; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12
Db 9 VVHCSAGVGRGTG 20
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Q9ULJ6 PRELIMINARY: PRT; 112 AA.
AC Q9ULJ6:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE PTP36-D isoform.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DDY;
RC MEDLINE=20068798; PubMed=10600535;
RA Aoyama K., Matsuda T., Aoki N.;
RT "Characterization of newly identified four isoforms for a putative
RT cytosolic protein tyrosine phosphatase PTP36.";
RL Biochem. Biophys. Res. Commun. 266:523-531(1999).
DR EMBL: AF170905; AAF27551.1; -.
DR HSSP: P18052; IYFO.
DR InterPro: IPR003595; PTPc_motif.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00102; Y_phosphatase; 1.
DR PRINTS: PR00700; PRTYPHPTASE.
DR SMART: SM00404; PTPc_motif; 1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.

```

KW Hydrolase. 112 AA; 13195 MW; BD4656A8512B3466 CRC64;  
SQ SEQUENCE

Query Match 100.0%; Score 65; DB 11; Length 112;  
Best Local Similarity 100.0%; Pred. No. 0.00038;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12  
Db 43 VVHCSAGVGRGTG 54  
|||||

## RESULT 4

```

Q23433 ID Q23433 PRELIMINARY: PRT; 198 AA.
AC Q23433:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE ZK1251.5 protein.
GN ZK1251.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurray A.A.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2010(1998).
DR EMBL: Z68222; CA92501.1; -.
DR HSSP: P18052; IYFO.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00102; Y_phosphatase; 1.
DR SMART: SM00194; FTRC; 1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
SQ SEQUENCE 198 AA; 22551 MW; CB586BF32D06375D CRC64;

Query Match 100.0%; Score 65; DB 5; Length 198;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12
Db 105 VVHCSAGVGRGTG 116
|||||
Q9NL00 PRELIMINARY: PRT; 253 AA.
AC Q9NL00:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE HgPFR5b protein (Fragment).
GN HgPFR5B.
OS Epplatretus burgeri (Inshore hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
OC Myxiniidae; Epplatretinae; Epplatretus.
OX NCBI_TaxID=7764;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20219325; PubMed=10754074;

```

RA Ono Koyanagi K., Suga H., Katoh K., Miyata T.;  
 RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:  
 RT divergence of tissue-specific isoform genes in the early evolution of  
 RT vertebrates.";  
 RL J. Mol. Evol. 50:302-311(2000).  
 DR EMBL: AB033577; BAA95184.1; -.  
 DR HSSP: P28827; IRPM.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR InterPro: IPR000242; Tyr\_PP.  
 DR Pfam: PF00102; Y\_phosphatase; 1.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SM00194; PTPc; 1.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 KM Hydrolyase.  
 FT NON\_TER  
 SQ SEQUENCE 253 AA; 28315 MW; 27845DD6FC154C96 CRC64;

Query Match 100.0%; Score 65; DB 13; Length 253;  
 Best Local Similarity 100.0%; Pred. No. 0.0009;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12  
 |||||  
 DB 143 VVHCSAGVGRG 154

## RESULT 6

ID 062604 PRELIMINARY; PRT; 398 AA.  
 AC 062604;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Hypothetical 45.6 kDa protein (Fragment).  
 GN CPPI.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE DAWLEY; TISSUE=OCCIPITAL CORTEX;  
 RX MEDLINE=94045925; PubMed=8229209;  
 RA Sahin M., Hookfield S.;  
 RT "Protein tyrosine phosphatases expressed in the developing rat  
 RT brain.";  
 RL J. Neurosci. 13:4968-4978(1993).  
 DR EMBL: U03273; AAC52124.1; -.  
 DR HSSP: P18052; IYFO.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR InterPro: IPR000242; Tyr\_PP.  
 DR Pfam: PF00102; Y\_phosphatase; 2.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SM00194; PTPc; 2.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
 KM Hydrolyase; Hypothetical protein.  
 FT NON\_TER  
 SQ SEQUENCE 398 AA; 45618 MW; A7CAB3AE6D589E17 CRC64;

Query Match 100.0%; Score 65; DB 11; Length 398;  
 Best Local Similarity 100.0%; Pred. No. 0.0015;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12  
 |||||  
 DB 106 VVHCSAGVGRG 117

## RESULT 7

ID 062917 PRELIMINARY; PRT; 460 AA.  
 AC 062917;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE LAR receptor-linked tyrosine phosphatase.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE DAWLEY; TISSUE=BRAIN;  
 RX MEDLINE=94075340; PubMed=8253779;  
 RA Longo F.M., Martignetti J.A., Le Beau J.M., Zhang J.S., Barnes J.P.,  
 RA Brosius J.;  
 RT "Leukocyte common antigen-related receptor-linked tyrosine  
 RT phosphatase. Regulation of mRNA expression.";  
 RL J. Biol. Chem. 268:26503-26511(1993).  
 DR EMBL: U00477; AAC04306.1; -.  
 DR HSSP: P18052; IYFO.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR InterPro: IPR000242; Tyr\_PP.  
 DR Pfam: PF00102; Y\_phosphatase; 2.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SM00194; PTPc; 2.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 2.  
 DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 2.  
 KM Hydrolyase; Receptor.  
 SQ SEQUENCE 460 AA; 52989 MW; B78C8E504F1260FA CRC64;

Query Match 100.0%; Score 65; DB 11; Length 460;  
 Best Local Similarity 100.0%; Pred. No. 0.0017;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12  
 |||||  
 DB 98 VVHCSAGVGRG 109

## RESULT 8

ID 09N106 PRELIMINARY; PRT; 468 AA.  
 AC 09N106;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE HgptPr2Ab protein (Fragment).  
 GN HGPTPR2AB.  
 OS Eplatreus burgeri (Inshore hagfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;  
 OC Myxiniidae; Eplatreinae; Eplatreus.  
 OX NCBI\_TaxID=7764;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20219325; PubMed=10754074;  
 RX Ono Koyanagi K., Suga H., Katoh K., Miyata T.;  
 RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:  
 RT divergence of tissue-specific isoform genes in the early evolution of  
 RT vertebrates.";  
 RL J. Mol. Evol. 50:302-311(2000).  
 DR EMBL: AB033571; BAA95178.1; -.  
 DR HSSP: P18052; IYFO.  
 DR InterPro: IPR000387; TYR\_phosphatase.  
 DR InterPro: IPR000242; Tyr\_PP.  
 DR Pfam: PF00102; Y\_phosphatase; 2.  
 DR PRINTS: PR00700; PRTYPHPTASE.  
 DR SMART: SM00194; PTPc; 2.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 2.  
 DR PROSITE: PS50056; TYR\_PHOSPHATASE\_2; 2.

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DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase.
FT NON_TER
SQ SEQUENCE 468 AA; 53952 MW; 7E123B7D3EAD69D CRC64;

Query Match
Best Local Similarity 100.0%; Score 65; DB 13; Length 468;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12
DB 106 VVHCSAGVGRG 117

RESULT 9
O91BA5 PRELIMINARY; PRT; 468 AA.
AC O91BA5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE RYPRR2Aa protein (Fragment).
GN RYPRR2Aa.
OS Potamotrygon motoro (South American freshwater stingray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalea; Hypnosqualea; Pristiogryae; Batoidae;
OC Myliobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.
OX NCBI_TaxID=86373;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20219325; PubMed=10754074;
RX Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray;
RT divergence of tissue-specific isoform genes in the early evolution of
RT vertebrates.";
RL J. Mol. Evol. 50:302-311(2000).
DR EMBL; AB033581; BAA95188.1; -.
DR HSSP; P18052; 1YFO.
DR InterPro; IPR000387; TYR-phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y-phosphatase; 2.
DR RYPRR2AC protein (Fragment).
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase.
FT NON_TER
SQ SEQUENCE 468 AA; 53862 MW; 0051F5E0EDD7A580 CRC64;

Query Match
Best Local Similarity 100.0%; Score 65; DB 13; Length 468;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12
DB 106 VVHCSAGVGRG 117

RESULT 10
O91BA2 PRELIMINARY; PRT; 468 AA.
AC O91BA2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE RYPRR2Ab protein (Fragment).
GN RYPRR2Ab.
OS Potamotrygon motoro (South American freshwater stingray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalea; Hypnosqualea; Pristiogryae; Batoidae;
OC Myliobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.
OX NCBI_TaxID=86373;

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RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20219325; PubMed=10754074;
RX Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray;
RT divergence of tissue-specific isoform genes in the early evolution of
RT vertebrates.";
RL J. Mol. Evol. 50:302-311(2000).
DR EMBL; AB033584; BAA95191.1; -.
DR HSSP; P18052; 1YFO.
DR InterPro; IPR000387; TYR-phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y-phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase.
FT NON_TER
SQ SEQUENCE 468 AA; 53885 MW; 8B1CABE0E9692E4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 65; DB 13; Length 468;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12
DB 106 VVHCSAGVGRG 117

RESULT 11
O91BA0 PRELIMINARY; PRT; 468 AA.
AC O91BA0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE RYPRR2Ac protein (Fragment).
GN RYPRR2Ac.
OS Potamotrygon motoro (South American freshwater stingray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalea; Hypnosqualea; Pristiogryae; Batoidae;
OC Myliobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.
OX NCBI_TaxID=86373;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20219325; PubMed=10754074;
RX Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray;
RT divergence of tissue-specific isoform genes in the early evolution of
RT vertebrates.";
RL J. Mol. Evol. 50:302-311(2000).
DR EMBL; AB033586; BAA95193.1; -.
DR HSSP; P18052; 1YFO.
DR InterPro; IPR000387; TYR-phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y-phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase.
FT NON_TER
SQ SEQUENCE 468 AA; 53976 MW; 76C975D92D437A86 CRC64;

Query Match
Best Local Similarity 100.0%; Score 65; DB 13; Length 468;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12
DB 106 VVHCSAGVGRG 117

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Db 106 VVHCSAGVGRG 117

RESULT 12

Q9NL14 ID Q9NL14 PRELIMINARY; PRT; 469 AA.

AC Q9NL14; 01-OCT-2000 (TREMblrel. 15, Created)

DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)

DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)

DE AMPPR4b protein (Fragment).

GN AMPPR4B.

OS Branchiostoma belcheri (Amphioxus).

OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;

OC Branchiostoma.

OX NCBI\_TaxID=7741;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20219325; PubMed=10754074;

RA Oho-Koyanagi K., Suga H., Katoh K., Miyata T.;

RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray;

RT divergence of tissue-specific isoform genes in the early evolution of

RT vertebrates.";

RT RT

RL J. Mol. Evol. 50:302-311(2000).

DR EMBL; AB033563; BAA95170.1; -.

DR HSSP; P18052; IYFO.

DR InterPro; IPR001664; IF.

DR InterPro; IPR000387; TYR\_phosphatase.

DR InterPro; IPR000242; TYR\_PP.

DR Pfam; PF00102; Y\_phosphatase; 2.

DR PRINTS; PR00700; PRYPPHPTASE.

DR SMART; SM00194; PTPC; 2.

DR PROSITE; PS00236; IF; UNKNOWN.1.

DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.

DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 2.

DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 2.

KW Hydroxylase.

FT NON\_TER

SQ SEQUENCE 469 AA; 53631 MW; C2CBREDE629815317 CRC64;

Query Match 100.0%; Score 65; DB 5; Length 469;

Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12

Db 105 VVHCSAGVGRG 116

RESULT 13

Q9NL08 ID Q9NL08 PRELIMINARY; PRT; 469 AA.

AC Q9NL08; 01-OCT-2000 (TREMblrel. 15, Created)

DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)

DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)

DE HGPTR2Aa protein (Fragment).

GN HGPTR2A.

OS Eptatretus burgeri (Inshore hagfish).

OC Eukaryota; Metazoa; Chordata; Granata; Hyperotretti; Myxiniiformes;

OC Myxiniidae; Eptatretinae; Eptatretus.

OX NCBI\_TaxID=7764;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20219325; PubMed=10754074;

RA Oho-Koyanagi K., Suga H., Katoh K., Miyata T.;

RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray;

RT divergence of tissue-specific isoform genes in the early evolution of

RT vertebrates.";

RT RT

RL J. Mol. Evol. 50:302-311(2000).

DR EMBL; AB033569; BAA95176.1; -.

DR HSSP; P18052; IYFO.

DR InterPro; IPR000387; TYR\_phosphatase.

DR InterPro; IPR000242; TYR\_PP.

DR Pfam; PF00102; Y\_phosphatase; 2.

DR PRINTS; PR00700; PRYPPHPTASE.

DR SMART; SM00194; PTPC; 2.

DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.

DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 2.

DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 2.

KW Hydroxylase.

FT NON\_TER

SQ SEQUENCE 469 AA; 53435 MW; 35BEB50A99B92C9 CRC64;

Query Match 100.0%; Score 65; DB 13; Length 469;

Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12

Db 106 VVHCSAGVGRG 117

RESULT 14

Q9NL15 ID Q9NL15 PRELIMINARY; PRT; 470 AA.

AC Q9NL15; 01-OCT-2000 (TREMblrel. 15, Created)

DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)

DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)

DE AMPTR4a protein (Fragment).

GN AMPTR4A.

OS Branchiostoma belcheri (Amphioxus).

OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;

OC Branchiostoma.

OX NCBI\_TaxID=7741;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20219325; PubMed=10754074;

RA Oho-Koyanagi K., Suga H., Katoh K., Miyata T.;

RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray;

RT divergence of tissue-specific isoform genes in the early evolution of

RT vertebrates.";

RT RT

RL J. Mol. Evol. 50:302-311(2000).

DR EMBL; AB033562; BAA95169.1; -.

DR HSSP; P18052; IYFO.

DR InterPro; IPR000387; TYR\_phosphatase.

DR InterPro; IPR000242; TYR\_PP.

DR Pfam; PF00102; Y\_phosphatase; 2.

DR PRINTS; PR00700; PRYPPHPTASE.

DR SMART; SM00194; PTPC; 2.

DR PROSITE; PS00383; TYR\_PHOSPHATASE\_1; 2.

DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 2.

DR PROSITE; PS50055; TYR\_PHOSPHATASE\_PTP; 2.

KW Hydroxylase.

FT NON\_TER

SQ SEQUENCE 470 AA; 53329 MW; CDA72BCF423B75D4 CRC64;

Query Match 100.0%; Score 65; DB 5; Length 470;

Best Local Similarity 100.0%; Pred. No. 0.0018;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12

Db 107 VVHCSAGVGRG 118

RESULT 15

Q9Y1X6 ID Q9Y1X6 PRELIMINARY; PRT; 471 AA.

AC Q9Y1X6; 01-NOV-1999 (TREMblrel. 12, Created)

DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)

DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)

DE SPMPR4 (Fragment).

OS Ephydatia fluviatilis.

OC	Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
OC	Harposclerida; Spongillidae; Ephydatia.
OX	NCBI_TaxID=31330;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=99246376; PubMed=10229569;
RA	Ono K., Suga H., Iwabe N., Kuma K., Miyata T.;
RT	"Multiple protein tyrosine phosphatases in sponges and explosive gene duplication in the early evolution of animals before the parazoan-
RT	eumetazoan split.";
RL	J. Mol. Evol. 48:654-662(1999).
DR	EMBL; AB019125; BAA82558.1; -.
DR	HSSP; P18052; 1YFO.
DR	InterPro; IPR000387; TYR_phosphatase.
DR	InterPro; IPR000242; TYR_PP.
DR	Pfam; PF00102; Y_phosphatase; 2.
DR	PRINTS; PR00700; PRTPPHPTASE.
DR	SMART; SM00194; PTPc; 2.
DR	PROSITE; PS00383; TYR_PHOSPHATASE.1; 2.
DR	PROSITE; PS50056; TYR_PHOSPHATASE.2; 2.
DR	PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW	Hydrolase.
FT	NON_TER
FT	1
FT	1
SEQ	SEQUENCE 471 AA; 54509 MW; 7DA62456154A6A56 CRC64;
QY	Query Match 100.0%; Score 65; DB 5; Length 471;
	Best Local Similarity 100.0%; Pred. No. 0.0018;
	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	1 VVHCASGVRGTG 12
	106 VVHCASGVRGTG 117

Search completed: January 17, 2003, 09:38:30  
Job time : 30 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 17, 2003, 09:10:56 : Search time 36 seconds

(without alignments)  
44.417 Million cell updates/sec

Title: US-09-743-492-4

Perfect score: 65

Sequence: 1 VVHCSAGYGRFG 12

Scoring table: BLOSUM62

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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1981.DAT:\*

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4: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1983.DAT:\*

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7: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1986.DAT:\*

8: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1987.DAT:\*

9: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1988.DAT:\*

10: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1989.DAT:\*

11: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1990.DAT:\*

12: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1991.DAT:\*

13: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1992.DAT:\*

14: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1993.DAT:\*

15: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1994.DAT:\*

16: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1995.DAT:\*

17: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1996.DAT:\*

18: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1997.DAT:\*

19: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1998.DAT:\*

20: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1999.DAT:\*

21: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT:\*

22: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:\*

23: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	12	21	AA181786
2	65	100.0	236	20	AA104707
3	65	100.0	236	20	AA104700
4	65	100.0	240	13	AA120745
5	65	100.0	250	22	AA159370
6	65	100.0	253	22	AA159373
7	65	100.0	253	22	AA159374
8	65	100.0	254	22	AA159372
9	65	100.0	254	22	AA159377
10	65	100.0	257	22	AA159369

11	65	100.0	260	22	AA159367
12	65	100.0	260	22	AA159388
13	65	100.0	261	22	AA159366
14	65	100.0	306	22	AA159368
15	65	100.0	309	22	AA159371
16	65	100.0	309	22	AA159372
17	65	100.0	310	22	AA159373
18	65	100.0	310	22	AA159375
19	65	100.0	313	22	AA159367
20	65	100.0	316	22	AA159365
21	65	100.0	317	22	AA159366
22	65	100.0	442	21	AA159372
23	65	100.0	579	21	AA159373
24	65	100.0	607	21	AA159373
25	65	100.0	607	21	AA159373
26	65	100.0	607	21	AA159373
27	65	100.0	647	22	AA159374
28	65	100.0	647	22	AA159374
29	65	100.0	659	20	AA159372
30	65	100.0	659	20	AA159372
31	65	100.0	699	22	AA159372
32	65	100.0	699	22	AA159372
33	65	100.0	700	22	AA159372
34	65	100.0	700	22	AA159372
35	65	100.0	717	22	AA159372
36	65	100.0	793	13	AA159373
37	65	100.0	793	17	AA159373
38	65	100.0	793	20	AA159373
39	65	100.0	802	13	AA159373
40	65	100.0	802	17	AA159373
41	65	100.0	802	20	AA159373
42	65	100.0	807	23	AA159373
43	65	100.0	807	23	AA159373
44	65	100.0	1149	22	AA159373
45	65	100.0	1237	19	AA159373

#### ALIGNMENTS

RESULT 1	AA181786	standard; Peptide; 12 AA.
ID	AA181786	
XX	AA181786	
AC	07-JUN-2000	(first entry)
XX		
DT		
XX		
DE		Protein tyrosine phosphatase motif #1.
XX		
KW		Human; protein tyrosine phosphatase; antibody; intracellular domain; IAR;
KW		CD45; PTP; diagnosis; insulin resistance related disease; syndrome X;
KW		non-insulin dependent diabetes mellitus; arteriosclerosis; therapy;
KW		heart disorder; signature motif.
XX		
OS		Unidentified.
XX		
PN		WO200002922-A1.
PD		20-JAN-2000.
XX		
PF		06-JUL-1999; 99WO-JP03656.
XX		
PR		10-JUL-1998; 98WO-JP03120.
XX		
PA		(FUSO ) FUSO PHARM IND LTD.
XX		
PI		Yamamoto H, Tsujikawa K, Uchino Y;
XX		
DR		WPI; 2000-182215/16.
XX		
PT		Antibody for diagnosis and treatment of insulin resistance disorders and syndrome X recognises the intracellular domains of tyrosine

PT phosphatase -  
XX  
PS Example 3; Page 32; 83pp; Japanese.  
XX  
CC This sequence represents a motif of a protein tyrosine  
phosphatases. The invention relates to an antibody of the  
CC phosphatases. The invention relates to an antibody of the  
CC has sites specifically recognising the intracellular domain  
CC of two or more protein tyrosine phosphatases (PTPs). The antibody is  
CC useful for the detection and assay of PTP including novel phosphatases  
CC generated by cloning; and diagnosis, treatment and prevention of insulin  
CC resistance related diseases and non-insulin dependent diabetes mellitus,  
CC syndrome x and arteriosclerosis and heart disorders.  
XX  
SQ Sequence 12 AA;  
Query Match 100.0%; Score 65; DB 21; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00021;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VVHCSAGVGRTG 12  
Db 1 VVHCSAGVGRTG 12  
IIIIIIIIIIII  
RESULT 2  
AA04707  
ID AA04707 standard; Protein; 236 AA.  
XX  
AC AA04707;  
XX  
DT 22-JUN-1999 (first entry)  
XX  
DE Mouse RPTPa amino acids 265-500.  
XX  
KW Receptor-type protein tyrosine phosphatase; RPTP; mouse; enzyme; cancer;  
cellular metabolism; regulation; insulin; diabetes; oncoprotein;  
KM negative growth regulator.  
XX  
OS Mus sp.  
XX  
PN US5888794-A.  
XX  
PD 30-MAR-1999.  
XX  
PF 23-MAY-1995; 95US-0448288.  
XX  
PR 10-FEB-1993; 93US-0015985.  
PR 11-JUL-1990; 90US-0551270.  
PR 26-FEB-1991; 91US-0654188.  
PR 23-MAY-1995; 95US-0448288.  
XX  
PA (UYNV ) UNIV NEW YORK STATE.  
XX  
PI Sap JM, Schlessinger J;  
XX  
DR WPI; 1999-253232/21.  
XX  
PT Receptor-type protein tyrosine phosphatase from mouse and human  
XX  
PS Claim 6; Page -: 50pp; English.  
XX  
CC This sequence represents a claimed peptide comprising amino acids  
265-500 of the receptor-type protein tyrosine phosphatase alpha (RPTPa)  
CC present in mice (AA04695). The protein, optionally immobilized or  
CC present in cells, is used to screen for specific binding agents or agents  
CC that stimulate/inhibit its enzymatic activity. These agents may be used  
CC to regulate major pathways of cellular metabolism. Activation of RPTPa  
CC may be an endogenous regulatory mechanism against cancer and may counter  
CC the effects of insulin (possibly causing insulin-resistant diabetes),  
CC i.e. RPTPa may be a recessive oncoprotein and negative growth regulator.  
CC (Note: this sequence is not given in the specification but is generated  
CC from information disclosed in the specification by the inventors).  
XX

SQ Sequence 236 AA;  
Query Match 100.0%; Score 65; DB 20; Length 236;  
Best Local Similarity 100.0%; Pred. No. 0.004;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VVHCSAGVGRTG 12  
Db 166 VVHCSAGVGRTG 177  
IIIIIIIIIIII  
RESULT 3  
AA04700  
ID AA04700 standard; Protein; 236 AA.  
XX  
AC AA04700;  
XX  
DT 22-JUN-1999 (first entry)  
XX  
DE Human RPTPa amino acids 265-500.  
XX  
KW Receptor-type protein tyrosine phosphatase; RPTP; human; enzyme; cancer;  
cellular metabolism; regulation; insulin; diabetes; oncoprotein;  
KM negative growth regulator.  
XX  
OS Homo sapiens.  
XX  
PN US5888794-A.  
XX  
PD 30-MAR-1999.  
XX  
PF 23-MAY-1995; 95US-0448288.  
XX  
PR 10-FEB-1993; 93US-0015985.  
PR 11-JUL-1990; 90US-0551270.  
PR 26-FEB-1991; 91US-0654188.  
PR 23-MAY-1995; 95US-0448288.  
XX  
PA (UYNV ) UNIV NEW YORK STATE.  
XX  
PI Sap JM, Schlessinger J;  
XX  
DR WPI; 1999-253232/21.  
XX  
PT Receptor-type protein tyrosine phosphatase from mouse and human  
XX  
PS Claim 2; Page -: 50pp; English.  
XX  
CC This sequence represents a claimed peptide comprising amino acids  
265-500 of the receptor-type protein tyrosine phosphatase alpha (RPTPa)  
CC protein from humans (AA04694). The protein, optionally immobilized or  
CC present in cells, is used to screen for specific binding agents or agents  
CC that stimulate/inhibit its enzymatic activity. These agents may be used  
CC to regulate major pathways of cellular metabolism. Activation of RPTPa  
CC may be an endogenous regulatory mechanism against cancer and may counter  
CC the effects of insulin (possibly causing insulin-resistant diabetes),  
CC i.e. RPTPa may be a recessive oncoprotein and negative growth regulator.  
CC (Note: this sequence is not given in the specification but is generated  
CC from information disclosed in the specification by the inventors).  
XX  
SQ Sequence 236 AA;  
Query Match 100.0%; Score 65; DB 20; Length 236;  
Best Local Similarity 100.0%; Pred. No. 0.004;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VVHCSAGVGRTG 12  
Db 175 VVHCSAGVGRTG 186  
IIIIIIIIIIII  
RESULT 4  
AAR20745



ID AAK20745 standard; Protein; 240 AA.  
 XX  
 AC AAR20745;  
 XX  
 DT 28-MAY-1992 (first entry)  
 XX  
 DE Human R-PTPase beta first conserved phosphatase.  
 XX  
 KM Receptor-type protein tyrosine phosphatase; cellular metabolism;  
 cancer; diabetes.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9201050-A.  
 XX  
 PD 23-JUN-1992.  
 XX  
 PF 11-JUL-1991; 91WO-US04892.  
 XX  
 PR 26-FEB-1991; 91US-065418.  
 PR 11-JUL-1990; 90US-0551270.  
 XX  
 PA (UYNV-) NEW YORK UNIV.  
 XX  
 PI Schlessinger J;  
 XX  
 DR WPI; 1992-056865/07.  
 XX  
 PT Human receptor-type protein tyrosine phosphatase - has DNA  
 encoding it and antibodies specific for it, useful for screening  
 PT drugs affecting R-PTPase activity, and detection of mutant genes  
 XX  
 PS Claim 5; Fig 5A; 77pp; English.  
 XX  
 CC The amino acid sequence is that of human receptor-type protein  
 CC tyrosine phosphatase (R-PTPase) beta first conserved phosphatase. It  
 CC is useful in methods for screening drugs and other agents which are  
 CC capable of activating or inhibiting the R-PTPase activity and thereby  
 CC affecting major pathways of cellular metabolism. Activation of  
 CC R-PTPases, leading to dephosphorylation would serve as a counter-  
 CC regulatory mechanism to prevent or inhibit growth, and may serve as  
 CC an endogenous regulatory mechanism against cancer. Mutation or  
 CC dysregulation of this receptor/enzyme system may promote susceptibility  
 CC to cancer, diabetes, or other diseases associated with alterations in  
 CC cellular phosphotyrosine metabolism. It can be used to raise antibodies  
 CC which can be used in immunoassays to determine the presence and amt.  
 CC of R-PTPases, or in immunoelectron microscopy for in situ detection of  
 CC R-PTPase. See also AAR20743-R20748.  
 CC  
 SQ Sequence 240 AA;  
 QY  
 Db 1 VVHCSAGVGRTG 12  
 179 VVHCSAGVGRTG 190

Query Match 100.0%; Score 65; DB 13; Length 240;  
 Best Local Similarity 100.0%; Pred. No. 0.0041;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5  
 AAB59370  
 ID AAB59370 standard; Protein; 250 AA.  
 XX  
 AC AAB59370;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Human protein tyrosine phosphatase #6.  
 XX  
 KM Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;  
 substrate trapping.  
 XX

OS Homo sapiens.  
 XX  
 PN WO200075339-A1.  
 XX  
 PD 14-DEC-2000.  
 XX  
 PF 24-MAY-2000; 2000WO-US14211.  
 XX  
 PR 03-JUN-1999; 99US-0137319.  
 PR 16-JUN-1999; 99US-0334575.  
 XX  
 PA (COLD-) COLD SPRING HARBOR LAB.  
 XX  
 PI Tonks NK, Zhang S;  
 XX  
 DR WPI; 2001-080598/09.  
 XX  
 PT New substrate trapping mutant protein tyrosine phosphatases (PTP) in  
 PT which the wild type PTP catalytic domain invariant aspartate is  
 PT replaced with an unphosphorylated amino acid, useful in gene therapy  
 XX  
 PS Disclosure; Fig 1; 109pp; English.  
 XX  
 CC The present invention provides substrate trapping mutant protein tyrosine  
 CC phosphatases (PTPs). They can be used to reduce the activity of tyrosine  
 CC phosphorylated proteins and to screen for modulators capable of altering  
 CC the binding of protein tyrosine phosphatases to their substrate. These  
 CC may be used in disease diagnosis and treatment.  
 CC  
 SQ Sequence 250 AA;  
 QY  
 Db 1 VVHCSAGVGRTG 12  
 180 VVHCSAGVGRTG 191

Query Match 100.0%; Score 65; DB 22; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 0.0043;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6  
 AAB59373  
 ID AAB59373 standard; Protein; 253 AA.  
 XX  
 AC AAB59373;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Human protein tyrosine phosphatase #9.  
 XX  
 KM Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;  
 substrate trapping.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200075339-A1.  
 XX  
 PD 14-DEC-2000.  
 XX  
 PF 24-MAY-2000; 2000WO-US14211.  
 XX  
 PR 03-JUN-1999; 99US-0137319.  
 PR 16-JUN-1999; 99US-0334575.  
 XX  
 PA (COLD-) COLD SPRING HARBOR LAB.  
 XX  
 PI Tonks NK, Zhang S;  
 XX  
 DR WPI; 2001-080598/09.  
 XX  
 PT New substrate trapping mutant protein tyrosine phosphatases (PTP) in  
 PT which the wild type PTP catalytic domain invariant aspartate is  
 PT replaced with an unphosphorylated amino acid, useful in gene therapy  
 XX

XX Disclosure; Fig 1; 109pp; English.

CC The present invention provides substrate trapping mutant protein tyrosine  
phosphatases (PTPs). They can be used to reduce the activity of tyrosine  
phosphorylated proteins and to screen for modulators capable of altering  
the binding of protein tyrosine phosphatases to their substrate. These  
CC may be used in disease diagnosis and treatment.

XX Sequence 253 AA;

Query Match 100.0%; Score 65; DB 22; Length 253;

Best Local Similarity 100.0%; Pred. No. 0.0043;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12  
|||||  
DB 183 VVHCSAGVGRG 194

RESULT 7

AAB59374

ID AAB59374 standard; Protein; 253 AA.

XX AAB59374;

DT 21-MAR-2001 (first entry)

DE Murine protein tyrosine phosphatase #1.

KM Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;

KW substrate trapping.

XX Mus sp.

PN WO200075339-A1.

PD 14-DEC-2000.

PF 24-MAY-2000; 2000WO-US14211.

PR 03-JUN-1999; 99US-0137319.

PR 16-JUN-1999; 99US-0334575.

XX (COLD-) COLD SPRING HARBOR LAB.

PI Tonks NK, Zhang S;

DR WPI; 2001-080598/09.

PT New substrate trapping mutant protein tyrosine phosphatases (PTP) in  
PT which the wild type PTP catalytic domain invariant aspartate is  
PT replaced with an unphosphorylated amino acid, useful in gene therapy

XX Disclosure; Fig 1; 109pp; English.

CC The present invention provides substrate trapping mutant protein tyrosine  
phosphatases (PTPs). They can be used to reduce the activity of tyrosine  
phosphorylated proteins and to screen for modulators capable of altering  
the binding of protein tyrosine phosphatases to their substrate. These  
CC may be used in disease diagnosis and treatment.

XX Sequence 253 AA;

Query Match 100.0%; Score 65; DB 22; Length 253;

Best Local Similarity 100.0%; Pred. No. 0.0043;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12  
|||||  
DB 183 VVHCSAGVGRG 194

RESULT 8

AAB59372

ID AAB59372 standard; Protein; 254 AA.

XX AAB59372;

DT 21-MAR-2001 (first entry)

DE Human protein tyrosine phosphatase #8.

KM Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;

KW substrate trapping.

XX Homo sapiens.

PN WO200075339-A1.

PD 14-DEC-2000.

PF 24-MAY-2000; 2000WO-US14211.

PR 03-JUN-1999; 99US-0137319.

PR 16-JUN-1999; 99US-0334575.

XX (COLD-) COLD SPRING HARBOR LAB.

PI Tonks NK, Zhang S;

DR WPI; 2001-080598/09.

PT New substrate trapping mutant protein tyrosine phosphatases (PTP) in  
PT which the wild type PTP catalytic domain invariant aspartate is  
PT replaced with an unphosphorylated amino acid, useful in gene therapy

XX Disclosure; Fig 1; 109pp; English.

CC The present invention provides substrate trapping mutant protein tyrosine  
phosphatases (PTPs). They can be used to reduce the activity of tyrosine  
phosphorylated proteins and to screen for modulators capable of altering  
the binding of protein tyrosine phosphatases to their substrate. These  
CC may be used in disease diagnosis and treatment.

XX Sequence 254 AA;

Query Match 100.0%; Score 65; DB 22; Length 254;

Best Local Similarity 100.0%; Pred. No. 0.0043;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRG 12  
|||||  
DB 184 VVHCSAGVGRG 195

RESULT 9

AAB59377

ID AAB59377 standard; Protein; 254 AA.

XX AAB59377;

DT 21-MAR-2001 (first entry)

DE Human protein tyrosine phosphatase #12.

KM Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;

KW substrate trapping.

XX Homo sapiens.

PN WO200075339-A1.

PD 14-DEC-2000.

PF 24-MAY-2000; 2000WO-US14211.

XX 03-JUN-1999; 99US-0137319.  
PR 16-JUN-1999; 99US-0334575.  
XX  
PA (COLD-) COLD SPRING HARBOR LAB.  
XX  
PI Tonks NK, Zhang S;  
XX  
DR WPI: 2001-080598/09.  
XX  
PT New substrate trapping mutant protein tyrosine phosphatases (PTP) in  
PT which the wild type PTP catalytic domain invariant aspartate is  
PT replaced with an unphosphorylated amino acid, useful in gene therapy  
XX  
PS Disclosure; Fig 1; 109pp; English.  
XX  
CC The present invention provides substrate trapping mutant protein tyrosine  
CC phosphatases (PTPs). They can be used to reduce the activity of tyrosine  
CC phosphorylated proteins and to screen for modulators capable of altering  
CC the binding of protein tyrosine phosphatases to their substrate. These  
CC may be used in disease diagnosis and treatment.  
XX  
SQ Sequence 254 AA;  
  
Query Match 100.0%; Score 65; DB 22; Length 254;  
Best Local Similarity 100.0%; Pred. No. 0.0043;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VVHCSAGVGRGTG 12  
DB 184 VVHCSAGVGRGTG 195  
IIIIIIIIII  
  
RESULT 10  
AAB59369  
ID AAB59369 standard; Protein; 257 AA.  
XX  
AC AAB59369;  
XX  
DT 21-MAR-2001 (first entry)  
XX  
DE Drosophila protein tyrosine phosphatase #1.  
XX  
KW Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;  
KM Substrate trapping.  
XX  
OS Drosophila sp.  
XX  
PN WO200075339-A1.  
XX  
PD 14-DEC-2000.  
XX  
PF 24-MAY-2000; 2000WO-US14211.  
XX  
PR 03-JUN-1999; 99US-0137319.  
PR 16-JUN-1999; 99US-0334575.  
XX  
PA (COLD-) COLD SPRING HARBOR LAB.  
XX  
PI Tonks NK, Zhang S;  
XX  
DR WPI: 2001-080598/09.  
XX  
PT New substrate trapping mutant protein tyrosine phosphatases (PTP) in  
PT which the wild type PTP catalytic domain invariant aspartate is  
PT replaced with an unphosphorylated amino acid, useful in gene therapy  
XX  
PS Disclosure; Fig 1; 109pp; English.  
XX  
CC The present invention provides substrate trapping mutant protein tyrosine  
CC phosphatases (PTPs). They can be used to reduce the activity of tyrosine  
CC phosphorylated proteins and to screen for modulators capable of altering  
CC the binding of protein tyrosine phosphatases to their substrate. These

CC may be used in disease diagnosis and treatment.  
XX  
SQ Sequence 257 AA;  
  
Query Match 100.0%; Score 65; DB 22; Length 257;  
Best Local Similarity 100.0%; Pred. No. 0.0044;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VVHCSAGVGRGTG 12  
DB 187 VVHCSAGVGRGTG 198  
IIIIIIIIII  
  
RESULT 11  
AAB59367  
ID AAB59367 standard; Protein; 260 AA.  
XX  
AC AAB59367;  
XX  
DT 21-MAR-2001 (first entry)  
XX  
DE Human protein tyrosine phosphatase #4.  
XX  
KW Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;  
KM Substrate trapping.  
XX  
OS Homo sapiens.  
XX  
PN WO200075339-A1.  
XX  
PD 14-DEC-2000.  
XX  
PF 24-MAY-2000; 2000WO-US14211.  
XX  
PR 03-JUN-1999; 99US-0137319.  
PR 16-JUN-1999; 99US-0334575.  
XX  
PA (COLD-) COLD SPRING HARBOR LAB.  
XX  
PI Tonks NK, Zhang S;  
XX  
DR WPI: 2001-080598/09.  
XX  
PT New substrate trapping mutant protein tyrosine phosphatases (PTP) in  
PT which the wild type PTP catalytic domain invariant aspartate is  
PT replaced with an unphosphorylated amino acid, useful in gene therapy  
XX  
PS Disclosure; Fig 1; 109pp; English.  
XX  
CC The present invention provides substrate trapping mutant protein tyrosine  
CC phosphatases (PTPs). They can be used to reduce the activity of tyrosine  
CC phosphorylated proteins and to screen for modulators capable of altering  
CC the binding of protein tyrosine phosphatases to their substrate. These  
CC may be used in disease diagnosis and treatment.  
XX  
SQ Sequence 260 AA;  
  
Query Match 100.0%; Score 65; DB 22; Length 260;  
Best Local Similarity 100.0%; Pred. No. 0.0044;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VVHCSAGVGRGTG 12  
DB 190 VVHCSAGVGRGTG 201  
IIIIIIIIII  
  
RESULT 12  
AAB59388  
ID AAB59388 standard; Protein; 260 AA.  
XX  
AC AAB59388;  
XX  
DT 21-MAR-2001 (first entry)

XX Human protein tyrosine phosphatase #16.  
DE Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;  
XX substrate trapping.  
KW Homo sapiens.  
XX WO200075339-A1.  
XX 14-DEC-2000.  
XX 24-MAY-2000; 2000WO-US14211.  
XX 03-JUN-1999; 99US-0137319.  
XX 16-JUN-1999; 99US-0334575.  
XX (COLD-) COLD SPRING HARBOR LAB.  
PA Tonks NK, Zhang S;  
XX WPI; 2001-080598/09.  
XX New substrate trapping mutant protein tyrosine phosphatases (PTP) in  
PT which the wild type PTP catalytic domain invariant aspartate is  
PT replaced with an unphosphorylated amino acid, useful in gene therapy  
XX  
XX Disclosure; Fig 1; 109pp; English.  
XX The present invention provides substrate trapping mutant protein tyrosine  
CC phosphatases (PTPs). They can be used to reduce the activity of tyrosine  
CC phosphorylated proteins and to screen for modulators capable of altering  
CC the binding of protein tyrosine phosphatases to their substrate. These  
CC may be used in disease diagnosis and treatment.  
XX  
SQ Sequence 260 AA:  
Query Match 100.0%; Score 65; DB 22; Length 260;  
Best Local Similarity 100.0%; Pred. No. 0.0044;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VVHCSAGVGRGTG 12  
DB 190 VVHCSAGVGRGTG 201  
RESULT 13  
AAB59366  
ID AAB59366 standard; Protein; 261 AA.  
XX AAB59366;  
XX AAB59366;  
XX 21-MAR-2001 (first entry)  
XX Human protein tyrosine phosphatase #3.  
DE Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;  
KW substrate trapping.  
XX Homo sapiens.  
XX WO200075339-A1.  
XX 14-DEC-2000.  
XX 24-MAY-2000; 2000WO-US14211.  
XX 03-JUN-1999; 99US-0137319.  
XX 16-JUN-1999; 99US-0334575.  
XX (COLD-) COLD SPRING HARBOR LAB.  
PA Tonks NK, Zhang S;  
XX

XX WPI; 2001-080598/09.  
XX New substrate trapping mutant protein tyrosine phosphatases (PTP) in  
PT which the wild type PTP catalytic domain invariant aspartate is  
PT replaced with an unphosphorylated amino acid, useful in gene therapy  
XX  
XX Disclosure; Fig 1; 109pp; English.  
XX The present invention provides substrate trapping mutant protein tyrosine  
CC phosphatases (PTPs). They can be used to reduce the activity of tyrosine  
CC phosphorylated proteins and to screen for modulators capable of altering  
CC the binding of protein tyrosine phosphatases to their substrate. These  
CC may be used in disease diagnosis and treatment.  
XX  
SQ Sequence 261 AA:  
Query Match 100.0%; Score 65; DB 22; Length 261;  
Best Local Similarity 100.0%; Pred. No. 0.0045;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VVHCSAGVGRGTG 12  
DB 191 VVHCSAGVGRGTG 202  
RESULT 14  
AAG78268  
ID AAG78268 standard; Protein; 306 AA.  
XX AAG78268;  
XX AAG78268;  
XX 19-DEC-2001 (first entry)  
XX Human DCA-D1.  
DE PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;  
KW dephosphorylation; phosphotyrosine; human; PTPB; mouse; fruit fly;  
KW yeast.  
XX Homo sapiens.  
XX WO200161031-A2.  
XX 23-AUG-2001.  
XX 13-FEB-2001; 2001WO-US05180.  
XX 14-FEB-2000; 2000US-0181769.  
XX (CEPT-) CEPTYR INC.  
XX Flint AJ, Cool DE;  
XX WPI; 2001-570570/64.  
XX Screening assays to identify agents that alter protein tyrosine  
PT phosphatase (PTP) binding to, and PTP-mediated catalytic  
PT dephosphorylation of phosphotyrosine peptide substrates  
XX  
XX Disclosure; Fig 1; 79pp; English.  
XX The invention relates to identifying agents which alter the interaction  
CC between a protein tyrosine phosphatase (PTP) and a tyrosine  
CC phosphorylated polypeptide using fluorescence energy signals. The methods  
CC are useful for performing screening assay to identify agents that alter  
CC PTP binding to and PTP-mediated catalytic dephosphorylation of  
CC phosphotyrosine peptide substrates. The present sequence is that of a  
CC catalytic domain of a PTP for comparison with human PTPB (AAG78262).  
XX  
SQ Sequence 306 AA:  
Query Match 100.0%; Score 65; DB 22; Length 306;

Best Local Similarity 100.0%; Pred. No. 0.0052;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRGTG 12  
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DB 180 VVHCSAGVGRGTG 191

## RESULT 15

AAG78271  
ID AAG78271 standard; Protein; 309 AA.

AC AAG78271;

DT 19-DEC-2001 (first entry)

DE Human PTP-epsilon-DL.

KM PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;  
KW dephosphorylation; phosphotyrosine; human; PTPB; mouse; fruit fly;  
yeast.

OS Homo sapiens.

PN W0200161031-A2.

PD 23-AUG-2001.

PF 13-FEB-2001; 2001WO-US05180.

PR 14-FEB-2000; 2000US-0181769.

PA (CEPT-) CEPTYR INC.

PI Flint AJ, COOL DE;

DR WPI; 2001-570570/64.

PT Screening assays to identify agents that alter protein tyrosine  
phosphatase (PTP) binding to, and PTP-mediated catalytic  
dephosphorylation of phosphotyrosine peptide substrates -

PS Disclosure; Fig 1; 79pp; English.

CC The invention relates to identifying agents which alter the interaction  
between a protein tyrosine phosphatase (PTP) and a tyrosine  
phosphorylated polypeptide using fluorescence energy signals. The methods  
are useful for performing screening assay to identify agents that alter  
PTP binding to and PTP-mediated catalytic dephosphorylation of  
phosphotyrosine peptide substrates. The present sequence is that of a  
catalytic domain of a PTP for comparison with human PTPB (AAG78262).

SQ Sequence 309 AA;

## Query Match

100.0%; Score 65; DB 22; Length 309;

Best Local Similarity 100.0%; Pred. No. 0.0053;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRGTG 12  
|||||  
DB 183 VVHCSAGVGRGTG 194

Search completed: January 17, 2003, 09:11:41  
Job time : 37 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2003, 09:12:06 : Search time 11 Seconds  
(without alignments)  
21.686 Million cell updates/sec

Title: US-09-743-492-4

Perfect score: 65  
Sequence: 1 VVHCSAGVGRG 12

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubppa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubppa/PCUS\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubppa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubppa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	100.0	248	10	US-09-848-294-10
2	65	100.0	306	10	US-09-788-626-8
3	65	100.0	309	10	US-09-788-626-11
4	65	100.0	309	10	US-09-788-626-12
5	65	100.0	310	10	US-09-788-626-10
6	65	100.0	310	10	US-09-788-626-15
7	65	100.0	313	10	US-09-788-626-7
8	65	100.0	316	10	US-09-788-626-5
9	65	100.0	316	10	US-09-788-626-26
10	65	100.0	317	10	US-09-788-626-4
11	65	100.0	442	10	US-09-925-300-950
12	65	100.0	1502	9	US-09-808-602-54
13	65	100.0	1948	9	US-09-808-602-55
14	65	100.0	2308	12	US-10-000-954-2
15	64	98.5	307	10	US-09-788-626-20
16	64	98.5	312	10	US-09-788-626-24
17	64	98.5	313	10	US-09-788-626-17
18	64	98.5	325	10	US-09-788-626-13
19	64	98.5	341	10	US-09-788-626-23

20	64	98.5	360	12	US-10-028-748-2	Sequence 2, Appl1
21	64	98.5	593	10	US-09-820-021A-3	Sequence 3, Appl1
22	63	96.9	291	10	US-09-788-626-18	Sequence 18, Appl1
23	63	96.9	322	10	US-09-788-626-14	Sequence 14, Appl1
24	63	96.9	595	10	US-09-920-021A-1	Sequence 1, Appl1
25	62	95.4	313	10	US-09-788-626-19	Sequence 19, Appl1
26	62	95.4	319	10	US-09-788-626-6	Sequence 6, Appl1
27	61	93.8	244	10	US-09-848-294-7	Sequence 7, Appl1
28	61	93.8	291	10	US-09-788-626-22	Sequence 22, Appl1
29	61	93.8	294	10	US-09-788-626-27	Sequence 27, Appl1
30	61	93.8	305	10	US-09-788-626-9	Sequence 9, Appl1
31	61	93.8	307	10	US-09-788-626-25	Sequence 25, Appl1
32	61	93.8	309	10	US-09-788-626-16	Sequence 16, Appl1
33	61	93.8	523	10	US-09-799-777-76	Sequence 76, Appl1
34	61	93.8	603	10	US-09-906-779-4	Sequence 4, Appl1
35	61	93.8	913	10	US-09-848-294-2	Sequence 2, Appl1
36	61	93.8	1274	9	US-10-020-215-2	Sequence 2, Appl1
37	60	92.3	250	10	US-09-848-294-8	Sequence 8, Appl1
38	60	92.3	254	10	US-09-788-626-2	Sequence 2, Appl1
39	60	92.3	435	10	US-09-986-240-1	Sequence 1, Appl1
40	59	90.8	246	10	US-09-848-294-9	Sequence 9, Appl1
41	59	90.8	251	10	US-09-788-626-3	Sequence 3, Appl1
42	58	89.2	13	10	US-09-906-779-6	Sequence 6, Appl1
43	57	87.7	281	10	US-09-788-626-28	Sequence 28, Appl1
44	57	87.7	298	10	US-09-788-626-29	Sequence 29, Appl1
45	57	87.7	750	10	US-09-801-368-280	Sequence 280, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-848-294-10  
Sequence 10, Application US/09848294  
Patent No. US20020049179A1  
GENERAL INFORMATION:  
APPLICANT: Tunks, Nicholas K.  
TITLE OF INVENTION: Isolation of A cDNA Encoding A NO. US20020049179A1el  
TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal  
FILE REFERENCE: CSHL90-04F2A  
CURRENT APPLICATION NUMBER: US/09/848,294  
CURRENT FILING DATE: 2001-05-03  
PRIOR APPLICATION NUMBER: 09/235,251  
PRIOR FILING DATE: 1999-01-22  
PRIOR APPLICATION NUMBER: 08/759,536  
PRIOR FILING DATE: 1996-12-04  
PRIOR APPLICATION NUMBER: 08/107,420  
PRIOR FILING DATE: 1993-08-16  
PRIOR APPLICATION NUMBER: 07/663,579  
PRIOR FILING DATE: 1991-03-01  
PRIOR APPLICATION NUMBER: 07/494,036  
PRIOR FILING DATE: 1990-03-14  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 10  
LENGTH: 248  
TYPE: PRT  
ORGANISM: Homosapiens  
US-09-848-294-10  
Query Match 100.0%; Score 65; DB 10; Length 248;  
Best Local Similarity 100.0%; Pred. No. 0.00085;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VVHCSAGVGRG 12  
Db 174 VVHCSAGVGRG 185  
RESULT 2  
US-09-788-626-8  
Sequence 8, Application US/09788626

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; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-788-626-8

Query Match
Best Local Similarity 100.0%; Score 65; DB 10; Length 306;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12
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Db 180 VVHCSAGVGRGTG 191

RESULT 3
; US-09-788-626-11
; Sequence 11, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-788-626-11

Query Match
Best Local Similarity 100.0%; Score 65; DB 10; Length 309;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12
    |||||
Db 183 VVHCSAGVGRGTG 194

RESULT 4
; US-09-788-626-12
; Sequence 12, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Mus musculus
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US-09-788-626-12

Query Match
Best Local Similarity 100.0%; Score 65; DB 10; Length 309;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12
    |||||
Db 183 VVHCSAGVGRGTG 194

RESULT 5
; US-09-788-626-10
; Sequence 10, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-788-626-10

Query Match
Best Local Similarity 100.0%; Score 65; DB 10; Length 310;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12
    |||||
Db 184 VVHCSAGVGRGTG 195

RESULT 6
; US-09-788-626-15
; Sequence 15, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-788-626-15

Query Match
Best Local Similarity 100.0%; Score 65; DB 10; Length 310;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRGTG 12
    |||||
Db 184 VVHCSAGVGRGTG 195

RESULT 7
; US-09-788-626-7
; Sequence 7, Application US/09788626
; Patent No. US20020009762A1
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; GENERAL INFORMATION:
; APPLICANT: Flint, Deborah J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-788-626-7

Query Match          100.0%; Score 65; DB 10; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12
Db 187 VVHCSAGVGRG 198

RESULT 8
US-09-788-626-5
; Sequence 5; Application US/09788626
; Patent No. US2002009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-5

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Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12
Db 190 VVHCSAGVGRG 201

RESULT 9
US-09-788-626-26
; Sequence 26; Application US/09788626
; Patent No. US2002009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-26

Query Match          100.0%; Score 65; DB 10; Length 316;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12
Db 190 VVHCSAGVGRG 201

RESULT 10
US-09-788-626-4
; Sequence 4; Application US/09788626
; Patent No. US2002009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-4

Query Match          100.0%; Score 65; DB 10; Length 317;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12
Db 191 VVHCSAGVGRG 202

RESULT 11
US-09-925-300-950
; Sequence 950; Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 950
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-950

Query Match          100.0%; Score 65; DB 10; Length 442;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12
Db 80 VVHCSAGVGRG 91

RESULT 12
US-09-808-602-54
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; Sequence 54, Application US/09808602
; Patent No. US2002015115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shinkets, Richard A
; APPLICANT: Herrman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: No. US2002015115A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 1502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-602-54
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Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 VVHCSAGVGRGTG 12
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DB      1140 VVHCSAGVGRGTG 1151
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RESULT 13
US-09-808-602-55
; Sequence 55, Application US/09808602
; Patent No. US2002015115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shinkets, Richard A
; APPLICANT: Herrman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: No. US2002015115A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 1948
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-602-55
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Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 VVHCSAGVGRGTG 12
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DB      1586 VVHCSAGVGRGTG 1597
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RESULT 14
US-10-000-954-2
; Sequence 2, Application US/10000954
; Patent No. US20020127226A1
; GENERAL INFORMATION:
; APPLICANT: Schllessinger, Joseph
; APPLICANT: Barnea, Giliad
; APPLICANT: Grumet, Martin H.
; APPLICANT: Margolis, Richard U.
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; TITLE OF INVENTION: A NEW CLASS OF REPRESSORS: THEIR
; STRUCTURAL DOMAINS AND LIGANDS
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```
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/10/000,954
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; FILING DATE: 04-Dec-2001
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; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 09/644,293
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; FILING DATE: 23-Aug-2000
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```
; APPLICATION NUMBER: 08/081,929
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; FILING DATE: <Unknown>
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; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Coruzzi, Laura A.
```

```
; REGISTRATION NUMBER: 30742
```

```
; REFERENCE/DOCKET NUMBER: 7683-041-999
```

```
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: 212 790-9090
```

```
; TELEFAX: 212 869-8864/9741
```

```
; TELEX: 66141 PENNIE
```

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; INFORMATION FOR SEQ ID NO: 2:
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; SEQUENCE CHARACTERISTICS:
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; LENGTH: 2308 amino acids
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; TYPE: amino acid
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```
; STRANDEDNESS: single
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; TOPOLOGY: unknown
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; MOLECULE TYPE: protein
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; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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Query Match      100.0%; Score 65; DB 12; Length 2308;
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Best Local Similarity 100.0%; Pred. No. 0.0077;
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 VVHCSAGVGRGTG 12
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DB      1923 VVHCSAGVGRGTG 1934
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RESULT 15
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US-09-788-626-20
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; Sequence 20, Application US/09788626
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; Patent No. US20020009762A1
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; GENERAL INFORMATION:
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```
; APPLICANT: Flint, Andrew J.
```

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; APPLICANT: Cool, Deborah E.
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; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
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; FILE REFERENCE: 200125.401
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; CURRENT APPLICATION NUMBER: US/09/788,626
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; CURRENT FILING DATE: 2001-02-13
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; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-20

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Query Match          98.5%; Score 64; DB 10; Length 307;
Best Local Similarity 91.7%; Pred. No. 0.0015;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VVHCSAGVGRG 12
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Db      195 VVHCSAGIGRTG 206

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Search completed: January 17, 2003, 09:15:47  
 Job time : 11 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2003, 09:11:01 : Search time 15 Seconds  
(Without alignments)  
23.538 Million cell updates/sec

Title: US-09-743-492-4

Perfect score: 65  
Sequence: 1 VVHCSAGVGRG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued\_Patents\_AA\*

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2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
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4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	100.0	235	1	US-08-015-985-5
2	65	100.0	236	1	US-08-015-985-6
3	65	100.0	242	1	US-08-015-985-7
4	65	100.0	248	1	US-08-015-985-9
5	65	100.0	250	2	US-08-685-992-7
6	65	100.0	250	2	US-09-144-925-7
7	65	100.0	253	2	US-08-685-992-11
8	65	100.0	253	2	US-08-685-992-10
9	65	100.0	253	2	US-09-144-925-10
10	65	100.0	253	2	US-09-144-925-11
11	65	100.0	254	2	US-08-685-992-9
12	65	100.0	254	2	US-08-685-992-14
13	65	100.0	254	2	US-09-144-925-5
14	65	100.0	254	2	US-09-144-925-14
15	65	100.0	257	2	US-08-685-992-6
16	65	100.0	257	2	US-09-144-925-6
17	65	100.0	260	2	US-08-685-992-4
18	65	100.0	260	2	US-08-685-992-25
19	65	100.0	260	2	US-09-144-925-4
20	65	100.0	260	2	US-09-144-925-25
21	65	100.0	261	2	US-08-685-992-3
22	65	100.0	261	2	US-09-144-925-3
23	65	100.0	278	1	US-08-201-697-16
24	65	100.0	289	1	US-08-036-210-13
25	65	100.0	289	2	US-08-449-609-13
26	65	100.0	292	1	US-08-036-210-12
27	65	100.0	292	2	US-08-449-609-12

#### ALIGNMENTS

28	65	100.0	699	1	US-08-348-006B-7	Sequence 7, Appl1
29	65	100.0	699	2	US-08-800-825A-7	Sequence 7, Appl1
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31	65	100.0	793	1	US-08-015-985-3	Sequence 3, Appl1
32	65	100.0	802	1	US-08-015-985-1	Sequence 1, Appl1
33	65	100.0	1237	1	US-08-241-853-2	Sequence 2, Appl1
34	65	100.0	1237	2	US-08-850-917-2	Sequence 2, Appl1
35	65	100.0	1501	2	US-08-447-464-3	Sequence 3, Appl1
36	65	100.0	1501	2	US-08-716-679-3	Sequence 3, Appl1
37	65	100.0	1911	1	US-08-348-006B-5	Sequence 5, Appl1
38	65	100.0	1911	2	US-08-800-825A-5	Sequence 5, Appl1
39	65	100.0	1911	4	US-09-158-657-5	Sequence 5, Appl1
40	65	100.0	1911	5	PCT-US94-10166-5	Sequence 5, Appl1
41	65	100.0	2308	1	US-08-015-973-1	Sequence 1, Appl1
42	65	100.0	2308	2	US-08-448-164-1	Sequence 1, Appl1
43	65	100.0	2308	4	US-08-081-929-2	Sequence 2, Appl1
44	65	100.0	2314	4	US-09-816-703A-2	Sequence 2, Appl1
45	64	98.5	126	1	US-08-202-389-10	Sequence 10, Appl1

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RESULT 1
US-08-015-985-5
: Sequence 5, Application US/08015985
: Patent No. 5538886
: GENERAL INFORMATION:
: APPLICANT: Schlessler, Joseph
: APPLICANT: Sap, Jan M.
: TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
: TITLE OF INVENTION: PHOSPHATASE ALPHA
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: PENNIE & EDMONDS
: STREET: 1155 AVENUE OF THE AMERICAS
: CITY: NEW YORK
: STATE: NEW YORK
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/015,985
: FILING DATE: 10-FEB-1993
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Coruzzi, Laura A.
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 7683-020
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 869-9741/8690
: TELEFAX: (212) 869-9741/8664
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 235 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
: US-08-015-985-5

Query Match 100.0%; Score 65; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VVHCSAGVGRG 12
Db 174 VVHCSAGVGRG 185

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```
RESULT 2
US-08-015-985-6
; Sequence 6, Application US/08015985
; Patent No. 5538886
; GENERAL INFORMATION:
; APPLICANT: Schlessinger, Joseph
; APPLICANT: Sap, Jan M.
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
; TITLE OF INVENTION: PHOSPHATASE-ALPHA
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/015,985
; FILING DATE: 10-FEB-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-015-985-6

Query Match          100.0%; Score 65; DB 1; Length 236;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVHCSAGVGRGTG 12
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DB      175 VVHCSAGVGRGTG 186

RESULT 3
US-08-015-985-7
; Sequence 7, Application US/08015985
; Patent No. 5538886
; GENERAL INFORMATION:
; APPLICANT: Schlessinger, Joseph
; APPLICANT: Sap, Jan M.
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
; TITLE OF INVENTION: PHOSPHATASE-ALPHA
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/015,985
; FILING DATE: 10-FEB-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-015-985-7

Query Match          100.0%; Score 65; DB 1; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVHCSAGVGRGTG 12
        |||||
DB      181 VVHCSAGVGRGTG 192

RESULT 4
US-08-015-985-9
; Sequence 9, Application US/08015985
; Patent No. 5538886
; GENERAL INFORMATION:
; APPLICANT: Schlessinger, Joseph
; APPLICANT: Sap, Jan M.
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
; TITLE OF INVENTION: PHOSPHATASE-ALPHA
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/015,985
; FILING DATE: 10-FEB-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
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MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Modified-sites  
LOCATION: 1..248  
OTHER INFORMATION: /label=Xaa  
OTHER INFORMATION: /note="For the Consensus Sequence, Xaa = Lack of  
OTHER INFORMATION: Consensus"  
US-08-015-985-9

Query Match 100.0%; Score 65; DB 1; Length 248;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12  
DB 187 VVHCSAGVGRG 198

## RESULT 5

US-08-685-992-7  
Sequence 7, Application US/08685992  
Patent No. 5912138  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,992  
FILING DATE: 25-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ. ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-685-992-7

Query Match 100.0%; Score 65; DB 2; Length 250;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12  
DB 180 VVHCSAGVGRG 191

## RESULT 6

US-09-144-925-7  
Sequence 7, Application US/09144925  
Patent No. 5951979  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02421-4799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/144,925  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/685,992  
FILING DATE: July 25, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ. ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-144-925-7

Query Match 100.0%; Score 65; DB 2; Length 250;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12  
DB 180 VVHCSAGVGRG 191

## RESULT 7

US-08-685-992-10  
Sequence 10, Application US/08685992  
Patent No. 5912138  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,992  
FILING DATE: 25-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 253 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-685-992-10

Query Match 100.0%; Score 65; DB 2; Length 253;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRGTG 12  
|||||  
DB 183 VVHCSAGVGRGTG 194

RESULT 8  
US-08-685-992-11  
Sequence 11, Application US/08685992  
Patent No. 5912138  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Millitia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,992  
FILING DATE: 25-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540

TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 253 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-685-992-11

Query Match 100.0%; Score 65; DB 2; Length 253;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRGTG 12  
|||||  
DB 183 VVHCSAGVGRGTG 194

RESULT 9  
US-09-144-925-10  
Sequence 10, Application US/09144925  
Patent No. 5951979  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Millitia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02421-4799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/144,925  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/685,992  
FILING DATE: July 25, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 253 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-144-925-10

Query Match 100.0%; Score 65; DB 2; Length 253;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVHCSAGVGRGTG 12  
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DB 183 VVHCSAGVGRGTG 194



```
RESULT 10
US-09-144-925-11
; Sequence 11, Application US/09144925
; Patent No. 5951979
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas
; APPLICANT: Flint, Andrew J.
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02421-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,925
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,992
; FILING DATE: July 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-144-925-11

Query Match      100.0%; Score 65; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VVHCSAGVGRGTG 12
Db      183 VVHCSAGVGRGTG 194
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RESULT 11
US-08-685-992-9
; Sequence 9, Application US/08685992
; Patent No. 5912138
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas
; APPLICANT: Flint, Andrew J.
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,992
; FILING DATE: 25-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-685-992-9

Query Match      100.0%; Score 65; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VVHCSAGVGRGTG 12
Db      184 VVHCSAGVGRGTG 195

RESULT 12
US-08-685-992-14
; Sequence 14, Application US/08685992
; Patent No. 5912138
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas
; APPLICANT: Flint, Andrew J.
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,992
; FILING DATE: 25-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
```

TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 254 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-685-992-14

Query Match 100.0%; Score 65; DB 2; Length 254;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12  
|||||  
DB 184 VVHCSAGVGRG 195

RESULT 13  
US-09-144-925-9  
Sequence 9, Application US/09144925  
Patent No. 5951979  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02421-4799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/144,925  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/685,992  
FILING DATE: July 25, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 254 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-144-925-9

Query Match 100.0%; Score 65; DB 2; Length 254;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12  
|||||  
DB 184 VVHCSAGVGRG 195

RESULT 14  
US-09-144-925-14  
Sequence 14, Application US/09144925  
Patent No. 5951979

GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02421-4799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/144,925  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/685,992  
FILING DATE: July 25, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: CSHL96-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:

INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 254 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-144-925-14

Query Match 100.0%; Score 65; DB 2; Length 254;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVHCSAGVGRG 12  
|||||  
DB 184 VVHCSAGVGRG 195

RESULT 15  
US-08-685-992-6  
Sequence 6, Application US/08685992  
Patent No. 5912138  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas  
APPLICANT: Flint, Andrew J.  
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA

```

; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,992
; FILING DATE: 25-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
;
; TELEEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-685-992-6

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Query Match 100.0%; Score 65; DB 2; Length 257;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVHCSAGVGRTG 12  
| | | | | | | | | |  
Db 187 VVHCSAGVGRTG 198

Search completed: January 17, 2003, 09:12:42  
Job time : 16 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run On: January 17, 2003, 10:58:57 ; Search time 15 Seconds  
(without alignments)  
76.908 Million cell updates/sec

Title: US-09-743-492-4  
Perfect score: 65  
Sequence: 1 VHCAGVGRGTG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 1580

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR-73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	41.5	12	2 PH0931	T-cell receptor be
2	24	36.9	12	2 S47394	T-cell antigen rec
3	23	35.4	8	2 PH0803	T-cell receptor al
4	23	35.4	11	2 PT0218	T-cell receptor be
5	23	35.4	12	2 S26549	T-cell receptor be
6	23	35.4	12	2 PH1463	T-cell receptor be
7	22	33.8	11	2 PH0938	T-cell receptor be
8	22	33.8	12	2 S28215	glucan endo-1,3-be
9	22	33.8	12	2 PH1464	T-cell receptor be
10	22	33.8	12	2 PT0216	T-cell receptor be
11	21	32.3	9	2 A11497	transaldolase (EC
12	21	32.3	9	2 I50633	C-rel protein - ch
13	21	32.3	11	2 S33782	acetylactate synth
14	21	32.3	12	2 S29764	alpha-macroglobuli
15	21	32.3	12	2 S26552	T-cell receptor be
16	21	32.3	12	2 PH1470	T-cell receptor be
17	21	32.3	12	2 PH1469	T-cell receptor be
18	21	32.3	12	2 PH1468	T-cell receptor be
19	20	30.8	7	2 PT0623	T-cell receptor be
20	20	30.8	8	2 PT0691	T-cell receptor be
21	20	30.8	9	2 A12872	transaldolase (EC
22	20	30.8	12	2 S26557	T-cell receptor be
23	20	30.8	12	2 S29830	dimethylalanine mo
24	20	30.8	12	2 S47391	T-cell antigen rec
25	19	29.2	10	2 E41946	T-cell receptor ga
26	19	29.2	11	2 S66196	alcohol dehydrogen
27	19	29.2	11	2 PH1600	ig H chain V-D-J r
28	19	29.2	12	2 S26553	T-cell receptor be
29	19	29.2	12	2 PH1180	T-cell receptor al

30	19	29.2	12	2 PH1466	T-cell receptor be
31	18	27.7	6	2 PT0718	T-cell receptor be
32	18	27.7	7	2 S08606	hypothetical prote
33	18	27.7	7	2 PT0663	T-cell receptor be
34	18	27.7	8	2 PT0279	Ig heavy chain CRD
35	18	27.7	10	2 S77990	cytochrome-c oxida
36	18	27.7	11	2 C49037	TCR gamma V-J regi
37	18	27.7	12	2 S47395	T-cell antigen rec
38	17	26.2	6	2 JU0355	lipopeptide WS1279
39	17	26.2	6	2 PT0643	T-cell receptor be
40	17	26.2	6	2 PT0668	T-cell receptor be
41	17	26.2	6	2 PT0727	T-cell receptor be
42	17	26.2	7	2 PT0719	T-cell receptor be
43	17	26.2	8	2 I48934	apolipoprotein A-I
44	17	26.2	8	2 PT0627	T-cell receptor be
45	17	26.2	8	2 A25836	L-serine ammonia-1

## ALIGNMENTS

## RESULT 1

PH0931  
T-cell receptor beta chain V-D-J region (clone 2) - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C:Accession: PH0931  
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991

A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle  
A:Reference number: PH0891; MUID:92078857; PMID:1836012  
A:Accession: PH0931  
A:Molecule type: mRNA  
A:Residues: 1-12 <GOL>  
A:Experimental source: complete Freund's adjuvant-immunized lymph node  
C:Keywords: T-cell receptor

Query Match 41.5%; Score 27; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CSAGVGRGT 11  
I:: IIII  
Db 1 CASSAGRT 8

## RESULT 2

S47394  
T-cell antigen receptor VJ junction beta chain - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
C:Accession: S47394; S47369  
R:Lehner, P.J.

submitted to the EMBL Data Library, August 1994  
A:Description: Human HLA-A0201 restricted recognition of Influenza A is dominated by  
A:Reference number: S47355  
A:Accession: S47394  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-12 <LEH>  
A:Cross-references: EMBL:Z35714; NID:g527523; PID:CAA84783.1; PID:g527524; EMBL:Z356  
C:Keywords: T-cell receptor

Query Match 36.9%; Score 24; DB 2; Length 12;  
Best Local Similarity 33.3%; Pred. No. 6.3e+02;  
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CSAGVGRGT 12  
I::: I I  
Db 1 CASSIGNYG 9

## RESULT 3

## PH0803

T-cell receptor alpha chain (J2) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PH0803  
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-I allelic exclusion and antigen-specific repertoire.  
A;Reference number: PH0746; MUID:92078846; PMID:1836010  
A;Accession: PH0803  
A;Molecule type: mRNA  
A;Residues: 1-8 <CAS>  
A;Cross-references: EMBL:X60912  
A;Experimental source: T lymphocyte  
C;Keywords: T-cell receptor

Query Match 35.4%; Score 23; DB 2; Length 8;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 CSAGV 8  
I::: I I  
Db 1 CAGI 5

## RESULT 4

PT0218  
T-cell receptor beta chain V-J region (7-10-D.3) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997  
C;Accession: PT0218  
R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.  
J. Exp. Med. 173, 1091-1097, 1991  
A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted.  
A;Reference number: PT0209; MUID:91217621; PMID:1902501  
A;Accession: PT0218  
A;Molecule type: mRNA  
A;Residues: 1-11 <NAK>  
C;Keywords: T-cell receptor

Query Match 35.4%; Score 23; DB 2; Length 11;  
Best Local Similarity 66.7%; Pred. No. 8.7e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CSAGVG 9  
I::: I I  
Db 1 CGAGQG 6

## RESULT 5

S26549  
T-cell receptor beta chain (clone Cw3/A8, Cw3/Cas1) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 13-Jan-1995 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999  
C;Accession: S26549; S26550  
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Widmann, J.  
J. Exp. Med. 176, 439-447, 1992  
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
A;Reference number: S26512; MUID:92364546; PMID:1380061  
A;Accession: S26549  
A;Molecule type: mRNA  
A;Residues: 1-12 <CAS>  
A;Cross-references: EMBL:X67999  
A;Experimental source: cytolytic T-lymphocyte, clone Cw3/A8  
A;Accession: S26550  
A;Molecule type: mRNA  
A;Residues: 1-12 <CA2>  
A;Cross-references: EMBL:X68000  
A;Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: T-cell receptor

## Query Match

Best Local Similarity 37.5%; Score 23; DB 2; Length 12;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 CSAGVGRT 11  
I::: I I  
Db 1 CASSLGET 8

## RESULT 6

PH1463  
T-cell receptor beta chain (clone A24/10.1) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995  
C;Accession: PH1463  
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; J. Exp. Med. 177, 811-820, 1993  
A;Title: T cell receptor selection by and recognition of two class I major histocomp  
A;Reference number: PH1430; MUID:93171821; PMID:8436911  
A;Accession: PH1463  
A;Molecule type: mRNA  
A;Residues: 1-12 <CAS>  
A;Experimental source: cytolytic T-lymphocyte  
C;Superfamily: immunoglobulin homology  
C;Keywords: receptor; T-cell

Query Match 35.4%; Score 23; DB 2; Length 12;  
Best Local Similarity 37.5%; Pred. No. 9.5e+02;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 CSAGVGRT 11  
I::: I I  
Db 1 CASSLGMT 8

## RESULT 7

PH0938  
T-cell receptor beta chain V-D-J region (clone 9) - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C;Accession: PH0938  
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991  
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle  
A;Reference number: PH0891; MUID:92078857; PMID:1836012  
A;Accession: PH0938  
A;Molecule type: mRNA  
A;Residues: 1-11 <GOL>  
A;Experimental source: complete Freund's adjuvant-immunized lymph node  
C;Keywords: T-cell receptor

Query Match 33.8%; Score 22; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GRG 12  
I::: I I I  
Db 7 GRG 10

## RESULT 8

S28215  
glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) GII - barley (fragment)  
N;Alternate names: (1-3)-beta-D-glucanase GII  
C;Species: Hordeum vulgare (barley)  
C;Date: 19-Mar-1997 #sequence\_revision 17-Jul-1998 #text\_change 07-May-1999  
C;Accession: S28215  
R;Hrmova, M.; Fincher, G.B.  
Biochem. J. 289, 453-461, 1993  
A;Title: Purification and properties of three (1->3)-beta-D-glucanase isoenzymes from  
A;Reference number: S28214; MUID:93143715; PMID:8424790  
A;Accession: S28215  
A;Molecule type: protein

A;Residues: 1-12 <HRM>  
A;Experimental source: cultivar clipper  
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 33.8%; Score 22; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 CSAGVG 9  
I : : :  
Db 4 CYGGIG 9

## RESULT 9

PHI464  
T-cell receptor beta chain (clone A3/63) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995  
C;Accession: PHI464  
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K  
J. Exp. Med. 177, 811-820, 1993  
A;Title: T cell receptor selection by and recognition of two class I major histocompatib  
A;Reference number: PHI430; MUID:93171821; PMID:8436911  
A;Accession: PHI464  
A;Molecule type: mRNA  
A;Residues: 1-12 <CAS>  
A;Experimental source: cytolytic T-lymphocyte  
C;Superfamily: immunoglobulin homology  
C;Keywords: receptor; T-cell

Query Match 33.8%; Score 22; DB 2; Length 12;  
Best Local Similarity 37.5%; Pred. No. 1.4e+03;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 CSAGVGRT 11  
I : : :  
Db 1 CASSTGNT 8

## RESULT 10

PT0216  
T-cell receptor beta chain V-J region (4-1-G.4) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997  
C;Accession: PT0216  
R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.  
J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restrict  
A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0216  
A;Molecule type: mRNA  
A;Residues: 1-12 <NAK>  
C;Keywords: T-cell receptor

Query Match 33.8%; Score 22; DB 2; Length 12;  
Best Local Similarity 37.5%; Pred. No. 1.4e+03;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 CSAGVGRT 11  
I : : :  
Db 1 CASSLGTT 8

## RESULT 11

All497  
transaldolase (EC 2.2.1.2) III - yeast (Pichia jadinii) (fragment)  
C;Species: Pichia jadinii, Candida utilis  
C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 30-Sep-1993  
C;Accession: All497  
R;Tsolas, O.; Sun, S.C.  
Arch. Biochem. Biophys. 167, 525-533, 1975  
A;Title: Isolation of a peptide containing a histidinyI-cysteinyI sequence from the acti  
A;Reference number: All497; MUID:75145197; PMID:1092268

A;Accession: All497  
A;Molecule type: protein  
A;Residues: 1-9 <TSO>  
C;Keywords: transferase

Query Match 32.3%; Score 21; DB 2; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHCS 5  
: : :  
Db 3 IHCN 6

## RESULT 12

I50633  
C-rel protein - chicken (fragment)  
C;Species: Gallus gallus (chicken)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C;Accession: I50633  
R;Hannink, M.; Temin, H.M.  
Oncogene 5, 1843-1850, 1990  
A;Title: Structure and autoregulation of the c-rel promoter.  
A;Reference number: I50633; MUID:91133738; PMID:2284104  
A;Accession: I50633  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-9 <HAN>  
A;Cross-references: EMBL:X56440; NID:g63338; PIDN:CAA39822.1; PID:g584483

Query Match 32.3%; Score 21; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 SAGVGR 10  
I : : :  
Db 4 SGGAGR 9

## RESULT 13

S33782  
acetolactate synthase (EC 4.1.3.18) small chain, valine-sensitive - Serratia marcesce  
C;Species: Serratia marcescens  
C;Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 24-Mar-1999  
C;Accession: S33782  
R;Yang, J.H.; Kim, S.S.  
Biochim. Biophys. Acta 1157, 178-184, 1993  
A;Title: Purification and characterization of the valine sensitive acetolactate synth  
A;Reference number: S33781; MUID:93283409; PMID:8507653  
A;Accession: S33782  
A;Molecule type: protein  
A;Residues: 1-11 <YAN>  
A;Experimental source: ATCC 25419  
C;Complex: heterotetramer; two small and two large chains  
C;Function:

A;Description: catalyzes the condensation of pyruvate and alpha-ketobutyrate to form  
A;Pathway: valine, leucine, and isoleucine biosynthesis  
A;Note: this isoenzyme exhibits homotropic allosterism with pyruvate  
C;Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein

Query Match 32.3%; Score 21; DB 2; Length 11;  
Best Local Similarity 80.0%; Pred. No. 1.9e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 VGRGTG 12  
I : : :  
Db 4 VGRNG 8

## RESULT 14

S29764  
alpha-macroglobulin proteinase inhibitor - bullfrog (fragment)  
C;Species: Rana catesbeiana (bullfrog)

C:Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 07-May-1999  
 C:Accession: S29764  
 R:Rubenstein, D.S.; Thøgersen, I.B.; Pizzo, S.V.; Enghild, J.J.  
 Biochem. J. 290, 85-95, 1993  
 A:Title: Identification of monomeric alpha-macroglobulin proteinase inhibitors in birds,  
 teinase inhibitor from the American bullfrog Rana catesbiana.  
 A:Reference number: S29764; MUID:93176138; PMID:7679897

A:Accession: S29764  
 A:Molecule type: protein  
 A:Residues: 1-12 <RUB>  
 A:Experimental source: plasma  
 C:Function:  
 A:Description: inhibits the proteinases of different catalytic class  
 C:Superfamily: alpha-2-macroglobulin  
 C:Keywords: monomer; proteinase inhibitor

Query Match 32.3%; Score 21; DB 2; Length 12;  
 Best Local Similarity 33.3%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VVHCSAGVG 9  
 : : | | |  
 Db 1 IHLPGCG 9

# RESULT 15

S26552  
 T-cell receptor beta chain (clone Cw3/701.1) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 13-Jan-1995 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999  
 C:Accession: S26552  
 R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid  
 J. Exp. Med. 176, 439-447, 1992  
 A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
 A:Reference number: S26512; MUID:92364546; PMID:1380061  
 A:Accession: S26552  
 A:Molecule type: mRNA  
 A:Residues: 1-12 <CAS>  
 A:Cross-references: EMBL:X68002  
 A:Experimental source: cytolytic T-lymphocyte, clone Cw3/701.1  
 C:Superfamily: immunoglobulin V region;--immunoglobulin homology  
 C:Keywords: T-cell receptor

Query Match 32.3%; Score 21; DB 2; Length 12;  
 Best Local Similarity 37.5%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 CSAGVGRT 11  
 : : | | |  
 Db 1 CASSYGET 8

Search completed: January 17, 2003, 11:01:06  
 Job time : 16 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 17, 2003, 10:58:12 ; Search time 10 Seconds  
(without alignments)  
49.772 Million cell updates/sec

Title: US-09-743-492-4

Perfect score: 65

Sequence: 1 VVHCSAGVGRTG 12

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 467

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	21	32.3	9	1 TAL3_PICJA	P17441 pichia jadi
2	20	30.8	9	1 TAL1_PICJA	P17440 pichia jadi
3	19	29.2	10	1 TRU2_UREUN	P40752 urechis uni
4	19	29.2	10	1 URAL1_HUMAN	P32118 homo sapien
5	18	27.7	10	1 COXO_THUOB	P80982 thunnus obe
6	17	26.2	9	1 CCAP_CARMA	P38556 carcinus ma
7	17	26.2	9	1 DNFL_LOEMI	P16339 locusta mig
8	17	26.2	10	1 COXO_RAT	P80432 rattus norv
9	16	24.6	9	1 OXYT_EISFO	P42998 eisenia foe
10	16	24.6	9	1 OXYV_SQUAC	P43000 squalus aca
11	16	24.6	10	1 FARP_MANSE	P18523 manduca sex
12	16	24.6	10	1 TPIS_NICPL	P19118 nicotiana p
13	16	24.6	12	1 OPS3_DROVI	P17645 drosophila
14	16	24.6	12	1 V14K_WSSV	P82006 white spot
15	15	23.1	9	1 ISOT_CYPCA	P42993 cyprinus ca
16	15	23.1	9	1 OXYA_SCYCA	P42996 scyllorhinu
17	15	23.1	9	1 OXYE_SCYCA	P42997 scyllorhinu
18	15	23.1	9	1 OXYT_CYPCA	P23879 cyprinus ca
19	15	23.1	9	1 OXYT_RABIT	P32878 oryctolagus
20	15	23.1	9	1 OXYT_FAJCL	P42994 raja clavav
21	15	23.1	10	1 CU30_LOEMI	P11735 locusta mig
22	15	23.1	10	1 GON1_ALLMI	P37041 alligator m
23	15	23.1	10	1 GON1_CLUPA	P81749 clupea pall
24	15	23.1	10	1 HTF_NAUCI	P10939 nauphoeta c
25	15	23.1	10	1 UPAS_HUMAN	P30091 homo sapien
26	14	21.5	5	1 UF01_MOUSE	P38639 mus musculu
27	14	21.5	9	1 CONO_CONGE	P05486 conus geogr
28	14	21.5	9	1 CONO_CONST	P05487 conus stria
29	14	21.5	9	1 OXYA_SQUAC	P42999 squalus aca
30	14	21.5	9	1 OXYT_OCIYU	P80027 octopus vul
31	14	21.5	9	1 PGLR_DIAAB	P81179 diaprepes a
32	14	21.5	10	1 GON2_CHICK	P37043 gallus gall
33	14	21.5	10	1 GON3_ONCKE	P20367 oncorhynch

34 14 21.5 10 1 GONL\_SQUAC P27429 squalus aca  
35 14 21.5 10 1 HTF\_HELZE P16353 heliothis z  
36 14 21.5 10 1 LABA\_JATMU P13270 jatrophia mu  
37 14 21.5 10 1 PNEU\_HUMAN P22103 homo sapien  
38 14 21.5 10 1 PNEU\_RAT P21996 rattus norv  
39 14 21.5 11 1 RS30\_ONCMY P83328 oncorhynchu  
40 14 21.5 12 1 SOI5\_BACSU P80863 bacillus su  
41 13 20.0 8 1 AKHG\_GRYBI P14086 gryllus bim  
42 13 20.0 9 1 FAR9\_ASCSU P43172 ascaris suu  
43 13 20.0 9 1 OXYT\_BUFRE P42995 bufo regula  
44 13 20.0 9 1 SAP\_STOVA P21047 stomopneute  
45 13 20.0 9 1 XYLA\_STRSQ P19149 streptomyce

## ALIGNMENTS

## RESULT 1

TAL3\_PICJA  
ID TAL3\_PICJA STANDARD; PRT; 9 AA.  
AC P17441;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Transaldolase III (EC 2.2.1.2) (Fragment).  
OS Pichia jadinii (Yeast) (Candida utilis).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Pichia.  
OX NCBI\_TaxID=4903;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75145197; PubMed=1092268;  
RA Tsolas O., Sun S.C.;  
RT "Isolation of a peptide containing a histidyl-cysteiny sequence  
from the active center of transaldolase.";  
RL Arch. Biochem. Biophys. 167:525-533(1975).  
CC -!- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF  
METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.  
CC -!- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde  
3-phosphate -> D-erythrose 4-phosphate + D-fructose 6-phosphate.  
CC -!- PATHWAY: Pentose phosphate pathway; nonoxidative part.  
CC -!- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY. SUBFAMILY 1.  
DR PIR; A11497; A11497.  
DR InterPro; IPR001585; Transaldolase.  
DR PROSITE; PS00958; TRANSALDOLASE\_2; PARTIAL.  
DR PROSITE; PS01054; TRANSALDOLASE\_1; PARTIAL.  
KW Transferase; Pentose shunt.  
FT NON\_TER 1  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1033 MW; 325A31A44EB1E058 CRC64;

Query Match 32.3%; Score 21; DB 1; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.1e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 2 VHCS 5  
Db 3 IHCN 6

## RESULT 2

TAL1\_PICJA  
ID TAL1\_PICJA STANDARD; PRT; 9 AA.  
AC P17440;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Transaldolase I (EC 2.2.1.2) (Fragment).  
OS Pichia jadinii (Yeast) (Candida utilis).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Pichia.  
OX NCBI\_TaxID=4903;  
RN [1]

RP SEQUENCE.  
 RX MEDLINE=77110646; PubMed=556924;  
 RA Sun S.C., Joris L., Tsolas O.;  
 RT "Purification of crystallization of transaldolase isozyme I and  
 RT evidence for different genetic origin of isozymes I and III in  
 RT Candida utilis.";  
 RL Arch. Biochem. Biophys. 178:69-78(1977).  
 CC -1- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF  
 CC METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.  
 CC -1- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde  
 CC 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.  
 CC -1- PATHWAY: Pentose phosphate pathway; nonoxidative part.  
 CC -1- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY. SUBFAMILY 1.  
 DR PIR; A12872; A12872.  
 DR InterPro; IPR001585; Transaldolase.  
 DR PROSITE; PS00958; TRANSALDOLASE\_2; PARTIAL.  
 DR PROSITE; PS01054; TRANSALDOLASE\_1; PARTIAL.  
 KW Transferase; Pentose shunt.  
 FT NON\_TER 1 1  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1008 MW; 274F31AF0EB1E058 CRC64;  
 Query Match 30.8%; Score 20; DB 1; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.1e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VHC 4  
 Db |||  
 3 IHC 5

RESULT 3  
 TKU2\_UREUN STANDARD; PRT; 10 AA.  
 ID TKU2\_UREUN  
 AC P40752;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Urechis tacyhkinin II.  
 OS Urechis unicinctus.  
 OC Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.  
 OX NCBI\_TaxID=6432;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Ventral nerve cord;  
 RX MEDLINE=93236558; PubMed=8476410;  
 RA Ikeda T., Minakata H., Nomoto K., Kubota I., Muneoka Y.;  
 RT "Two novel tacyhkinin-related neuropeptides in the echiuroid worm,  
 RT Urechis unicinctus.";  
 RL Biochem. Biophys. Res. Commun. 192:1-6(1993).  
 CC -1- FUNCTION: CONTRACTILE ACTION ON THE INNER CIRCULAR BODY-WALL  
 CC MUSCLE OF THE ANIMAL.  
 CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 10 10  
 FT AMIDATION.  
 SQ SEQUENCE 10 AA; 984 MW; 3F58DD79C9C87698 CRC64;  
 Query Match 29.2%; Score 19; DB 1; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 SAGVGRGT 12  
 Db |||:|  
 1 AAGMGFFG 8

RESULT 4  
 URAL\_HUMAN STANDARD; PRT; 10 AA.  
 ID URAL\_HUMAN  
 AC P32118;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 16-OCT-2003 (Rel. 40, Last annotation update)

DE Unknown protein from 2D-page of red blood cells (Spot 1) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Erythrocyte;  
 RX MEDLINE=94147970; PubMed=8313871;  
 RA Golaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,  
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,  
 RA Balant L., Hochstrasser D.F.;  
 RT "Plasma and red blood cell protein maps: update 1993.";  
 RL Electrophoresis 14:1223-1231(1993).  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.4, ITS MW IS: 23 Kda.  
 DR SWISS-2DPAGE; P32118; HUMAN.  
 FT NON\_TER 1 1  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 977 MW; 723C65BIADD0587B CRC64;  
 Query Match 29.2%; Score 19; DB 1; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 7 GVGRTG 12  
 Db ||:||  
 4 GIATG 9

RESULT 5  
 COXO\_THUOB STANDARD; PRT; 10 AA.  
 ID COXO\_THUOB  
 AC P80982;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cytochrome c oxidase polypeptide VIIC (EC 1.9.3.1) (Fragment).  
 OS Thunus obesus (Bigeye tuna).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;  
 OC Scombridae; Thunnus.  
 OX NCBI\_TaxID=8241;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart, and Liver;  
 RX MEDLINE=97454291; PubMed=9310366;  
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,  
 RA Kadenbach B.;  
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and  
 RT liver.";  
 RL Eur. J. Biochem. 248:99-103(1997).  
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.  
 KW Oxidoreductase; Inner membrane; Mitochondrion.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1059 MW; 126DE767687B1DCB CRC64;  
 Query Match 27.7%; Score 18; DB 1; Length 10;  
 Best Local Similarity 37.5%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 HCSAGVGR 10  
 Db |::|:  
 2 HYAEGPGK 9

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RESULT 6 .
CCAP_CARMA          STANDARD;          PRT;          9 AA.
ID  CCAP_CARMA
AC  P38556;
DT  01-OCT-1994 (Rel. 30, Created)
DT  01-OCT-1994 (Rel. 30, Last sequence update)
DT  15-DEC-1998 (Rel. 37, Last annotation update)
DE  Cardioactive peptide (CCAP).
OS  Carcinus maenas (Common shore crab) (Green crab),
OS  Mandauca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS  Tenebrio molitor (Yellow mealworm), and
OS  Spodoptera eridania (Southern armyworm);
OC  Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
OC  Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
OC  Brachyura; Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX  NCBI_TaxID=6759, 7130, 7067, 37547;
RN  [1]
RN  SEQUENCE.
RP  SPECIES=C.maenas; TISSUE=Pericardial organs;
RC  Stangier J., Hilbich C., Beyreuther K., Keller R.;
RA  "Unusual cardioactive peptide (CCAP) from pericardial organs of the
RT  shore crab Carcinus maenas.";
RL  Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RN  [2]
RN  SEQUENCE.
RP  SPECIES=M.sexata;
RC  MEDLINE=93050243; PubMed=1426284;
RA  Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RT  "Primary structure of a cardioactive neuropeptide from the tobacco
RN  hawkmoth, Mandauca sexta.";
RL  FEBS Lett. 313:165-168(1992).
RN  [3]
RN  SEQUENCE.
RP  SPECIES=T.molitor, and S.eridania; TISSUE=Head;
RC  MEDLINE=94176032; PubMed=8129851;
RA  Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA  Schooley D.A.;
RT  "Isolation and identification of a cardioactive peptide from Tenebrio
RN  molitor and Spodoptera eridania.";
RL  Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
CC  -1- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
CC  -1- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
CC  INTO THE HEMOLYMPH.
DR  PIR: A26363; A26363.
DR  PIR: S27233; S27233.
KW  Neuropeptide; Amidation.
FT  DISULFID 3 9
FT  MOD_RES 9 9
FT  SEQUENCE 9 AA; 959 MW; CSA861A9CDD44EB9 CRC64;

Query Match 26.2%; Score 17; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CSAGVG 9
    | | |
Db 3 CNAFTG 8

RESULT 7
DNFL_LOCMI          STANDARD;          PRT;          9 AA.
ID  DNFL_LOCMI
AC  P16339;
DT  01-AUG-1990 (Rel. 15, Created)
DT  01-AUG-1990 (Rel. 15, Last sequence update)
DT  15-DEC-1998 (Rel. 37, Last annotation update)
DE  Locupressin (Diuretic neuropeptide Fl/F2).
OS  Locusta migratoria (Migratory locust).
OC  Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC  Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC  Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
OX  NCBI_TaxID=7004;
RN  [1]
RN  SEQUENCE.
RP  TISSUE=Suboesophageal ganglion, and Thoracic ganglion;
RC  MEDLINE=88077077; PubMed=3689410;
RA  Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
RA  Delaage M., Schooley D.A.;
RT  "Identification of an arginine vasopressin-like diuretic hormone from
RN  Locusta migratoria.";
RL  Biochem. Biophys. Res. Commun. 149:180-186(1987).
CC  -1- FUNCTION: DIURETIC HORMONE.
CC  -1- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.
CC  -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR  PIR: A29477; A29477.
DR  InterPro; IPR000981; Neurhyp_horm.
DR  Pfam; PF00220; hormone4; 1.
DR  PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW  Hormone; Neuropeptide; Amidation
FT  DISULFID 1 6
FT  DISULFID 1 1
FT  DISULFID 6 6
FT  MOD_RES 9 9
FT  SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match 26.2%; Score 17; DB 1; Length 9;
Best Local Similarity 28.6%; Pred. No. 1.1e+05;
Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VVHCSAG 7
    : | | |
Db 3 ITNCPRG 9

RESULT 8
COXO_RAT
ID  COXO_RAT          STANDARD;          PRT;          10 AA.
AC  P80432;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Cytochrome c oxidase polypeptide Viic, mitochondrial (EC 1.9.3.1)
DE  (VIIIa) (Fragment).
DE  COX7C OR COX7C1.
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RN  SEQUENCE.
RP  STRAIN=Wistar; TISSUE=Liver, and Heart;
RC  MEDLINE=95324529; PubMed=7601105;
RA  Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT  "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RN  amino-terminal sequences suggest identity of the fetal heart and the
adult liver isoform.";
RL  Eur. J. Biochem. 230:235-241(1995).
CC  -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC  CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC  MITOCHONDRIAL ELECTRON TRANSPORT.
CC  -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) -> 4 ferricytochrome
CC  c + 2 H(2)O.
CC  -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
KW  Oxidoreductase; Mitochondrion.
FT  NON_TER 10
FT  SEQUENCE 10 AA; 1117 MW; 126DE76767B1B0B CRC64;

Query Match 26.2%; Score 17; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 2.6e+03;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 HCSAGVGR 10
    | | |
Db 2 HYEKGPGK 9

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RESULT 9
OXYT_EISFO STANDARD; PRT; 9 AA.
AC P42998;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Annetocin.
OS Eisenia foetida (Common brandling worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Eisenia.
OX NCBI_TaxID=6396;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=94121660; PubMed=8292046;
RA Oumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,
RT Eisenia foetida.";
RL Biochem. Biophys. Res. Commun. 198:393-399(1994).
CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO
CC PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE
CC NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH
CC NEPHRIDIAL FUNCTION.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR: PC2021; PC2021.
DR InterPro: IPR000981; Neurhyp_horm.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 996 MW; D4EB76EB45412C9 CRC64;
QY Query Match 24.6%; Score 16; DB 1; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.1e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 VVHCASG 7
DB | : | |
3 VRNCPTG 9

RESULT 10
OXYV_SQUAC STANDARD; PRT; 9 AA.
AC P43000;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Valitocin.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro: IPR000981; Neurhyp_horm.
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DR InterPro: IPR001230; Prenyl_site.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 996 MW; 17EDD76EB456D04B CRC64;
QY Query Match 24.6%; Score 16; DB 1; Length 9;
Best Local Similarity 28.8%; Pred. No. 1.1e+05;
Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 VVHCASG 7
DB | : | |
3 IQNCPVG 9

RESULT 11
FARP_MANSE STANDARD; PRT; 10 AA.
AC P18523;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
OC Ditrysia; Sphingioidea; Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE.
RX MEDLINE=91045350; PubMed=2235684;
RA Kington T.G., Teplow D.B., Phillips J.M., Riehm J.P., Rao K.R.,
RA Hilgbrand J.G., Homborg U., Kammer A.E., Jardine I., Griffin P.R.,
RA Hunt D.F.;
RT "A new peptide in the FMRFamide family isolated from the CNS of the
RT hawkmoth, Manduca sexta.";
RL Peptides 11:849-856(1990).
CC -!- FUNCTION: INCREASES THE FORCE OF NEURALLY EVOKED CONTRACTIONS IN
CC THE MAJOR POWER-PRODUCING FLIGHT MUSCLES, THE DORSAL LONGITUDINAL
CC MUSCLES AND SO IS LIKELY TO PLAY A ROLE IN SUSTAINING OR PROMOTING
CC FLIGHT BEHAVIOR PATTERNS.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR: A43977; A43977.
KW Amidation; Neuropeptide.
FT MOD_RES 1 1
FT MOD_RES 10 10
FT SEQUENCE 10 AA; 1247 MW; D3C45229D5B1F2D2 CRC64;
QY Query Match 24.6%; Score 16; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVH 3
DB | | |
3 VVH 5

RESULT 12
TPIS_NICPL STANDARD; PRT; 10 AA.
AC P19118;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fragment).
OS Nicotiana glumaginifolia (Leadwort-leaved tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4092;
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RN      [1]
RP      SEQUENCE.
RA      Bouw G., de Loose M., Inze D., van Montagu M., Vandekerckhove J.;
RT      "Alterations in the phenotype of plant cells studied by NH2-terminal
RT      amino acid-sequence analysis of proteins electrophoretically from two-
RT      dimensional gel-separated total extracts.";
RL      Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810(1987).
CC      -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
CC      phosphate.
CC      -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC      -1- SUBUNIT: HOMODIMER.
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC      -1- MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TPIS, CYTOSOLIC
CC      AND PLASTID.
CC      -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR      PIR; A27617; A27617.
DR      InterPro: IPR000652; Triophos_1smrse.
DR      PROSITE: PS00171; TIM; PARTIAL.
KM      Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW      Pentose shunt.
FT      NON_TER
SQ      SEQUENCE 10 AA; 1140 MW; 80B9D37862C9C9D1 CRC64;

Query Match
Best Local Similarity 24.6%; Score 16; DB 1; Length 10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GRT 11
       |||
Db      1 GRT 3

RESULT 13
OPS3_DROVI STANDARD; PRT; 12 AA.
ID OPS3_DROVI
AC P17645;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Opsin Rh3 (inner R7 photoreceptor cells opsin) (Fragment).
GN Rh3.
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7244;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90249748; PubMed-2140105;
RA Fortini M.E., Rubin G.M.;
RT "Analysis of cis-acting requirements of the Rh3 and Rh4 genes reveals
RT a bipartite organization to rhodopsin promoters in Drosophila
RT melanogaster.";
RL Genes Dev. 4:444-463(1990).
CC -1- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
CC MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
CC LINKED TO CIS-RETINAL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- MISCELLANEOUS: EACH DROSOPHILA EYE IS COMPOSED OF 800 FACETS OR
CC OMATIDIA. EACH OMATIDIUM CONTAINS 8 PHOTORECEPTOR CELLS (R1-R8),
CC THE R1 TO R6 CELLS ARE OUTER CELLS, WHILE R7 AND R8 ARE INNER
CC CELLS.
CC -1- MISCELLANEOUS: OPSIN RH3 IS SENSITIVE TO UV LIGHT.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC OPSIN SUBFAMILY.
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CC      -----
DR      EMBL; X51350; CA35742.1;
DR      FlyBase; FBgn0013091; Dvir\Rh3.
DR      InterPro: IPR000276; GPCR_Rhodopsn.
DR      InterPro: IPR001760; Opsin.
DR      PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; PARTIAL.
DR      PROSITE: PS00238; OPSIN; PARTIAL.
KM      Photoreceptor; Retinal protein; Transmembrane; Phosphorylation;
KW      Glycoprotein; G-Protein coupled receptor; Vision.
FT      CARBOHYD
FT      NON_TER
SQ      SEQUENCE 12 AA; 1253 MW; 04024EA3495865B0 CRC64;

Query Match
Best Local Similarity 24.6%; Score 16; DB 1; Length 12;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      6 AGVG 9
       :||
Db      6 SGIG 9

RESULT 14
V14K_MSSV STANDARD; PRT; 12 AA.
ID V14K_MSSV
AC P82006;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 14.5 kDa structural polypeptide (Fragment).
OS White spot syndrome virus (WSSV).
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae.
OX NCBI_TaxID=92652;
RN [1]
RP SEQUENCE.
RC STRAIN-South Carolina;
RX MEDLINE-20214217; PubMed-10752552;
RA Wang Q., Poulos B.T., Lightner D.V.;
RT "Protein analysis of geographically isolates of shrimp white spot syndrome
RT virus.";
RL Arch. Virol. 145:263-274(2000).
CC -1- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
FT NON_TER
SQ      SEQUENCE 12 AA; 1242 MW; 24B8DE4FFD21A338 CRC64;

Query Match
Best Local Similarity 24.6%; Score 16; DB 1; Length 12;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 GRTG 12
       |||
Db      9 GRRG 12

RESULT 15
ISOT_CYPCA STANDARD; PRT; 9 AA.
ID ISOT_CYPCA
AC P42993;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Isotocin.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE.
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea

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RT water bony fishs."  
 RL Comp. Biochem. Physiol. 14:245-254(1965).  
 CC -1- FUNCTION: ANTIDIURETIC HORMONE.  
 CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR PIR; A61364; A61364.  
 DR InterPro: IPR000981; Neuhyp\_horm.  
 DR InterPro: IPR001230; Prenyl\_site.  
 DR Pfam; PF00220; hormone4; 1.  
 DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Amidation.  
 FT DISULFID 1 6  
 FT MOD\_RES 9 9  
 SQ SEQUENCE 9 AA; 969 MW; 17FF476EB455B04B CRC64;

Query Match 23.1%; Score 15; DB 1; Length 9;  
 Best local Similarity 28.6%; Pred. No. 1.1e+05;  
 Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VVHCSAG 7  
 : : 1 1  
 Db 3 ISNCPIG 9

Search completed: January 17, 2003, 11:00:09  
 Job time : 10 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 17, 2003, 10:58:32 ; Search time 28 Seconds  
(without alignments)  
88.306 Million cell updates/sec

Title: US-09-743-492-4  
Perfect score: 65  
Sequence: 1 VVHCSAGVGRG 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 2041

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL.21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	25	38.5	12	11	Q61331
2	23	35.4	12	5	Q9TY79
3	21	32.3	9	13	Q92009
4	21	32.3	12	10	Q945C2
5	20	30.8	10	6	Q8WP04
6	20	30.8	12	13	Q9PS67
7	19	29.2	12	6	Q9TRT8
8	18	27.7	9	4	Q99887
9	18	27.7	11	12	Q66874
10	18	27.7	11	12	Q66874
11	18	27.7	11	4	Q16452
12	18	27.7	12	10	Q945C4
13	18	27.7	12	12	Q91F00
14	18	27.7	12	12	Q91E29
15	18	27.7	12	15	Q12074
16	18	27.7	12	15	Q12074

17	18	27.7	12	15	Q12076	012076 caprine art
18	18	27.7	12	15	Q12078	012078 caprine art
19	18	27.7	12	15	Q12080	012080 caprine art
20	18	27.7	12	15	Q12082	012082 caprine art
21	18	27.7	12	15	Q12084	012084 caprine art
22	18	27.7	12	15	Q12086	012086 caprine art
23	18	27.7	12	15	Q12088	012088 caprine art
24	18	27.7	12	15	Q12090	012090 caprine art
25	18	27.7	12	15	Q12092	012092 caprine art
26	18	27.7	12	15	Q12094	012094 caprine art
27	18	27.7	12	15	Q12106	012106 caprine art
28	18	27.7	12	15	Q12108	012108 caprine art
29	18	27.7	12	15	Q12110	012110 caprine art
30	18	27.7	12	15	Q12112	012112 caprine art
31	18	27.7	12	15	Q12114	012114 caprine art
32	18	27.7	12	15	Q12116	012116 caprine art
33	18	27.7	12	15	Q12118	012118 caprine art
34	18	27.7	12	15	Q78845	078845 human immun
35	17	26.2	8	4	Q15900	Q15900 homo sapien
36	17	26.2	8	11	Q60615	Q60615 mus musculu
37	17	26.2	10	3	Q90VW2	Q90VW2 schizophyll
38	17	26.2	11	11	Q99JC3	Q99JC3 rattus sp.
39	17	26.2	12	3	Q9UR22	Q9UR22 cryptococcu
40	17	26.2	12	6	Q9TRU2	Q9TRU2 bos taurus
41	17	26.2	12	10	Q02319	Q02319 pinus sylve
42	17	26.2	12	10	Q02320	Q02320 pinus sylve
43	17	26.2	12	10	Q38715	Q38715 arachis hyp
44	16	25.4	11	5	P82698	P82698 leucophaea
45	16	24.6	7	2	Q47505	Q47505 escherichia

## ALIGNMENTS

RESULT 1	061331	PRELIMINARY:	PRT:	12 AA.
ID	Q61331			
AC	Q61331			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DR	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	N-acetylglucosamine (Beta1-4) galactosyl transferase (EC 2.4.1.90)			
DE	(Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RP	[1]			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE=89033997; PubMed=3141392;			
RA	Nakazawa K., Ando T., Kimura T., Narimatsu H.;			
RT	"Cloning and sequencing of a full-length cDNA of mouse N-			
RT	acetylglucosamine (beta1-4)galactosyltransferase.";			
RL	J. Biochem. 104:165-168(1988).			
DR	EMBL; D00315; BAA00217.1;--			
KW	Glycosyltransferase; Transferase.			
FT	NON_TER			
FT	NON_TER			
SO	SEQUENCE	12 AA;	1283 MW;	304EA0668387728 CRC64;
Query Match		38.5%;	Score 25;	DB 11;
Best Local Similarity		57.1%;	Pred. No. 5.3e+02;	Length 12;
Matches	4;	Conservative	3;	Mismatches 0;
				Indels 0;
				Gaps 0;
QY	5 SAGVGR 11			
DB	1:1:1:1			
	3 SSGIGRT 9			
RESULT 2	Q9TY79	PRELIMINARY:	PRT:	12 AA.
ID	Q9TY79			
AC	Q9TY79;			

DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Potassium channel (Fragment).  
 GN SHAKER.  
 OS Panulirus interruptus (California spiny lobster).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Palinura;  
 OC Palinuroidea; Palinuridae; Panulirus.  
 OX NCBI\_Taxid=6735;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98330950; PubMed=9665521;  
 RA Kim M., Baro D.J., Lanning C.C., Doshi M., Moskowitz H.S., Farnham J.,  
 RA Harris-Warlick R.M.;  
 RT "Expression of Panulirus shaker potassium channel splice variants";  
 RL Recept. Channels 5:291-304(1998).  
 DR EMBL: AF017131; AAC05911.1; -.  
 FT NON\_TER  
 SQ SEQUENCE 12 AA; 1227 MW; 049050CA44D4DD4 CRC64;

Query Match 35.4%; Score 23; DB 5; Length 12;  
 Best Local Similarity 33.3%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VHCAGVG 9  
 : : : : :  
 Db 1 MISCNANAG 9

RESULT 3  
 ID 092009 PRELIMINARY; PRT; 9 AA.  
 AC 092009;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-NOV-1996 (TReMBLrel. 08, Last annotation update)  
 DE C-REL protein (Chicken).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_Taxid=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91133738; PubMed=2284104;  
 RA Hannink M., Temin H.M.;  
 RT "Structure and autoregulation of the c-rel promoter";  
 RL Oncogene 5:1843-1850(1990).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RA Hannink M., Temin H.M.;  
 RL Oncogene 0:0-0(1990).  
 DR EMBL: X56440; CAA38822.1; -.  
 DR EMBL: X56515; CAA39866.1; -.  
 FT NON\_TER  
 SQ SEQUENCE 9 AA; 805 MW; DE317DD87865A2CD CRC64;

Query Match 32.3%; Score 21; DB 13; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 6.7e+05;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 SAGVGR 10  
 : : : : :  
 Db 4 SGCAGR 9

RESULT 4  
 ID 0945C2 PRELIMINARY; PRT; 12 AA.  
 AC 0945C2;  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE DapC protein (Fragment).  
 OS Cryptocodinium cornii (Dinoflagellate).  
 OC Eukaryota; Alveolata; Dinophyceae; Gonyaulacales; Cryptocodiniaceae;  
 OC Cryptocodinium.  
 OX NCBI\_Taxid=2866;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21428164; PubMed=11545436;  
 RA Guillebaud D., Derelle E., Bhaud Y., Moreau H.;  
 RT "Role of nuclear MW domains and proline-rich proteins in  
 RT dinoflagellate transcription";  
 RL Proclst 152:127-138(2001).  
 DR EMBL: AF417569; AAL15907.1; -.  
 FT NON\_TER  
 SQ SEQUENCE 12 AA; 1436 MW; C4831B7517B1F2CD CRC64;

Query Match 32.3%; Score 21; DB 10; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHC 4  
 : : : : :  
 Db 6 VHC 8

RESULT 5  
 ID 08WP04 PRELIMINARY; PRT; 10 AA.  
 AC 08WP04;  
 DT 01-MAR-2002 (TReMBLrel. 20, Created)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
 DE Oculocutaneous albinism type II (Fragment).  
 GN OCA2.  
 OS Ateles belzebuth chamek (Chamek spider monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateles.  
 OX NCBI\_Taxid=118643;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21636947; PubMed=11778686;  
 RA Senquez H.N., Lima C.R., Lemos B., Bonvicino C.R., Moreira M.A.M.,  
 RA Canavez F.C.;  
 RT "Gene assignment in Ateles paniscus chamek (Platyrrhini, Primates).  
 RT Allocation of 18 markers of human syntenic groups 1,2,7,14,15,17 and  
 RT 22";  
 RL Chromosome Res. 9:631-639(2001).  
 DR EMBL: AF375652; AAL31489.1; -.  
 FT NON\_TER  
 SQ SEQUENCE 10 AA; 901 MW; 22DF47DD87EA5B8 CRC64;

Query Match 30.8%; Score 20; DB 6; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CSAGV 8  
 : : : : :  
 Db 5 CGAGM 9

RESULT 6  
 ID 09PS67 PRELIMINARY; PRT; 12 AA.  
 AC 09PS67;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE Myosin (Fragment).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.



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OX NCBI_TaxID=9031;
RP [1]
RP SEQUENCE.
RX MEDLINE=92031443; PubMed=1931944;
RA Garabedian T.E., Yount R.G.;
RT "Direct photoaffinity labeling of gizzard myosin with vanadate-trapped
RL adenosine diphosphate.";
RL Biochemistry 30:10126-10132(1991).
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 12 AA; 1178 MW; C1FC2E0D9AA3387D CRC64;

Query March 30.8%; Score 20; DB 13; Length 12;
Best Local Similarity 50.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 AGVGR 11
DB 3 SGAGKT 8

RESULT 7
O17140 PRELIMINARY; PRT; 12 AA.
AC O17140;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Putative c-myc homolog (Fragment).
OS Crassostrea virginica (Eastern oyster).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
OC Ostreoida; Ostreidae; Crassostrea.
OX NCBI_TaxID=6565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WESTERN NORTH ATLANTIC WILD OYSTER;
RA Hare M.P., Avise J.C.;
RT "Population structure in the American Oyster as inferred by Nuclear
RT Gene Genealogies.";
RL Mol. Biol. Evol. 0:0-0(1997).
DR EMBL; AF024522; AAB82269.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 12 AA; 1334 MW; FF6312ABFE1775AA CRC64;

Query Match 29.2%; Score 19; DB 5; Length 12;
Best Local Similarity 42.9%; Pred. No. 6.3e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 HCSAGVG 9
DB 3 HXSAPRG 9

RESULT 8
O9TRT8 PRELIMINARY; PRT; 12 AA.
AC O9TRT8;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE 15 kDa histone H4 homolog (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=92132498; PubMed=1734497;
RA Velby O.P., Sletten K., Husby G., Nordstoga K.;
RT "Amino acid sequence analyses of non-AA proteins from amyloid fibrils
RT of bovine kidney.";
```

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RL Scand. J. Immunol. 35:63-69(1992).
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 12 AA; 1406 MW; CA8BC4BC9003372D CRC64;

Query Match 29.2%; Score 19; DB 6; Length 12;
Best Local Similarity 45.5%; Pred. No. 6.3e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 VVHCAGVGR 11
DB 2 VVYALKRQGR 12

RESULT 9
O99887 PRELIMINARY; PRT; 9 AA.
AC O99887;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE I1 <beta>-HSD2 protein (Fragment).
GN I1 <BETA>-HSD2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96133030; PubMed=8538347;
RA Stewart P.M., Krozowski Z.S., Gupta A., Milford D.V., Howie A.J.,
RA Sheppard M.C., Whorwood C.B.;
RT "Hypertension in the syndrome of apparent mineralocorticoid excess due
RT to mutation of the I1 beta-hydroxysteroid dehydrogenase type 2 gene.";
RL Lancet 347:88-91(1996).
DR EMBL; S80133; AAD14324.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 9 AA; 1020 MW; CERC2EB1F5B059C9 CRC64;

Query Match 27.7%; Score 18; DB 4; Length 9;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVHC 4
DB 4 ISHC 7

RESULT 10
O66874 PRELIMINARY; PRT; 11 AA.
AC O66874;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE Polymerase (Fragment).
OS Feline calicivirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Vesivirus.
OX NCBI_TaxID=11978;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=255;
RX MEDLINE=95250311; PubMed=7732664;
RA Seal B.S., Neill J.D.;
RT "Capsid protein gene sequence of feline calicivirus isolates 255 and
RT LUK: further evidence for capsid protein configuration among feline
RT caliciviruses.";
RL Virus Genes 9:183-187(1995).
DR EMBL; U07130; AAA74412.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1232 MW; 4EBE5F5CMAEB1E7 CRC64;
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Query Match 27.7%; Score 18; DB 12; Length 11;  
Best Local Similarity 66.7%; Pred. No. 8.6e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 VHC 4  
: 11  
Db 4 LHC 6

RESULT 11  
066877 PRELIMINARY; PRT; 11 AA.  
AC 066877;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DE 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
DE Polymerase (Fragment).  
OS Feline calicivirus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;  
OC Vesivirus.  
OX NCBI\_TaxID=11978;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LIK:  
RX MEDLINE=95250311; PubMed=7732664;  
RA Seal B.S., Neill J.D.;  
RT "Capsid protein gene sequence of feline calicivirus isolates 255 and  
RT LK: further evidence for capsid protein configuration among feline  
RT caliciviruses";  
RL Virus Genes 9:183-187(1995).  
DR EMBL, U07131; AAA74415.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1264 MW; 5E9F43BCCAEB1E7 CRC64;

Query Match 27.7%; Score 18; DB 12; Length 11;  
Best Local Similarity 66.7%; Pred. No. 8.6e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 VHC 4  
: 11  
Db 4 LHC 6

RESULT 12  
016452 PRELIMINARY; PRT; 12 AA.  
AC 016452;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Mutant collagen alpha 2(I) chain CB peptide alpha 2CBA  
DE (Fragment).  
GN COL1A2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92201825; PubMed=1551666;  
RA Nicholls A.C., Oliver J., Renouf D.V., Heath D.A., Pope F.M.;  
RT "The molecular defect in a family with mild atypical osteogenesis  
RT imperfecta and extreme joint hypermobility: exon skipping caused by an  
RT 11-bp deletion from an intron in one COL1A2 allele";  
RL Hum. Genet. 88:627-633(1992).  
DR EMBL, S89896; AAB21862.1; -.  
KW Collagen.  
FT NON\_TER 1 1  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1161 MW; D5BD7D21FAE861B6 CRC64;

Query Match 27.7%; Score 18; DB 4; Length 12;  
Best Local Similarity 75.0%; Pred. No. 9.5e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 9 GRTG 12  
: 11  
Db 4 GRTG 7

RESULT 13  
0945C4 PRELIMINARY; PRT; 12 AA.  
AC 0945C4;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DE Beta-tubulin (Fragment).  
OS Cryptocodium cohnii (Dinoflagellate).  
OC Eukaryota; Alveolata; Dinophyceae; Gonyaulacales; Cryptophocodiniaceae;  
OC Cryptocodium.  
OX NCBI\_TaxID=2866;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Guillebaud D., Derelle E., Lozano J.C., Bingham S., Moreau H.;  
RT "A single TBP-like protein is present in the marine unicellular  
RT organism: the dinoflagellate Cryptocodium cohnii";  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL, AF417567; AAL15905.1; -.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1299 MW; F2AE9D1D4166D051 CRC64;

Query Match 27.7%; Score 18; DB 10; Length 12;  
Best Local Similarity 42.9%; Pred. No. 9.5e+03;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VHCASG 7  
: 11  
Db 3 LVHIOGG 9

RESULT 14  
091F00 PRELIMINARY; PRT; 12 AA.  
AC 091F00;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)  
DE E1A nucleoprotein (Fragment).  
OS Human adenovirus type 5.  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
OX NCBI\_TaxID=28285;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hayashi S., Gillam I.C., McDonald T., Way D., Harris T.,  
RA Sedgwick E.G.;  
RT "E1A DNA of group C adenovirus integrates into human chromosomes";  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL, AF288220; AAF91488.1; -.  
KW Nucleocapsid.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1337 MW; 06D6D0D4171EEB0 CRC64;

Query Match 27.7%; Score 18; DB 12; Length 12;  
Best Local Similarity 60.0%; Pred. No. 9.5e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CSACV 8  
: 11  
Db 6 CHGCV 10

RESULT 15  
091E29 PRELIMINARY; PRT; 12 AA.  
AC 091E29;  
AC 091E29;

DT 01-OCT-2000 (TRENBLrel. 15, Created)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)  
 DE E1A nucleoprotein (Fragment).  
 OS Human adenovirus type 5.  
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
 OX NCBI\_TaxID=28285;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hayashi S., Gilliam I.C., McDonald T., Way D., Harris T.,  
 RA Sedgwick E.G.;  
 RT "E1A DNA of group C adenovirus integrates into human chromosomes.";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF288641; AAF91494.1; -.  
 KW Nucleocapsid.  
 FT NON\_TER 12  
 SQ SEQUENCE 12 AA; 1337 MW; 06D66DD4171EEB0 CRC64;

Query Match 27.7%; Score 18; DB 12; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 9.5e+03;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CSAGV 8  
 1 11  
 Db 6 CHGV 10

Search completed: January 17, 2003, 11:00:44  
 Job time : 28 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 17, 2003, 10:55:47 : Search time 34 Seconds  
(without alignments)  
47.030 Million cell updates/sec

Title: US-09-743-492-4

Perfect score: 65

Sequence: 1 VVHCSAGVGRTG 12

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

204235

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
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6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
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21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result NO.	Score	Query Match	Length	DB	ID	Description
1	65	100.0	12	21	AAV81786	Protein tyrosine p
2	61	93.8	11	20	AAV34167	PTP-D1 binding reg
3	51	78.5	9	21	AAV19775	Protein tyrosine p
4	50	76.9	11	19	AAV64787	Human tumour suppr
5	50	76.9	11	20	AAV07459	Protein tyrosine p
6	45	69.2	8	20	AAV94026	PTP-OB tyrosine p
7	45	69.2	8	22	AAU01458	Conserved amino ac
8	45	69.2	9	21	AAV19777	Protein tyrosine p
9	43	66.2	10	23	AAV07849	Protein tyrosine p
10	43	66.2	12	22	AAV59247	Peptide associated

11	42	64.6	10	21	AAV19603	Human dual-specific
12	42	64.6	11	18	AAV35299	Tyrosine phosphatase
13	41	63.1	7	20	AAV14759	Protein tyrosine p
14	41	63.1	9	21	AAV19776	Protein tyrosine p
15	40	61.5	7	16	AAV85205	Tyrosine phosphatase
16	40	61.5	7	20	AAV14760	Human PTPB protein
17	40	61.5	7	20	AAV25413	Human dual-specific
18	39	60.0	10	22	AAV32999	Human dual-specific
19	39	60.0	10	22	AAV67168	Human dual-specific
20	39	60.0	10	22	AAV64332	Human DSP-3 active
21	38	58.5	7	20	AAV14758	Tyrosine phosphatase
22	36	55.4	7	15	AAV6291	PTP-D1/D2 primer #
23	36	55.4	7	16	AAV49154	Corresp. to human
24	36	55.4	7	16	AAV71502	Conserved region o
25	36	55.4	7	19	AAV49916	Protein tyrosine p
26	36	55.4	8	23	AAV17886	Human PTPN catalyt
27	36	55.4	10	23	AAV22730	Human dual-specific
28	36	55.4	11	16	AAV72863	Rat receptor type-
29	36	55.4	11	19	AAV52305	PTP catalytic doma
30	36	55.4	11	21	AAV81784	Protein tyrosine p
31	36	55.4	11	21	AAV79019	Protein tyrosine p
32	36	55.4	11	21	AAV56099	Phosphatase domain
33	36	55.4	11	22	AAV78257	Generic conserved
34	36	55.4	11	22	AAV59585	Non-receptor PTPas
35	36	55.4	11	22	AAV59358	Protein tyrosine p
36	35	53.8	7	20	AAV14757	Tyrosine phosphatase
37	35	53.8	11	18	AAV29151	Consensus catalytic
38	35	53.8	12	21	AAV70337	Subsequence-2 of A
39	34	52.3	9	20	AAV39372	Protein tyrosine p
40	32	49.2	11	23	AAV13602	Protein tyrosine p
41	31	47.7	5	20	AAV89256	Human PTP04 conser
42	31	47.7	6	19	AAV3022	Protein tyrosine p
43	31	47.7	10	22	AAV94324	Human complementar
44	31	47.7	10	22	AAV94326	Human complementar
45	31	47.7	10	22	AAV6427	Saccharomycetes cere

#### ALIGNMENTS

RESULT 1  
ID AAV81786 standard; Peptide: 12 AA.  
AAV81786;  
07-JUN-2000 (first entry)  
Protein tyrosine phosphatase motif #1.  
Human; protein tyrosine phosphatase; antibody; intracellular domain; LAR; CD45; PTP; diagnosis; insulin resistance related disease; syndrome X; non-insulin dependent diabetes mellitus; arteriosclerosis; therapy.  
heart disorder; signature motif.  
Unidentified.  
WO200002922-A1.  
20-JAN-2000.  
06-JUL-1999; 99WO-JP03656.  
10-JUL-1998; 98WO-JP03120.  
(FUSO ) FUSO PHARM IND LTD.  
Yamamoto H, Tsujikawa K, Uchino Y;  
WPI: 2000-182215/16.  
Antibody for diagnosis and treatment of insulin resistance disorders  
and syndrome X recognises the intracellular domains of tyrosine

PT phosphatase -  
 XX  
 PS Example 3; Page 32; 83pp; Japanese.  
 XX  
 CC This sequence represents a motif of a protein tyrosine  
 CC phosphatases. The invention relates to an antibody of the invention that  
 CC has sites specifically recognising the intracellular domain  
 CC of two or more protein tyrosine phosphatases (PTPs). The antibody is  
 CC useful for the detection and assay of PTP including novel phosphatases  
 CC generated by cloning; and diagnosis, treatment and prevention of insulin  
 CC resistance related diseases and non-insulin dependent diabetes mellitus,  
 CC syndrome X and arteriosclerosis and heart disorders.  
 XX  
 SQ Sequence 12 AA:  
 Query Match 100.0%; Score 65; DB 21; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.00021;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VVHCSAGVGRG 12  
 DB 1 VVHCSAGVGRG 12  
 RESULT 2  
 AAY34167  
 ID AAY34167 standard; peptide; 11 AA.  
 XX  
 AC AAY34167;  
 XX  
 DT 09-NOV-1999 (first entry)  
 XX  
 DE PTP-DI binding region.  
 XX  
 KM PTP-DI; human; protein tyrosine phosphatase; neoplastic formation;  
 KM PTPase; growth factor signal transduction; cell cycle progression;  
 KM cancer; diabetes; cellular phosphotyrosine metabolism; binding site.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5955592-A.  
 XX  
 PD 21-SEP-1999.  
 XX  
 PF 27-APR-1994; 94US-0234440.  
 XX  
 PR 27-APR-1994; 94US-0234440.  
 PR 05-AUG-1992; 92US-0923740.  
 XX  
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX  
 PI Moller KB, Moller NPH, Ullrich A;  
 XX  
 DR WPI; 1999-539559/45.  
 XX  
 PT Nucleic acids encoding protein tyrosine phosphatase PTP-DI  
 XX useful for identification of PTP-DI modulators  
 XX  
 PS Example 8; Column 37; 63pp; English.  
 XX  
 CC This sequence represents a fragment of the protein tyrosine phosphatase  
 CC of the invention, designated PTP-DI. This sequence is thought to promote  
 CC binding of specific molecules to PTP-DI. The new PTP proteins are a  
 CC subfamily of protein tyrosine phosphatases (PTPases) involved with growth  
 CC factor signal transduction, cell cycle progression, and neoplastic  
 CC formation. The DNA sequence may be used in the recombinant production of  
 CC PTP-DI according to standard DNA methodology. The protein expressed may  
 CC then be used in assays to identify modulators of its enzymatic activity  
 CC and in the production of antibodies. The nucleic acids may also be used  
 CC in assays to detect and quantify expression of PTP-DI in samples. Methods  
 CC identifying normal or mutant PTP-D genes, or for measuring amount or  
 CC activity of the protein can serve as methods for identifying  
 CC susceptibility to cancer, diabetes, or other disorders associated with

CC alterations in cellular phosphotyrosine metabolism.  
 XX  
 SQ Sequence 11 AA:  
 Query Match 93.8%; Score 61; DB 20; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.00089;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VVHCSAGVGRG 12  
 DB 1 VVHCSAGVGRG 11  
 RESULT 3  
 AAB19775  
 ID AAB19775 standard; Peptide; 9 AA.  
 XX  
 AC AAB19775;  
 XX  
 DT 19-FEB-2001 (first entry)  
 XX  
 DE Protein tyrosine phosphatase HPTP-beta catalytic core.  
 XX  
 KM Vascular endothelial protein tyrosine phosphatase; HPTP-beta;  
 KM Tie-2; receptor-type tyrosine kinase; antiangiogenic; antitumour;  
 KM antimetastatic; tumour; metastasis; angiogenesis; therapy; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1046715-A1.  
 XX  
 PD 25-OCT-2000.  
 XX  
 PF 23-APR-1999; 99EP-0108074.  
 XX  
 PR 23-APR-1999; 99EP-0108074.  
 XX  
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX  
 PI Fachinger G, Ritsau B, Deutsch U;  
 XX  
 DR WPI; 2000-648932/63.  
 XX  
 PT Monitoring or modulating Tie-2 tyrosine kinase activity, useful e.g.  
 XX for regulating tumor growth, using vascular-endothelial protein  
 XX tyrosine phosphatase -  
 XX  
 PS Example 4; Fig 1a; 60pp; English.  
 XX  
 CC The present sequence is that of the catalytic core of HPTP-beta  
 CC (see AAB19774), a human protein tyrosine phosphatase. Trapping  
 CC mutants were engineered by replacing the Cys residue of this  
 CC motif with Ser (see AAB19776) and the Arg residue with Ala (see  
 CC AAB19777). The proteins were expressed in COS-1 cells, and used to  
 CC to examine the interaction of HPTP-beta with the receptor tyrosine  
 CC kinases Tie-2 and VEGFR-2. HPTP-beta polypeptides, nucleic  
 CC acids and ligands are used in claimed methods for detecting and  
 CC modulating Tie-2 activity. This allows the monitoring or  
 CC modulation of angiogenesis, induction or inhibition of vascular  
 CC growth or remodelling and blood vessel maturation, and inhibition  
 CC of tumour growth or metastasis.  
 XX  
 SQ Sequence 9 AA:  
 Query Match 78.5%; Score 51; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 HCSAGVGRG 11  
 DB 1 HCSAGVGRG 9

```

RESULT 5
AAW64787
ID AAW64787 standard; Protein; 11 AA.
XX
XX AAW64787;
AC
XX
XX 03-NOV-1998 (first entry)
DT
XX
XX Human tumour suppressor TS10q23.3 protein fragment (aa 88-98).
DE
XX
XX Tumour suppressor; TS10q23.3; human; diagnosis; tumour; prostate; breast;
KM brain; glioma; metastasis; gene therapy; anti-cancer; transgenic animal;
KW drug screening.
XX
XX Homo sapiens.
OS
XX
XX WO9833907-A1.
PN
XX
XX 06-AUG-1998.
PD
XX
XX 08-JAN-1998; 98WO-US00353.
PF
XX
XX 30-JAN-1997; 97US-0791115.
PR
XX
XX (MYRI-) MYRIAD GENETICS INC.
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Jaaser SA, Pershouse MA, Steck P, Tavligian SV;
PI Yung WKA;
PS WPI; 1998-437461/37.
DR
XX
XX Tumour suppressor TS10q23.3 and related antibodies - useful for
PT diagnosis, staging and treatment of cancer, especially of breast,
PR prostate and brain
PS Example 5; Page 115; 161pp; English.
XX
XX This sequence represents a fragment of the human tumour suppressor
CC protein TS10q23.3 corresponding to residues 88-98. This suppressor can be
CC used to diagnose a wide range of tumours, particularly of prostate,
CC breast and brain (glioma), to stage cancers (particularly differentiation
CC between low grade brain cancer and glioma) and for prediction of
CC metastasis. This suppressor and its nucleic acid are also used to alter
CC the phenotype to specifically treat cancer cells, e.g. by in vivo or ex
CC vivo gene therapy, optionally together with other anti-cancer agents.
CC Fragments of the suppressor can be coupled to an immunogenic carrier and
CC are used to raise antibodies, to isolate antigens, as immunosassay
CC reagents, to clone related DNA or for immunotherapy. Antisense nucleic
CC acid can be used to produce transgenic animals (useful for drug
CC screening) or to eliminate dominant negative mutants.
XX
XX Sequence 11 AA;
SQ
Query Match 76.9%; Score 50; DB 19; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.061;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 VHCSAGVGRGTG 12
: || || || ||
DB 1 IHCKAGKGRGTG 11

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KW Mutation; mutant; tumour suppressor; TS10q23.3; diagnosis; breast; ovary;
KM Cowden's Syndrome; thyroid gland; endometrium; cancer; antibody; ELISA;
KW enzyme linked immunosorbant assay; gene expression; human.
XX
XX Homo sapiens.
OS
XX
XX WO9910537-A1.
PN
XX
XX 04-MAR-1999.
PD
XX
XX 26-AUG-1998; 98WO-US17636.
PF
XX
XX 30-APR-1998; 98US-0083563.
PR
XX
XX 26-AUG-1997; 97US-0057750.
PA (MYRI-) MYRIAD GENETICS INC.
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Jaaser SA, Pershouse MA, Steck P, Tavligian SV;
PI Yung WKA;
PS WPI; 1999-190638/16.
DR
XX
XX Newly isolated DNA or RNA polynucleotide encoding a mutant tumour
PT suppressor (TS10q23.3) - useful for the diagnosis of Cowden's
PR syndrome and susceptibility to breast cancer
PS Example 5; Page 110; 244pp; English.
XX
XX The invention relates to mutant genes encoding the tumour suppressor
CC TS10q23.3. The TS10q23.3 mutant gene is useful for the diagnosis of
CC Cowden's Syndrome in cells selected from the breast, ovaries, thyroid
CC gland and endometrium (claimed). The mutant gene is also useful for
CC diagnosing a subject who has a predisposition to breast cancer. Both
CC methods involve antibodies, which specifically bind to a TS10q23.3,
CC used in an ELISA assay to evaluate the level of TS10q23.3 expression.
XX
XX Sequence 11 AA;
SQ
Query Match 76.9%; Score 50; DB 20; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.061;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 VHCSAGVGRGTG 12
: || || || ||
DB 1 IHCKAGKGRGTG 11

```

PA (MERI ) MERCK & CO INC.  
 XX  
 PI Rodan GA, Rutledge SJ, Schmidt A;  
 XX  
 DR WPI; 1999-141930/12.  
 XX  
 PT Protein tyrosine phosphatase denoted PTP-OB - useful for drug  
 PT screening  
 XX  
 PS Example 1; Column 11; 34pp; English.  
 XX  
 CC The invention relates to a human protein tyrosine phosphatase (PTP)  
 CC denoted as PTP-OB, produced by bone and brain cells. A recombinant  
 CC host cell transfected or transformed with a nucleic acid vector  
 CC comprising the nucleic acid can be used for the production of the  
 CC PTP-OB polypeptide. The protein can be used to screen for modulators of  
 CC PTP-OB activity, which might be useful for treating e.g. osteoporosis  
 CC and cancer. Sequences AA094025-26 represent peptide fragments from the  
 CC conserved tyrosine phosphatase domain of PTP-OB used for designing PCR  
 CC primers.  
 CC  
 SQ Sequence 8 AA;  
 XX  
 OY Query Match 69.2%; Score 45; DB 20; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 2 VHCSAGVG 9  
 1 VHCSAGVG 8  
 XX  
 RESULT 7  
 AA01458  
 ID AA01458 standard; Peptide: 8 AA.  
 AC AA01458;  
 XX  
 DT 18-JUL-2001 (first entry)  
 XX  
 DE Conserved amino acids of PTP domain used to make PCR primer PH2a.  
 XX  
 KW Protein tyrosine phosphatase; PTP; human; osteoporosis; bone formation;  
 KW PTP-OB; cell proliferation; cell death; neoplastic transformation;  
 KW metastasis; tumour; cancer; lung cancer; osteosarcoma.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6214564-B1.  
 XX  
 PD 10-APR-2001.  
 XX  
 PF 22-SEP-1998; 98US-0158657.  
 XX  
 PR 01-DEC-1994; 94US-0348006.  
 PR 14-FEB-1997; 97US-0800825.  
 PR 14-SEP-1993; 93US-0122032.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Rodan GA, Rutledge SJ, Schmidt A;  
 XX  
 DR WPI; 2001-280994/29.  
 DR N-PSDB; AAS02143.  
 XX  
 PT Identifying a compound which modulates protein tyrosine phosphatase  
 PT activity for treating osteoporosis, comprises contacting a polypeptide  
 PT with a compound and measuring the ability of the compound to modulate  
 PT polypeptide activity -  
 XX  
 PS Example 1; Column 11; 35pp; English.  
 XX  
 CC The sequence represents the conserved amino acids of protein tyrosine

CC phosphatase (PTP-OB) domain used to make degenerate PCR primer PH2a.  
 CC The PTP-OB nucleic acid and protein sequences (see AAS02144, AA01459)  
 CC were used in a method to identify a compound able to modulate PTP-OB  
 CC activity, involving contacting a recombinant polypeptide comprising the  
 CC entire cytoplasmic domain of PTP-OB with the compound, and measuring the  
 CC ability of the compound to modulate the activity of the polypeptide. The  
 CC compounds that modulate PTP-OB activity are useful in treating disease  
 CC states involving PTP-OB activity such as osteoporosis, for preventing and  
 CC treating bone loss, and stimulation of bone formation. The compounds are  
 CC also useful for treating diseases in which activation or inactivation of  
 CC PTP-OB protein results in either cellular proliferation, cell death,  
 CC nonproliferation, induction of cellular neoplastic transformations or  
 CC metastatic tumour growth, such as cancer, preferably lung cancer or  
 CC osteosarcoma.  
 CC  
 SQ Sequence 8 AA;  
 XX  
 OY Query Match 69.2%; Score 45; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 2 VHCSAGVG 9  
 1 VHCSAGVG 8  
 XX  
 RESULT 8  
 AAB19777  
 ID AAB19777 standard; Peptide: 9 AA.  
 AC AAB19777;  
 XX  
 DT 19-FEB-2001 (first entry)  
 XX  
 DE Protein tyrosine phosphatase HTPP-beta catalytic core R to A mutant.  
 XX  
 KW Vascular-endothelial protein tyrosine phosphatase; HTPP-beta;  
 KW Tie-2; receptor-type tyrosine kinase; antiangiogenic; antitumour;  
 KW antineoplastic; tumour; metastasis; angiogenesis; therapy; human;  
 KW mutant; mutlein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FT Key Location/Qualifiers  
 FT Misc-difference 8 /note= "Arg in native sequence"  
 FT  
 XX  
 PN EP1046715-A1.  
 XX  
 PD 25-OCT-2000.  
 XX  
 PF 23-APR-1999; 99EP-0108074.  
 XX  
 PR 23-APR-1999; 99EP-0108074.  
 XX  
 PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX  
 PI Fachinger G, Rissau B, Deutsch U;  
 XX  
 DR WPI; 2000-648932/63.  
 XX  
 PT Monitoring or modulating Tie-2 tyrosine kinase activity, useful e.g.  
 PT for regulating tumor growth, using vascular-endothelial protein  
 PT tyrosine phosphatase -  
 XX  
 PS Example 4; Fig 1a; 60pp; English.  
 XX  
 CC The present sequence is that of the catalytic core of HTPP-beta  
 CC (see AAB19774); mutated such that the native Arg residue at position  
 CC 9 is substituted by Ala. This trapping mutant of HTPP-beta, a  
 CC protein tyrosine phosphatase, was used in experiments to examine  
 CC the interaction of HTPP-beta with the receptor tyrosine kinases



CC Tie2 and VEGFR-2. HRP-beta polypeptides, nucleic acids and  
 CC ligands are used in claimed methods for detecting and modulating  
 CC Tie-2 activity. This allows the monitoring or modulation of  
 CC angiogenesis, induction or inhibition of vascular growth or  
 CC remodelling and blood vessel maturation, and inhibition of tumour  
 CC growth or metastasis.

XX Sequence 9 AA;

Query Match 69.2%; Score 45; DB 21; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 7.8e+05;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 HCSAGVGR 11  
 |||||  
 DB 1 HCSAGVGAR 9

RESULT 9  
 ABB07849

ID ABB07849 standard; peptide; 10 AA.

XX ABB07849;

DT 03-JUN-2002 (first entry)

DE Protein tyrosine phosphatase (PTP) catalytic domain conserved sequence.

XX Tyrosine phosphatase-like enzyme; antidiabetic; anorectic; cyostatic;  
 KW cardiatic; metabolic; immunomodulator; antiparkinsonian; anticonvulsant;  
 KW cerebroprotective; neuroprotective; nootropic; neuroleptic; anti-HIV;  
 KW antiarrhythmic; hypotensive; vulnerary; protein tyrosine phosphatase;  
 PTP.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1.10  
 FT /note= "residues Xaa are unknown"

XX WO200220747-A2.

XX 14-MAR-2002.

XX 05-SEP-2001; 2001WO-EP10205.

XX 11-SEP-2000; 2000US-231568P.

XX 06-DEC-2000; 2000US-251403P.

XX (FARB ) BAYER AG.

XX Kossida S;

XX WPI; 2002-339803/37.

XX New human tyrosine phosphatase-like enzyme polypeptide, regulators of  
 PT which are useful for preventing, treating diabetes, obesity, cancer,  
 PT cardiovascular and pulmonary diseases

XX Disclosure; Page 4; 117pp; English.

XX The invention relates to a purified human tyrosine phosphatase-like  
 CC enzyme polypeptide. The enzyme can be expressed by standard recombinant  
 CC methodology. The tyrosine phosphatase-like enzyme and encoding  
 CC polynucleotides are useful for screening for modulators which are used  
 CC for treating a tyrosine phosphatase-like enzyme dysfunction related  
 CC disease such as a central nervous system (CNS) disorder, diabetes,  
 CC obesity, chronic obstructive pulmonary disease, cardiovascular disease,  
 CC cancer, anorexia, cachexia, wasting disorders, appetite suppression, and  
 CC other eating disorder such as bulimia. CNS disorders include brain  
 CC injuries, Parkinson's disease, dementia, multiple sclerosis, stroke,  
 CC Alzheimer's disease, Huntington's disease, schizophrenia, Pick's disease,  
 CC Creutzfeldt-Jacob dementia, progressive nuclear palsy, and human

CC immunodeficiency virus (HIV) dementia, pain associated with CNS disorders  
 CC and cardiovascular diseases include myocardial infarction, ischemic  
 CC diseases of the heart, atrial and ventricular arrhythmia, hypertensive  
 CC vascular diseases and peripheral vascular diseases. The enzyme is useful  
 CC in diagnostic assays for detecting diseases and abnormalities or  
 CC susceptibility to diseases or abnormalities related to the presence of  
 CC mutations in the encoding nucleic acid sequences. The present sequence  
 CC represents a protein tyrosine phosphatase (PTP) catalytic domain  
 CC conserved fragment.

XX Sequence 10 AA;

Query Match 66.2%; Score 43; DB 23; Length 10;  
 Best Local Similarity 70.0%; Pred. No. 0.83;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 HCSAGVGR 12  
 |||||  
 DB 1 HCSXGGRXG 10

RESULT 10  
 AAB59247

ID AAB59247 standard; peptide; 12 AA.

XX AAB59247;

DT 26-MAR-2001 (first entry)

DE Peptide associated with SH2 domain containing proteins.

XX SHP-2; SHP-1; Src Homology-2; protein tyrosine phosphatase; mutant;  
 KW neoplastic disorder; obesity; angiogenesis; cancer; immune;  
 KW hematopoietic; allergy.

XX Unidentified.

XX US6156551-A.

XX 05-DEC-2000.

XX 05-JUN-1998; 98US-0092443.

XX 05-JUN-1998; 98US-0092443.

XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
 XX (JOSL-) JOSLIN DIABETES CENT.

XX Neel BG, Shoelson S, Pluskey S, O'Reilly AM;

XX WPI; 2001-060166/07.

XX Mutant SH2 domain-containing protein tyrosine phosphatase, useful in in  
 PT vitro assays to screen for binding partners, inhibitors of tyrosine  
 PT phosphatase and for treating tyrosine phosphatase-mediated diseases

XX Disclosure; Column 249; 161pp; English.

XX The present invention relates to an activated SH2 (Src Homology-2)  
 CC -domain containing protein tyrosine phosphatase (SHP-1 or SHP-2)  
 CC mutant with a mutation in the SH2-domain. Activated mutants of  
 CC SH2-domain-containing protein tyrosine phosphatases are useful in  
 CC in vitro assays to screen for binding partners and inhibitors of  
 CC the phosphatase and in the treatment of PTP-mediated diseases or  
 CC conditions in a mammal, including neoplastic disorders, obesity and  
 CC to inhibit angiogenesis. Inhibitors identified using the activated  
 CC mutants are useful for the treatment of cancer, immunosuppression,  
 CC immunostimulation, hematopoietic stimulation and anti-allergy  
 CC treatment.

XX Sequence 12 AA;

Query Match 66.2%; Score 43; DB 22; Length 12;

Best Local Similarity 58.3%; Pred. No. 1;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VHCAGVGRG 12  
: ||| | | |  
Db 1 IVHCAGXRRK 12

RESULT 11  
AAB19603  
ID AAB19603 standard; Peptide: 10 AA.

AC AAB19603;

DT 22-JAN-2001 (first entry)

DE Human dual-specificity phosphatase-1 (DSP-1) active site.

KW DSP-1: dual-specificity phosphatase-1; human; cell proliferation;  
KW cell differentiation; cell survival; cell cycle; dephosphorylation;  
KW signal transduction; MAP-kinase; cancer; graft versus host disease;  
KW allergy; autoimmune disease; metabolic disease; therapy.

OS Homo sapiens.

PN WO200053636-A2.

PD 14-SEP-2000.

PF 08-MAR-2000; 2000WO-US06154.

PR 08-MAR-1999; 99US-0123255.

PA (CEPT-) CEPTYR INC.

PI Luche RM, Wei B;

DR WPI: 2000-579365/54.

PT New isolated polypeptide having the sequence of dual-specificity  
phosphatase-1 (DSP-1) is useful for treating a patient with a disorder  
associated with DSP-1 activity e.g. cancer and autoimmune diseases -

PS Disclosure; Page 13; 74pp; English.

XX The present sequence is that of the active site of human  
XX dual-specificity phosphatase-1 (DSP-1), corresponding to amino acid  
XX residues 109-118 of the full-length protein (see AAB19602). DSP-1  
XX dephosphorylates phosphotyrosine and phosphothreonine/serine  
XX residues in DSP-1 substrates such as activated mitogen-activated  
XX protein kinase (MAP-kinase). Methods are provided for recombinant  
XX production of DSP-1 polypeptides, and for using DSP-1 polypeptides,  
XX antibodies and polynucleotides to detect DSP-1 expression, to screen  
XX for agents that modulate DSP-1 activity, and for using such agents to  
XX modulate cell proliferation, differentiation or survival. The cell  
XX may display contact inhibition of cell growth, anchorage-dependent  
XX growth or an altered intercellular adhesion property, or is a cell  
XX present in a patient afflicted with a disorder associated with  
XX DSP-1 activity, such as cancer, graft-versus host disease,  
XX autoimmune disease, allergy, metabolic disease, abnormal cell  
XX growth, abnormal cell proliferation and abnormal cell cycle.  
XX Variants of DSP-1 are also provided. These may have amino acid  
XX sequence modifications in non-critical regions so as to preserve  
XX the active site.

SO Sequence 10 AA;

Query Match 64.6%; Score 42; DB 21; Length 10;

Best Local Similarity 70.0%; Pred. No. 1.2;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VHCAGVGRG 11  
|||:~|||:

Db 1 VHCAAGVSRS 10

RESULT 12  
AAW35299  
ID AAW35299 standard; Peptide: 11 AA.

AC AAW35299;

DT 27-MAR-1998 (first entry)

DE Protein tyrosine phosphatase catalytic core consensus.

KW Islet cell antigen 1851; autoantigen; protein tyrosine phosphatase;  
KW insulin-dependent diabetes mellitus; IDDM; diagnosis; therapy;  
KW macaque; human.

OS Mammalia.

PN Key Location/Qualifiers

FT Misc-difference 3 /note= "the Cys residue appears to be essential  
to the catalytic mechanism"

FT Misc-difference 4 /note= "any amino acid"

FT Misc-difference 7 /note= "any amino acid"

FT Misc-difference 8 /note= "any amino acid"

FT Misc-difference 10 /label= Ser, thr

FT WO9732984-A1.

PN 12-SEP-1997.

PD 05-MAR-1997; 97WO-US03532.

PF 15-OCT-1996; 96US-0027540.

PR 06-MAR-1996; 96US-0012927.

PA (UNIW ) UNIV WASHINGTON.

PA (ZYMO ) ZYMOGENETICS INC.

PI Hagopian W, Jelinek L, Kinsvogel W, Lagasse J;

PI Sheppard PO;

DR WPI: 1997-457535/42.

PT Mammalian pancreatic islet cell antigen and related DNA - used to  
detect autoantibodies indicative of insulin-dependent diabetes or  
pre-disposition to it

PS Disclosure; Page 19; 134pp; English.

XX This peptide sequence comprises the conserved catalytic core  
XX within the cytoplasmic domain of the protein tyrosine phosphatase  
XX (PTP) family members. The catalytic core of macaque islet cell  
XX antigen 1851 (see AAW35296) and of the human homologue (see AAW35297)  
XX of 1815 differ from that of other PTP family members in that  
XX alanine is replaced by aspartic acid and the second variable amino  
XX acid is alanine. Islet cell antigen 1851 forms an immune complex  
XX with an autoantibody in patients at risk of, or predisposed to,  
XX insulin-dependent diabetes mellitus (IDDM), and can be used in  
XX methods for the diagnosis and treatment of IDDM.

SO Sequence 11 AA;

Query Match 64.6%; Score 42; DB 18; Length 11;

Best Local Similarity 63.6%; Pred. No. 1.3;

Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 VHCAGVGRG 12

DB 1 VHCXAGAAARXG 11

## RESULT 13

ID AAV14759 standard; peptide; 7 AA.

XX AAV14759;

DT 11-OCT-1999 (first entry)

DE Tyrosine phosphatase conserved domain.

KM Genetic proximity; gene expression; cell characterisation; homeobox gene;

KM genetic defect; reverse transcriptase polymerase chain reaction; RT-PCR;

KM kinase gene; protein phosphatase; P450; steroid receptor; cadherin.

XX Homo sapiens.

XX WO9934016-A2.

PD 08-JUL-1999.

XX 28-DEC-1998; 98MO-IL00625.

XX 16-OCT-1998; 98ITL-0126627.

PR 29-DEC-1997; 97ITL-0122793.

XX (GENE-) GENENAL LTD.

PI Vidler B;

DR WPI: 1999-419113/35.

XX N-PSDB: AA218225.

XX Examples; Page 48; 102pp; English.

XX The invention provides a new method for identifying and characterising

CC cells. The method for determining the genetic proximity of a first cell

CC and a second cell comprises: (a) obtaining the first cell and the second

CC cell; (b) determining in the first cell and the second cell the pattern

CC of expression of genes in a selected gene family; and (c) calculating a

CC proximity index using a specified formula. The methods can be used for

CC characterising cells, e.g. for determining the origin of a cell, its

CC genetic status, whether it carries a genetic defect, or whether it is

CC transformed. They can be used for detecting a selected genetic defect in

CC an individual, e.g. a fetus. They can also be used for determining the

CC effect of a selected treatment on a test cell. They can also be used for

CC obtaining cells capable of expressing an homeobox related desired

CC property. The method uses reverse transcriptase polymerase chain

CC reaction (RT-PCR) for determining the pattern of gene expression in a

CC selected gene family. Sequences AA217803-218342 represent primers that

CC can be used in the RT-PCR reactions to determine the pattern of gene

CC expression. The gene family can be selected from a set of homeobox genes,

CC kinase genes, protein phosphatase genes, P450 enzyme genes, steroid

CC receptor superfamily genes or cadherin superfamily genes. Sequences

CC AAV14603-813 represent conserved peptide motifs based on which the

CC primers of the invention were designed.

CC

XX Sequence 7 AA;

XX

XX Query Match 63.1%; Score 41; DB 20; Length 7;

XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;

XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

XX 3 HCSAGVG 9

XX 1 HCSAGVG 7

DB

## RESULT 14

ID AAB19776 standard; peptide; 9 AA.

XX AAB19776;

DT 19-FEB-2001 (first entry)

DE Protein tyrosine phosphatase HTPP-beta catalytic core C to S mutant.

KM Vascular-endothelial protein tyrosine phosphatase; HTPP-beta;

KM Tie-2; receptor-type tyrosine kinase; antiangiogenic; antitumour;

KM antimetastatic; tumour; metastasis; angiogenesis; therapy; human;

KM mutant; mutlein.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

XX FT Misc-difference 2 /note="Cys in native sequence"

XX EP1046715-A1.

PD 25-OCT-2000.

XX 23-APR-1999; 99EP-0108074.

XX 23-APR-1999; 99EP-0108074.

XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX Fachinger G, Risau B, Deutsch U;

XX WPI: 2000-648932/63.

XX Monitoring or modulating Tie-2 tyrosine kinase activity, useful e.g.

XX for regulating tumor growth, using vascular-endothelial protein

XX tyrosine phosphatase

XX Example 4; Fig 1a; 60pp; English.

XX The present sequence is that of the catalytic core of HTPP-beta

XX (see AAB19774), mutated such that the native Cys residue at position

XX 2 is substituted by Ser. This trapping mutant of HTPP-beta, a

XX protein tyrosine phosphatase, was used in experiments to examine

XX the interaction of HTPP-beta with the receptor tyrosine kinases

XX Tie-2 and VEGFR-2. HTPP-beta polypeptides, nucleic acids and

XX ligands are used in claimed methods for detecting and modulating

XX Tie-2 activity. This allows the monitoring or modulation of

XX angiogenesis, induction or inhibition of vascular growth or

XX remodelling and blood vessel maturation, and inhibition of tumour

XX growth or metastasis.

XX Sequence 9 AA;

XX

XX Query Match 63.1%; Score 41; DB 21; Length 9;

XX Best Local Similarity 88.9%; Pred. No. 7.8e+05;

XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX

XX 3 HCSAGVGRT 11

XX 1 HSSAGVGRT 9

DB

XX RESULT 15

XX AAR85205 standard; peptide; 7 AA.

XX AAR85205;

XX 12-FEB-1996 (first entry)

XX

XX Protein tyrosine phosphatase conserved sequence.  
DE  
XX  
XX Densily enhanced Type III receptor-like protein tyrosine phosphatase;  
KW huDEP-1.  
KM  
XX  
XX Synthetic.  
OS  
XX  
XX WO9530008-A1.  
PN  
XX  
XX 09-NOV-1995.  
PD  
XX  
XX 03-MAY-1995; 95WO-US05512.  
PF  
XX  
XX 03-MAY-1994; 94US-0237940.  
PR  
XX  
XX (COLD-) COLD SPRING HARBOR LAB.  
PA  
XX  
XX Oestman A, Tonks NK;  
PI  
XX  
XX WPI; 1995-393079/50.  
DR  
XX  
XX  
XX New density enhanced protein tyrosine phosphatase - used to develop  
PT prods. to modify transcription, translation and/or activity of  
PT tyrosine phosphatase(s).  
PS  
XX  
XX Example 1; Page 15; 51pp; English.  
PS  
XX  
XX 2 Conserved amino acid sequences (AAR85204-05) common to many protein  
CC tyrosine phosphatases (PTs) were used to design degenerate primers  
CC (see AAT06028-29) used for the PCR amplification of cDNA from a HeLa  
CC library, allowing isolation of a clone encoding a novel density-  
CC enhanced Type III receptor-like PTP, huDEP-1 (see AAT06027).  
XX  
XX  
SQ Sequence 7 AA:  
  
Query Match 61.5%; Score 40; DB 16; Length 7;  
Best Local Similarity 85.7%; Pred. No. 7.8e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 HCSAGVG 9  
| | | | | | |  
Db 1 HCSAGIG 7

Search completed: January 17, 2003, 10:59:52  
Job time : 35 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2003, 11:00:48 ; Search time 11 Seconds  
(Without alignments)  
21.686 Million cell updates/sec

Title: US-09-743-492-4  
Perfect score: 65  
Sequence: 1 VVHCSAGVGRTG 12

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 120991 seqs, 19878514 residues  
Total number of hits satisfying chosen parameters: 25634

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCRT\_NEW\_PUB pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCRTUS\_PUBCOMB pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	61.5	7	10	US-09-848-294-13
2	40	61.5	11	10	US-09-876-527-13
3	38	58.5	10	10	US-09-964-277-16
4	36	55.4	7	9	US-10-087-993-2
5	36	55.4	7	9	US-10-087-993-5
6	36	55.4	10	9	US-09-955-732-16
7	36	55.4	11	10	US-09-788-626-1
8	36	55.4	11	10	US-09-918-3968-1
9	36	55.4	11	12	US-10-000-954-1
10	35	53.8	10	10	US-09-770-595A-4
11	35	53.8	12	10	US-09-770-595A-7
12	34	52.3	10	10	US-09-770-595A-5
13	32	49.2	7	9	US-10-020-215-7
14	32	49.2	7	10	US-09-822-295-6
15	31	47.7	5	9	US-10-020-215-9
16	31	47.7	5	10	US-09-822-295-14
17	28	43.1	5	9	US-10-020-215-10
18	27	41.5	7	10	US-09-870-379-9
19	26	40.0	12	9	US-09-981-876-265

20	25	38.5	6	10	US-09-905-831-2	Sequence 2, Appl
21	25	38.5	11	10	US-09-756-594-31	Sequence 31, Appl
22	24	36.9	8	10	US-09-817-198A-12	Sequence 12, Appl
23	24	36.9	10	9	US-09-996-288-115	Sequence 115, Appl
24	24	36.9	10	9	US-09-996-288-144	Sequence 144, Appl
25	24	36.9	10	9	US-09-996-288-197	Sequence 197, Appl
26	24	36.9	10	9	US-09-910-557-59	Sequence 59, Appl
27	23	35.4	6	10	US-09-817-198A-11	Sequence 11, Appl
28	23	35.4	6	10	US-09-817-198A-10	Sequence 10, Appl
29	23	35.4	8	9	US-10-118-984-12	Sequence 12, Appl
30	23	35.4	8	9	US-10-118-984-29	Sequence 29, Appl
31	23	35.4	8	10	US-09-728-721-12	Sequence 12, Appl
32	23	35.4	8	10	US-09-728-721-29	Sequence 29, Appl
33	23	35.4	8	10	US-09-817-198A-14	Sequence 14, Appl
34	23	35.4	8	12	US-10-105-931-12	Sequence 12, Appl
35	23	35.4	8	12	US-10-105-931-29	Sequence 29, Appl
36	23	35.4	10	10	US-09-765-086-42	Sequence 42, Appl
37	23	35.4	11	8	US-08-424-550B-521	Sequence 521, Appl
38	23	35.4	11	10	US-09-867-852-111	Sequence 111, Appl
39	23	35.4	11	10	US-09-867-852-113	Sequence 113, Appl
40	22	33.8	8	9	US-10-012-756-18	Sequence 18, Appl
41	22	33.8	10	9	US-09-904-117-4	Sequence 4, Appl
42	22	33.8	10	9	US-09-996-288-112	Sequence 112, Appl
43	22	33.8	10	9	US-09-996-288-142	Sequence 142, Appl
44	22	33.8	10	9	US-09-996-288-146	Sequence 146, Appl
45	22	33.8	10	9	US-09-996-288-195	Sequence 195, Appl

## ALIGNMENTS

RESULT 1  
US-09-848-294-13  
Sequence 13, Application US/09848294  
Patent No. US20020049179A1  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas K.  
TITLE OF INVENTION: Isolation of A cDNA Encoding A NO. US20020049179A1el  
TITLE OF INVENTION: Protein Tyrosine Phosphatase which localizes to Focal  
FILE REFERENCE: CSH90-04FZA  
CURRENT APPLICATION NUMBER: US/09/848,294  
CURRENT FILING DATE: 2001-05-03  
PRIOR APPLICATION NUMBER: 09/235,251  
PRIOR FILING DATE: 1999-01-22  
PRIOR APPLICATION NUMBER: 08/759,536  
PRIOR FILING DATE: 1996-12-04  
PRIOR APPLICATION NUMBER: 08/107,420  
PRIOR FILING DATE: 1993-08-16  
PRIOR APPLICATION NUMBER: 07/663,579  
PRIOR FILING DATE: 1991-03-01  
PRIOR APPLICATION NUMBER: 07/494,036  
PRIOR FILING DATE: 1990-03-14  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 13  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Conserved Protein Sequence  
US-09-848-294-13

Query Match 61.5%; Score 40; DB 10; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1e+05; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 HCSAGVG 9  
|||||:  
DB 1 HCSAGIG 7

RESULT 2

```
US-09-876-527-13
; Sequence 13, Application US/09876527
; Patent No. US20020102616A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
;           Jelinek, Laura J.
;           Sheppard, Paul O.
;           Hagopian, William A.
;           Lagasse, James M.
; TITLE OF INVENTION: ISLET CELL ANTIGEN 1851
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/876,527
; FILING DATE: 07-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/811,481
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lingenfelter, Susan
; REGISTRATION NUMBER: P-41,156
; REFERENCE/DOCKET NUMBER: 95-36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6675
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-876-527-13

Query Match      61.5%  Score 40; DB 10; Length 11;
Best Local Similarity 63.6%  Pred. No. 0.5;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 VHCXAGVGRG 12
   |||  |||  |||
Db 1 VHCXAGXXRG 11

RESULT 3
US-09-964-277-16
; Sequence 16, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Lucche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16 *
; LENGTH: 10
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-277-16

Query Match      58.5%  Score 38; DB 10; Length 10;
Best Local Similarity 60.0%  Pred. No. 0.96;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 VHCXAGVGR 11
   |||  |||  |||
Db 1 VHCXAGISRS 10

RESULT 4
US-10-087-993-2
; Sequence 2, Application US/10087993
; Patent No. US20020169303A1
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
;           Aoki, Naohito
;           Kim, Yeong Woong
;           Wang, Hong Yang
;           Chen, Zhengjun
;           Naylor, Oliver
;           Kharitonov, Alexei Igorevich
; TITLE OF INVENTION: NOVEL PRP20, PCP-2, Bp1, CLK,
;           AND SIRP POLYPEPTIDES AND RELATED
;           PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
;           Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/087,993
; FILING DATE: 05-Mar-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,150
; FILING DATE: June 17, 1997
; APPLICATION NUMBER: U.S. 60/019,629
; FILING DATE: June 17, 1996
; APPLICATION NUMBER: U.S. 60/023,485
; FILING DATE: August 9, 1996
; APPLICATION NUMBER: U.S. 60/030,860
; FILING DATE: No. US20020169303A1ember 13, 1996
; APPLICATION NUMBER: U.S. 60/034,286
; FILING DATE: December 19, 1996
; APPLICATION NUMBER: U.S. 60/030,964
; FILING DATE: NO. US20020169303A1ember 15, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 225/298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: "Xaa" in position 6 stands for  
either Ser, Ile or Val.  
SEQUENCE DESCRIPTION: SEQ ID NO: 2  
US-10-087-993-2

Query Match 55.4%; Score 36; DB 9; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HCSAGVG 9  
111111  
DB 1 HCSAGXG 7

RESULT 5  
US-10-087-993-5  
Sequence 5, Application US/10087993  
Patent No. US20020169303A1  
GENERAL INFORMATION:  
APPLICANT: Ullrich, Axel  
Aoki, Naohito  
Kim, Yeong Woong  
Wang, Hong Yang  
Chen, Zhengjun  
Naylor, Oliver  
Kharitonkov, Alexei Igorevich  
TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDP1, CLK,  
AND STRP POLYPEPTIDES AND RELATED  
PRODUCTS AND METHODS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/087,993  
FILING DATE: 05-Mar-2002  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/877,150  
FILING DATE: June 17, 1997  
APPLICATION NUMBER: U.S. 60/019,629  
FILING DATE: June 17, 1996  
APPLICATION NUMBER: U.S. 60/023,485  
FILING DATE: August 9, 1996  
APPLICATION NUMBER: U.S. 60/030,860  
FILING DATE: NO. US20020169303A1member 13, 1996  
APPLICATION NUMBER: U.S. 60/034,286  
FILING DATE: December 19, 1996  
APPLICATION NUMBER: U.S. 60/030,964  
FILING DATE: NO. US20020169303A1member 15, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 225/298  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 955-0440  
TELEFAX: (213) 955-0440  
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: "Xaa" in position 6 stands for  
either Ser, Ile or Val.  
SEQUENCE DESCRIPTION: SEQ ID NO: 5  
US-10-087-993-5

Query Match 55.4%; Score 36; DB 9; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HCSAGVG 9  
111111  
DB 1 HCSAGXG 7

RESULT 6  
US-09-955-732-16  
Sequence 16, Application US/09955732  
Publication No. US20020182203A1  
GENERAL INFORMATION:  
APPLICANT: Lucche, Ralf M.  
APPLICANT: Wei, Bo  
TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE  
FILE REFERENCE: 200125,433  
CURRENT APPLICATION NUMBER: US/09/955,732  
CURRENT FILING DATE: 2001-09-18  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 16  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-955-732-16

Query Match 55.4%; Score 36; DB 9; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2.1;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 VHCSAGVGR 11  
111111  
DB 1 VHCKMVSRS 10

RESULT 7  
US-09-788-626-1  
Sequence 1, Application US/09788626  
Patent No. US20020009762A1  
GENERAL INFORMATION:  
APPLICANT: Flint, Andrew J.  
APPLICANT: Cool, Deborah E.  
TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE  
PHOSPHATASE  
FILE REFERENCE: 200125,401  
CURRENT APPLICATION NUMBER: US/09/788,626  
CURRENT FILING DATE: 2001-02-13  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 1  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (1)...(1)  
OTHER INFORMATION: Xaa = Ile or Val  
NAME/KEY: VARIANT  
LOCATION: (4)...(4)

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OTHER INFORMATION: Xaa = any amino acid
NAME/KEY: VARIANT
LOCATION: (7)...(7)
OTHER INFORMATION: Xaa = any amino acid
NAME/KEY: VARIANT
LOCATION: (8)...(8)
OTHER INFORMATION: Xaa = any amino acid
NAME/KEY: VARIANT
LOCATION: (10)...(10)
OTHER INFORMATION: Xaa = Ser or Thr
OTHER INFORMATION: Unique signature sequence motif which is invariant
OTHER INFORMATION: among all PTPs.
US-09-788-626-1

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Query Match      55.4%; Score 36; DB 10; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 HCSAGVGRGTG 12
Db 2 HCSAGVGRGTG 11

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RESULT 8
US-09-918-396B-1
Sequence 1, Application US/09918396B
Patent No. US20020138862A1
GENERAL INFORMATION:
APPLICANT: Kennedy, Brian
APPLICANT: Payette, Paul
APPLICANT: Gresser, Michael
APPLICANT: Ramachandran, Chidambaram
APPLICANT: Tremblay, Michel
APPLICANT: Eichelely, Mounib
TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE-1B (PTP-1B)
TITLE OF INVENTION: DEFICIENT MICE AND ASSAYS FOR PTP-1B MODULATORS
FILE REFERENCE: 20162PDA
CURRENT APPLICATION NUMBER: US/09/918,396B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: 09/744,383
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/093,975
PRIOR FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: SITE
LOCATION: 1
OTHER INFORMATION: Xaa = Ile or Val
FEATURE:
NAME/KEY: SITE
LOCATION: 4
OTHER INFORMATION: Xaa = Any Amino Acid
FEATURE:
NAME/KEY: SITE
LOCATION: 7
OTHER INFORMATION: Xaa = Any Amino Acid
FEATURE:
NAME/KEY: SITE
LOCATION: 8
OTHER INFORMATION: Xaa = Any Amino Acid
NAME/KEY: SITE
LOCATION: 10
OTHER INFORMATION: Xaa = Ser or Thr
FEATURE:
OTHER INFORMATION: Protein tyrosine phosphatase catalytic domain
US-09-918-396B-1

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Query Match      55.4%; Score 36; DB 10; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 HCSAGVGRGTG 12
Db 2 HCSAGVGRGTG 11

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RESULT 9
US-10-000-954-1
Sequence 1, Application US/10000954
Patent No. US20020127226A1
GENERAL INFORMATION:
APPLICANT: Schlusser, Joseph
APPLICANT: Barnea, Gilad
APPLICANT: Grunet, Martin H.
APPLICANT: Margolis, Richard U.
TITLE OF INVENTION: A NEW CLASS OF PTPases: THEIR
STRUCTURAL DOMAINS AND LIGANDS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/000,954
FILING DATE: 04-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/644,293
FILING DATE: 23-Aug-2000
APPLICATION NUMBER: 08/081,929
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 7683-041-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= Xaa
/note= "Xaa = Ile or Val"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /label= Xaa
/note= "Xaa = Any amino acid"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7..8
OTHER INFORMATION: /label= Xaa
/note= "Xaa = Any amino acid"
FEATURE:

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NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: /label= Xaa  
/note= "Xaa = Ser or Thr"  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-000-954-1

Query Match 55.4%; Score 36; DB 12; Length 11;  
Best Local Similarity 60.0%; Pred. No. 2.3;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 HCSAGVGRGT 12  
||| |||  
Db 2 HCXAGXRXG 11

RESULT 10  
US-09-770-595A-4  
Sequence 4, Application US/09770595A  
Patent No. US20020048803A1  
GENERAL INFORMATION:  
APPLICANT: Revenkova, Ekaterina  
APPLICANT: Paszkowski, Jurek  
TITLE OF INVENTION: Map Kinase Phosphatase Mutant  
FILE REFERENCE: S-30589A  
CURRENT APPLICATION NUMBER: US/09/770,595A  
CURRENT FILING DATE: 2001-01-26  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
US-09-770-595A-4

Query Match 53.8%; Score 35; DB 10; Length 10;  
Best Local Similarity 60.0%; Pred. No. 3;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 VHCSAGVGRGT 11  
||| |||  
Db 1 VHCCGVGSRS 10

RESULT 11  
US-09-770-595A-7  
Sequence 7, Application US/09770595A  
Patent No. US20020048803A1  
GENERAL INFORMATION:  
APPLICANT: Revenkova, Ekaterina  
APPLICANT: Paszkowski, Jurek  
TITLE OF INVENTION: Map Kinase Phosphatase Mutant  
FILE REFERENCE: S-30589A  
CURRENT APPLICATION NUMBER: US/09/770,595A  
CURRENT FILING DATE: 2001-01-26  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
US-09-770-595A-7

Query Match 53.8%; Score 35; DB 10; Length 12;  
Best Local Similarity 60.0%; Pred. No. 3.6;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 VHCSAGVGRGT 11  
||| |||  
Db 2 VHCCGVGSRS 11

RESULT 12

US-09-770-595A-5  
Sequence 5, Application US/09770595A  
Patent No. US20020048803A1  
GENERAL INFORMATION:  
APPLICANT: Revenkova, Ekaterina  
APPLICANT: Paszkowski, Jurek  
TITLE OF INVENTION: Map Kinase Phosphatase Mutant  
FILE REFERENCE: S-30589A  
CURRENT APPLICATION NUMBER: US/09/770,595A  
CURRENT FILING DATE: 2001-01-26  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: <221> MISC\_FEATURE<222> (1)..(10)<223> Xaa = any amino acid  
OTHER INFORMATION: Description of Artificial Sequence: mammalian  
US-09-770-595A-5

Query Match 52.3%; Score 34; DB 10; Length 10;  
Best Local Similarity 50.0%; Pred. No. 4.5;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 VHCSAGVGRGT 11  
||| |||  
Db 1 HCHXAGXRS 10

RESULT 13  
US-10-020-215-7  
Sequence 7, Application US/10020215  
Publication No. US20030008347A1  
GENERAL INFORMATION:  
APPLICANT: PLOWMAN, GREGORY  
APPLICANT: PILES, EIOR  
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF ALP RELATED DISORDERS  
FILE REFERENCE: 038602/1290  
CURRENT APPLICATION NUMBER: US/10/020,215  
CURRENT FILING DATE: 2001-12-18  
PRIOR APPLICATION NUMBER: 09/095,443  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/049,477  
PRIOR FILING DATE: 1997-06-11  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (3)  
OTHER INFORMATION: Unspecified amino acid  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (6)  
OTHER INFORMATION: Unspecified amino acid  
US-10-020-215-7

Query Match 49.2%; Score 32; DB 9; Length 7;  
Best Local Similarity 71.4%; Pred. No. 1e+05; 2; Indels 0; Gaps 0;

QY 3 HCSAGVG 9  
||| |||  
Db 1 HCHXAGXG 7

RESULT 14  
US-09-822-295-6  
; Sequence 6, Application US/09822295  
; Patent No. US20020119501A1  
; GENERAL INFORMATION:  
; APPLICANT: Bahija Jallal  
; Gregory D. Plowman  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF  
; PTP04 RELATED DISORDERS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FASTSEQ for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/822,295  
; FILING DATE: 02-Apr-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/081,345  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wardburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 234/253  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: "Xaa" in positions 3 and 6 stand  
; for an unspecified amino acid.  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-822-295-6  
Query Match 49.2%; Score 32; DB 10; Length 7;  
Best Local Similarity 71.4%; Pred. No. 1e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 HCSAGVG 9  
| | | | |  
Db 1 HCSAGVG 7  
RESULT 15  
US-10-020-215-9  
; Sequence 9, Application US/10020215  
; Publication No. US20030008347A1  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, GREGORY  
; APPLICANT: PELES, EIOR  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF ALP RELATED DISORDERS  
; FILE REFERENCE: 038602/1290  
; CURRENT APPLICATION NUMBER: US/10/020,215  
; FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: 09/095,443

; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/049,477  
; PRIOR FILING DATE: 1997-06-11  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Illustrative  
US-10-020-215-9  
Query Match 47.7%; Score 31; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 HCSAG 7  
| | | | |  
Db 1 HCSAG 5

Search completed: January 17, 2003, 11:04:24  
Job time : 11 secs

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## OM protein - protein search, using sw model

Run on: January 17, 2003, 10:59:18 : Search time 14 seconds  
(without alignments)  
25.220 Million cell updates/sec

Title: US-09-743-492-4  
Perfect score: 65  
Sequence: 1 VVHCSAGVGRG 12

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 91334

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
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6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	93.8	11	2	US-08-342-930-4
2	50	76.9	11	4	US-08-791-115B-17
3	46	70.8	8	2	US-08-342-930-12
4	45	69.2	8	1	US-08-348-006B-4
5	45	69.2	8	2	US-08-800-825A-4
6	45	69.2	8	4	US-09-158-657-4
7	43	66.2	10	1	US-08-036-210-2
8	43	66.2	10	1	US-08-036-210-32
9	43	66.2	10	2	US-08-449-609-2
10	43	66.2	10	2	US-08-449-609-32
11	40	61.5	7	3	US-08-854-585-4
12	40	61.5	7	5	PCT-US95-05512-4
13	40	61.5	7	4	US-08-791-115B-18
14	40	61.5	11	4	US-08-811-481-13
15	39	60.0	9	2	US-08-990-379-18
16	37	56.9	8	1	US-08-036-210-45
17	37	56.9	8	1	US-08-449-609-45
18	36	55.4	7	2	US-08-036-210-41
19	36	55.4	7	2	US-08-446-345-13
20	36	55.4	7	2	US-08-449-609-41
21	36	55.4	7	3	US-08-951-260A-3
22	36	55.4	7	3	US-09-100-804-9
23	36	55.4	11	1	US-08-201-697-9
24	36	55.4	11	2	US-08-342-930-3
25	36	55.4	11	2	US-08-447-464-1
26	36	55.4	11	2	US-08-716-679-1
27	36	55.4	11	2	US-08-685-992-36

28	36	55.4	11	2	US-09-144-925-36	Sequence 36, Appl
29	36	55.4	11	3	US-08-246-441-9	Sequence 9, Appl
30	36	55.4	11	4	US-08-081-929-1	Sequence 11, Appl
31	35	53.8	6	2	US-08-447-464-11	Sequence 1, Appl
32	35	53.8	6	2	US-08-716-679-11	Sequence 11, Appl
33	35	53.8	6	2	US-08-884-569A-15	Sequence 15, Appl
34	34	52.3	7	2	US-08-530-290-4	Sequence 4, Appl
35	32	49.2	7	4	US-09-081-345-6	Sequence 6, Appl
36	32	49.2	7	4	US-09-095-443-7	Sequence 7, Appl
37	31	47.7	5	4	US-09-081-345-14	Sequence 14, Appl
38	31	47.7	8	2	US-08-884-569A-13	Sequence 13, Appl
39	30	46.2	10	4	US-08-990-379-17	Sequence 17, Appl
40	30	46.2	10	4	US-09-164-193-11	Sequence 11, Appl
41	30	46.2	10	4	US-09-221-448A-11	Sequence 11, Appl
42	29	44.6	7	5	PCT-US94-10166-4	Sequence 4, Appl
43	28	43.1	11	1	US-07-732-114A-6	Sequence 6, Appl
44	28	43.1	11	1	US-08-170-114A-6	Sequence 6, Appl
45	26	40.0	6	4	US-09-020-880-50	Sequence 50, Appl

## ALIGNMENTS

RESULT 1  
US-08-342-930-4  
Sequence 4, Application US/08342930  
Patent No. 5821084  
GENERAL INFORMATION:  
APPLICANT: OLMSTED, ELIZABETH A.  
APPLICANT: MAURO, LAURA J.  
APPLICANT: DAVIS, ALAN R.  
APPLICANT: DIXON, JACK E.  
TITLE OF INVENTION: OSTEOBLAST-TESTICULAR PROTEIN TYROSINE  
TITLE OF INVENTION: 13  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & ROEBSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/342,930  
FILING DATE: 21-NOV-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KONSKI, ANTOINETTE F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 20344-20975.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-342-930-4  
Query Match 93.8%; Score 61; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00036;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VVHCSAGVGRG 12  
|||||



SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-348-006B-4

Query Match 69.2%; Score 45; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VHCSAGVG 9  
|||||  
Db 1 VHCSAGVG 8

RESULT 5  
US-08-800-825A-4  
Sequence 4, Application US/08800825A  
Patent No. 5866397  
GENERAL INFORMATION:  
APPLICANT: RODAN, GIDEON A.  
APPLICANT: SCHMIDT, AZRIEL  
APPLICANT: RUTLEDGE, SU JANE  
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASE  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: J. MARK HAND - MERCK & CO., INC.  
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000  
CITY: RAHWAY  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,825A  
FILING DATE: 14-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HAND, J. MARK  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 18992DA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-3905  
TELEFAX: 732-594-4720  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-800-825A-4

Query Match 69.2%; Score 45; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VHCSAGVG 9  
|||||  
Db 1 VHCSAGVG 8

RESULT 6  
US-09-158-657-4  
Sequence 4, Application US/09158657  
Patent No. 6214564

GENERAL INFORMATION:  
APPLICANT: RODAN, GIDEON A.  
APPLICANT: SCHMIDT, AZRIEL  
APPLICANT: RUTLEDGE, SU JANE  
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN  
TITLE OF INVENTION: TYROSINE PHOSPHATASE  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: J. MARK HAND - MERCK & CO., INC.  
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000  
CITY: RAHWAY  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/158,657  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/800,825  
FILING DATE: 14-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: HAND, J. MARK  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 18992DA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-3905  
TELEFAX: 732-594-4720  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-158-657-4

Query Match 69.2%; Score 45; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VHCSAGVG 9  
|||||  
Db 1 VHCSAGVG 8

RESULT 7  
US-08-036-210-2  
Sequence 2, Application US/08036210  
Patent No. 5585233  
GENERAL INFORMATION:  
APPLICANT: Moller, Niels P.H.  
APPLICANT: Moller, Karin B.  
APPLICANT: Ullrich, Axel  
TITLE OF INVENTION: PTP-631: A NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

```
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036,210
FILING DATE: 23-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-036-210-2

Query Match          66.2%  Score 43; DB 1; Length 10;
Best Local Similarity 70.0%  Pred. No. 0.29;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 HCSAGVGRGTG 12
      ||| | ||| |
Db      1 HCSXGXGRXG 10

RESULT 8
US-08-036-210-32
Sequence 32, Application US/08036210
Patent No. 5585233
GENERAL INFORMATION:
APPLICANT: Moller, Niels P.H.
APPLICANT: Ullrich, Karin B.
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036,210
FILING DATE: 23-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
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US-08-036-210-32

Query Match          66.2%  Score 43; DB 1; Length 10;
Best Local Similarity 70.0%  Pred. No. 0.29;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 HCSAGVGRGTG 12
      ||| | ||| |
Db      1 HCSXGXGRXG 10

RESULT 9
US-08-449-609-2
Sequence 2, Application US/08449609
Patent No. 5952212
GENERAL INFORMATION:
APPLICANT: Moller, Niels P.H.
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,609
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/036,210
FILING DATE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-449-609-2

Query Match          66.2%  Score 43; DB 2; Length 10;
Best Local Similarity 70.0%  Pred. No. 0.29;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 HCSAGVGRGTG 12
      ||| | ||| |
Db      1 HCSXGXGRXG 10

RESULT 10
US-08-449-609-32
Sequence 32, Application US/08449609
Patent No. 5952212
GENERAL INFORMATION:
APPLICANT: Moller, Niels P.H.
```

APPLICANT: Moller, Karin B.  
APPLICANT: Ullrich, Axel  
TITLE OF INVENTION: PEP-531: A NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,609  
FILING DATE: 24-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/036,210  
FILING DATE: 23-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: MISTOCK, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7683-025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-449-609-32

Query Match 66.2%; Score 43; DB 2; Length 10;  
Best Local Similarity 70.0%; Pred. No. 0.29;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 HCSAGVGTG 12  
||| ||| |  
Db 1 HCSXGGRXG 10

RESULT 11  
US-08-854-585-4  
Sequence 4, Application US/08854585  
Patent No. 6114140  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas K. and Stman, Arne  
TITLE OF INVENTION: Densily Enhanced Protein Tyrosine Phosphatase  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, Suite 6300  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/854,585  
FILING DATE:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/237,940  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 27866/31954  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-854-585-4

Query Match 61.5%; Score 40; DB 3; Length 7;  
Best Local Similarity 85.7%; Pred. No. 2e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HCSAGVG 9  
||| ||| |  
Db 1 HCSAGIG 7

RESULT 12  
PCT-US95-05512-4  
Sequence 4, Application PC/TUS9505512  
GENERAL INFORMATION:  
APPLICANT: Tonks, Nicholas K. and Stman, Arne  
TITLE OF INVENTION: Densily Enhanced Protein Tyrosine  
TITLE OF INVENTION: Phosphatase  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Borun  
STREET: 233 South Wacker Drive, Suite 6300  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05512  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 27866/31954  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US95-05512-4

Query Match 61.5%; Score 40; DB 5; Length 7;  
Best Local Similarity 85.7%; Pred. No. 2e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HCSAGVG 9

Db 1 HCSAGIG 7

|||||:1

RESULT 13

US-08-791-115B-18

; Sequence 18, Application US/08791115B

; Patent No. 6262242

; GENERAL INFORMATION:

; APPLICANT: Steck, Peter

; APPLICANT: Pershouse, Mark A.

; APPLICANT: Jasser, Samar

; APPLICANT: Yung, W.K. Alfred

; APPLICANT: Tavligian, Sean V.

; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10023.3

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rothwell, Flgg, Ernst & Kurz, P.C.

; STREET: 555 Thirteenth Street, N.W., Suite 701-E

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 22204

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentln Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/791,115B

; FILING DATE: 30-JAN-1997

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Ihnen, Jeffrey L.

; REGISTRATION NUMBER: 38,957

; REFERENCE/DOCKET NUMBER: 2318-134.A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-683-6040

; TELEFAX: 202-683-7031

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 1

; OTHER INFORMATION: /note="may be either I =

; OTHER INFORMATION: Isoleucine or V = Valine"

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 4..8

; OTHER INFORMATION: /note="X = Any amino acid"

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 10

; OTHER INFORMATION: /note="may be either S = Serine or

; OTHER INFORMATION: T = Threonine"

US-08-791-115B-18

Query Match 61.5%; Score 40; DB 4; Length 11;

Best Local Similarity 54.5%; Pred. No. 0.98;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 VHCSAGVGRFG 12

Db 1 IPCXAGXXRSG 11

RESULT 14

US-08-811-481-13

; Sequence 13, Application US/08811481

; Patent No. 6300093

; GENERAL INFORMATION:

; APPLICANT: Kindsvogel, Wayne

; APPLICANT: Jelinek, Laura J.

; APPLICANT: Sheppard, Paul O.

; APPLICANT: Hagopian, William A.

; APPLICANT: Lagasse, James M.

; TITLE OF INVENTION: ISLET CELL ANTIGEN 1851

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Zymogenetics, Inc.

; STREET: 1201 Eastlake Avenue East

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/811,481

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Lingenfelter, Susan

; REGISTRATION NUMBER: P-41,156

; REFERENCE/DOCKET NUMBER: 95-36

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-442-6675

; TELEFAX: 206-442-6678

; TEXES:

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

US-08-811-481-13

Query Match 61.5%; Score 40; DB 4; Length 11;

Best Local Similarity 63.6%; Pred. No. 0.98;

Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 VHCSAGVGRFG 12

Db 1 VHCSAGXXRSG 11

RESULT 15

US-08-990-379-18

; Sequence 18, Application US/08990379

; Patent No. 5998188

; GENERAL INFORMATION:

; APPLICANT: Stork, Philip J

; APPLICANT: Misra-Press, Anita

; TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase cDNAs and

; TITLE OF INVENTION: Their Biologically Active Expression Products

; FILE REFERENCE: 4104-000322USA

; CURRENT APPLICATION NUMBER: US/08/990,379

; CURRENT FILING DATE: 1997-12-15

; EARLIER APPLICATION NUMBER: PCT/US96/10402

; EARLIER FILING DATE: 1996-06-14

; EARLIER APPLICATION NUMBER: 60/000,263

; EARLIER FILING DATE: 1995-06-16

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: Patentln Ver. 2.0



; SEQ ID NO: 18  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 US-08-990-379-18

Query Match 60.0%; Score 39; DB 2; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 2e+05;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 VHCSAGVGR 10  
 ||| ||:  
 Db 1 VHCQAGISR 9

Search completed: January 17, 2003, 11:01:27  
 Job time : 15 secs

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